# Evaluation of Partially Converted Lines from the Sorghum Conversion Program to Determine Combining Ability and Heterosis for Early Testing

by

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## Abstract

Hybrid breeding technology has been very successful in increasing yield of many cereal crops including sorghum (*Sorghum bicolor* (L.) Moench). The process of developing and evaluating the performance of hybrids is the most expensive and time-consuming activity. In sorghum, developing parental inbred lines and evaluating their potential hybrid performance is very expensive and time-consuming. Predicting hybrid performance in any way possible might help reduce the number of crosses needed and evaluated. The study was comprised of 40 lines, selected by the percentage of exotic genome recovered and the generation ($BCF_{2:3}$ high, $BCF_{2:3}$ low, $F_{2:3}$ high, and $F_{2:3}$ low), and four elite testers. The 160 $F_1$ hybrids and parents were evaluated in a randomized complete block design with two replications for combining ability and heterosis during the 2015-2016 cropping season. The results indicated that sufficient genetic variability was observed for all characters evaluated. Analysis of general combining ability (GCA) revealed that among the parents, lines RSC117-4 $BCF_{2:3}$ high, RSC83-1 $BCF_{2:3}$ low, RSC83-14 $BCF_{2:3}$ high, and RSC112-19 $BCF_{2:3}$ high, and the testers A.301 and A.319 were promising general combiners for increasing grain yield and most other important traits. Therefore, the parents can be used in sorghum breeding programs aimed toward developing high-yielding hybrids. A.301*RSC83-14 $BCF_{2:3}$ high produced the third largest overall mean grain yield for hybrids, yielding slightly more than commercial check 301/41, with 67.3 days to anthesis and 127.5 cm total plant height. The hybrid had

significant midparent heterosis (MPH) with a positive specific combining ability (SCA) effect and GCA combining effect combination of high x high which provides complementary gene action.  The hybrid had good combination for earliness, dwarfing genes, and large yield.  A.319*RSC83-1 $F_{2:3}$ high had the largest overall mean for grain yield, out yielding four of the best six commercial check hybrids, with 72.2 days to anthesis and 153.0 cm total plant height, with a positive MPH and SCA effect with high x low GCA effects combination indicating additive x dominance type of gene interaction.  The cross could produce desirable transgressive segregates because of the additive genetic system in one general combiner of the parent and complementary epistatic effects in the other.  The hybrid was taller and yielded more, with heavier panicle weights and 1000-kernel weight, and significantly greater MPH *per se* parents.  Line x tester analysis revealed that the contribution of the lines to the total sum of squares was greater than testers in all studied traits except the number of days to anthesis.  The variance due to GCA ($\sigma^2_{gca}$) was less than for SCA ($\sigma^2_{sca}$) for all traits except plant exsertion and concentration of protein, starch, fiber, and fat in grain, suggesting preponderance of non-additive gene action controlling the characters.  Dominance variance ($\sigma^2_D$) was greater than additive variance ($\sigma^2_A$) for all traits except plant exsertion and concentration of protein, starch, fiber, and fat in the grain.  The results are supported by the ratio of variance of general to specific combining ability ($\sigma^2_{gca}/ \sigma^2_{sca}$) which was smaller than unity and by the degree of dominance ($\sigma^2_D/\sigma^2_A$) that uses values greater than unity for all traits except plant exsertion where $\sigma^2_A$ was larger than $\sigma^2_D,$ with the degree of dominance being less than unity.  Selections based on the predominance of dominance variance suggested the exploitation of heterosis.

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# Chapter I

## Introduction

Plant breeding is driven by the need to continually increase yield while improving the ability of crop plants to be sustainable across variable environments.  Increasing yield of cereal grains is an important aspect of "2050 - feeding the nine billion people" because it will require increasing food production by 70% during the next 33 years (FAO, 2011).

As the amount of water in the Ogallala Aquifer continues to decrease, there is an increased need to improve agricultural production under limited water or dryland conditions with minimal inputs.  Sorghum [*Sorghum bicolor* (L.) Moench] because of its drought tolerance is important in semi-arid regions.  Sorghum has been cultivated in arid and semi-arid regions of Africa for thousands of years.  Sorghum is the fifth-most important cereal crop in the world and the third-most important in the United States, after maize, *Zea mays* L., and wheat, *Triticum aestivum* L. (FAS/USDA, 2012).  Increasing global food demand and decreasing water, coupled with potential effects of climate change, push plant breeders to epic heights.

Worldwide, 66.2 million Mg of sorghum were produced during the 2010-2011 trade year (September through August), with the United States being the second largest producer in the world, behind Nigeria.  Worldwide sorghum production increased to 67.8 million Mg during the 2014-2015 trade year (September through August), with the United States leading world production, followed by Mexico and then Nigeria

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(FAS/USDA, 2015). In 2010, more than 7.5 million Mg of sorghum worth $1.7 billion were harvested in the United States (USDA, 2011). The United States, with 2.4 million Mg in trade year 2010-2011, is the largest exporter of grain sorghum in the world, while Mexico and Japan were the leading importers of sorghum (FAS/USDA, 2011). Chief importers during the 2014-2015 U.S. crop year (September through August) were China (97%) and Japan (2%) (U.S. Grains, 2016).

Sorghum has a high yield potential, and the greatest recorded yield of 20.1 tons per hectare for the crop was in Texas in the 1980s (Boyer, 1987). However, yields in Africa and India remain low. Access to modern machinery, improved technology, and irrigation, along with sorghum breeding efforts through hybrid production in developed countries might, in part, explain the vast difference in yield in developed countries compared to that in developing countries.

By 1905, the Texas Agricultural Experiment Station and USDA began research at Chillicothe, Texas that focused mainly on creating plants that were short statured for mechanical harvesting, early maturing, and higher yielding than varieties introduced from the tropics (Rooney and Smith, 2000). Dwarf sorghum cultivars were created by making three of the four independent height-gene alleles (Dw1 through Dw4) recessive (three-gene dwarfs). Maturity in grain sorghum was shortened by using six gene loci (Ma1 through Ma6) that can be manipulated to adapt the plants to shorter growing seasons (Quinby and Karper, 1954; Poehlman, 1987; Rooney and Aydin, 1999). Grain yield potential in the United States has increased markedly since the introduction of sorghum

in the 1800s, and the increase is attributed to development of hybrids and short-statured plants that yield well in different environments.

Commercial production of sorghum seed relies on development of hybrids. In sorghum, a mostly self-pollinated crop, development of hybrids depends on cytoplasmic-genetic male sterility, in which self-pollination is averted by using male-sterile lines as females, thus avoiding laborious emasculation by hand, yet enabling crossing between lines as if the crop had been cross-pollinated (Quinby and Martin, 1954; Stephens and Holland, 1954). Production of hybrid sorghum seed has evolved into a system where introduced germplasm can be used either as a male parent or a female parent. This classification depends on the presence or absence of fertility-restoring genes. If the line possesses fertility-restoring genes, it is designated an R line (restorer line) that can be used as a male; otherwise, it is designated a B line and can be sterilized by backcrossing with a male sterile designated as an A line. The system of hybrid development has caused sorghum breeding programs to develop two breeding groups: a male-parent group (R line/fertility-restorer) and a female-parent group (an A/B line, lacking the fertility-restoring gene of the A1 male-sterility system). New germplasm is usually placed in one of the two groups based on whether or not it possesses fertility-restoring genes. Stephens and Holland (1954) discovered the cytoplasmic male sterility (CMS) system that is dependent on the presence of male-sterile cytoplasm and nuclear fertility-restoring genes.

Heterosis or hybrid vigor is defined as the difference between a hybrid and the mean of the two parents (Falconer and Mackay, 1996). Exploitation of heterosis began in the United States in the 1950s, resulting in a dramatic increase in yields for maize. The

more genetically divergent a hybrid is, based on genetic relatedness of the parental lines, the greater the degree of heterosis.  Much sorghum research and advancement to date have been based on phenotypic classification.  Grain yield is a complex trait controlled by polygenes and has low heritability especially in stressful environments.  For example, selection for grain yield under severe drought stress has often been considered inefficient because the estimate of heritability of grain yield has been observed to decrease with reduced yield (Bolaños and Edmeades, 1993).

Such traits as grain yield and its components are governed by polygenes with complex gene action.  Hence, a comprehensive understanding of the nature and magnitude of gene action and knowledge of the combining ability of parents to develop new hybrids through suitable breeding methods were essential for implementing a systematic crop improvement program.  Combining ability analysis is a powerful tool to estimate combining ability effects and aids in selecting desirable parents and crosses for exploitation of heterosis and involving them in production of desirable hybrids and segregates (Sarker et al., 2002; Rashid et al., 2007).  Combining ability is useful for plant breeders to better understand genetic variance and inbred lines to identify desirable parents to use in commercial hybrid production.  Plant breeders use results of research on combining ability to help select the best parents for development of hybrids or varieties.  The concept of general and specific combining ability was introduced by Spraque and Tatum (1942) who designated general combining ability (GCA) as the average performance of a line in hybrid combination.  The term specific combining ability (SCA) was applied to cases where certain hybrid combinations did relatively better or worse

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than would be expected on the basis of the average performance of the lines involved. Commercial production of hybrids, however, depends upon two factors: the behavior of a line itself and the behavior of a line in hybrid combination assessed through the estimation of GCA and SCA effects. The importance of both GCA and SCA has been reported by Kambal and Webster (1965). GCA is the result of additive gene effect, while SCA is considered to be composed of non-allelic interaction.

The line x tester (L x T) mating design for combining ability suggested by Kempthorne (1957) is an appropriate method to identify superior parents and hybrids based on GCA and SCA, respectively. It is also helpful for assessing the nature and magnitude of gene action controlling quantitative traits. Information on combining ability and heterosis is a valuable tool in determining superior parents and hybrid combinations in a hybrid breeding program.

Correlation studies provide information on the association of yield with its component characters and help to formulate a selection index. Because yield is a complex quantitative character, it tends to be dependent on various component characters, and path analysis reveals the direct and indirect effects of component traits on grain yield.

The purpose of the present investigation was to obtain information on combining ability of sorghum lines for traits of economic value. The overall goal of this research was to determine if there was additional benefit for sorghum breeders to increase efficiency by decreasing the workload of the breeding process, thus allowing quicker

release of newly cultivated sorghum hybrids.  The primary objective of many plant breeding programs is to increase yield and its components to improve the quality (grain yield and its components including plant height) of crop plants.  The objective of this study was to use the recovered genetic proportion of exotic sorghum genotypes from different taxonomic groups through the evaluation of $F_1$ hybrids produced from exotic germplasm in the generation of $F_{2:3}$ or $BC_1F_{2:3}$ to determine if there was additional benefit from backcrossing to an exotic parent in the USDA ARS Sorghum Conversion Program.  Considering this, the investigation entitled "Evaluation of Partially Converted Lines from the Sorghum Conversion Program to Determine Combining Ability and Heterosis for Early Testing" was undertaken with the following objectives to determine:

1.  if a difference exists between high and low percentage of recovery for the genetic proportion recovered,

2.  if a difference exists between the $F_{2:3}$ and $BC_1F_{2:3}$ for high and low percentage of recovery for the genetic proportion recovered,

3.  effects of high and low percentage of recovery for genetic similarity to the recurrent parent across different levels of genetics and maturities, across different environments, and across the taxonomic groups used in this study,

4.  effects of combining ability across different females, with different genetics and maturity, within the Reinstated Sorghum Conversion (RSC) families and generation selections,

5.  effects of midparent heterosis (MPH) across different females, with different genetics and maturities, within a RSC population,

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6.  correlations among grain yield and yield components and to understand their direct and indirect effects on grain yield, and

7.  determine the benefits of early testing in the $F_2$ population

This should provide insight into combining ability of selected males across different levels of maturity for elite females in a current breeding program. The information will be useful to sorghum breeders who can more efficiently and systematically exploit heterosis through selection of high combining ability based on the parents used. Understanding combining ability is crucial for sorghum breeders to make much-needed advances in development of new hybrids. At present, yield potential of sorghum has reached a plateau, where increases in yield are minimal.

# Chapter II

# Review of Literature

**Texas Panhandle and the Ogallala Aquifer**

As the amount of water in the Ogallala Aquifer on the Great Plains of the United States continues to decrease, improved crop production under limited water or dryland conditions with minimal input is required. Producers will be making difficult decisions to grow crops that more efficiently use water with the decreasing amount of water in the Aquifer. Understanding the impact of the decreased availability of water in the Ogallala Aquifer increases the need to identify higher yielding food and feed crops that can be produced with limited irrigation or dryland conditions on the Texas High Plains.

The Ogallala Aquifer, one of the largest fresh-water aquifers in the world, underlies parts of the states of South Dakota, Nebraska, Wyoming, Colorado, Kansas, Oklahoma, New Mexico, and Texas (Colazzi et al., 2008). The Ogallala Aquifer is the main supplier of irrigation for agricultural production on the Texas High Plains, with 95% of the water pumped from the Aquifer used for irrigation (Conkwright, 2012; Dudensing et al., 2008). Colaizzi et al. (2008) stated that almost all irrigation water used on the Texas High Plains is from the Ogallala Aquifer. Infiltration and evaporation are key components to recharge the Aquifer, but currently, water is being removed faster than the natural recharge rate, which varies by region. Discharge from the Ogallala Aquifer occurs through natural outlets such as seeps, springs, and leakage to underlying

geological formations (Nativ and Smith, 1987). Thus far, withdrawal through irrigation is currently the most significant discharge component. Pumping from the Ogallala Aquifer started in 1911 and increased drastically after World War II (Nativ and Smith, 1987). Intensive irrigation on the Texas High Plains began in the 1930s and was facilitated mostly by the development of the internal combustion engine, turbine pumps, and rotary well drilling (Musick et al., 1988; Musick and Walker, 1987). The amount of water currently being withdrawn from the Aquifer is much greater than the annual recharge by precipitation. Annual recharge ranges from 0.15 to 2.1 cm $yr^{-1}$ (0.058 to 0.833 in $yr^{-1}$) (Knowles et al., 1984), while Nativ and Smith (1987) reviewed articles for the Ogallala Aquifer south of the Canadian River on the Southern High Plains of Texas and New Mexico and found that annual removal by pumping ranged from 16.6 to 113 cm $year^{-1}$ (0.5 to 6.55 in $yr^{-1}$). The Texas Panhandle is one of the areas where the amount of annual withdrawal exceeds the recharge rate. The sustainability of current agroecosystems depends on irrigation water on the Texas High Plains. Irrigation increases yield potential two to seven times and reduces yield risk by 75 to 90% over non-irrigated agricultural production (Lust et al., 2009). The increasing interest in agricultural production with limited irrigation (Norwood, 2000), coupled with producers seeking alternative crops that could reduce water consumption and lengthen the utility of the Aquifer (Howell et al., 2004), have become two of the agricultural priorities on the Southern High Plains.

Carpenter et al. (2011) reported that agricultural activities account for 76% of the global fresh water used by humans. Because water is becoming a scarce commodity

through erratic rainfall patterns, the water in aquifers is being depleted, and agricultural commodities are being produced in marginal areas to satiate the demand of the escalating number of humans in the world (Hanjra and Qureshi, 2010). To maintain or increase agricultural output, a more efficient water management system is needed to maximize crop water-use efficiency -- the concept of evaluating agricultural output based on the amount of water consumed rather than land area occupied (Bennett, 2003).

**Sorghum History and Characteristics**

Sorghum is a self-pollinating monocot in the grass family Poaceae. It is thought to have originated in the Ethiopia-Sudan region of northeastern Africa (Doggett, 1998; FAO, 1995), then spread throughout Africa, Southeast Asia, India, Australia, and the United States (FAO, 2007). Broomcorn might have been introduced into the United States by Benjamin Franklin, as early as 1757 (Kimber, 2000; Smith and Frederiksen, 2000). Grain sorghum was first carried from West Africa to the United States with the slave trade, when guinea corn and probably chicken corn were introduced (Doggett, 1970; Smith and Frederiksen, 2000). Introductions from North Africa included brown and white durras in 1874, milo about 1880, feterita in 1906, and hegari in 1908 (Doggett, 1970; Dillons et al., 2007).

Originally intended to feed slaves, sorghum continues to be the staple food of many of the poorest people in developing countries of the world (Rooney and Smith, 2000). Sorghum also has evolved as a primary feed source for livestock and is used in ethanol production in developed countries. This versatile crop is grown primarily in the semiarid regions of Africa, India, China, South America, and the United States. Grain

yields are significantly less in Africa and India, averaging 300-2,000 kg ha$^{-1}$ under rain-fed conditions, compared to 4,500-6,500 kg ha$^{-1}$ of hybrids grown under irrigated conditions in the United States (FAO, 2007).

Worldwide, sorghum ranks fifth behind maize, rice (*Oryza sativa* L.), wheat, and barley (*Hordeum vulgare* L.) with approximately 825, 680, 650, 150, and 60 million Mg of grain produced on 160, 162, 226, 54, and 40 million hectares, respectively (FAO, 2011; Grains, 2011; USDA-ERS, 2011). Sorghum is the third most-important cereal crop in the United States and the fifth most-important cereal crop in the world (Grains, 2007-2008). Assefa et al. (2010) and Assefa and Staggenborg (2010) reported that more than 80% of sorghum in the world is cultivated as a dryland crop because of its drought tolerance.

Sorghum is a frost-sensitive, short-day plant that grows on a wide range of soils at altitudes from sea level to 3,000 m (Kimber, 2000; FAO, 2007). As a C$_4$ species, sorghum has greater transpiration efficiency and hence survives and grows better than most other cereal crops under water-stress conditions (Doggett, 1988; Rooney, 2004). Sorghum is well known for its ability to tolerate limited water and produce during periods of extended drought that deter production of most other grain crops. Several factors that can limit sorghum yields include: prolonged drought or delayed rainfall; erratic rainfall; harsh rainfall and hail; early frost, snow, and extreme cold conditions; hot, dry summers; high-wind conditions; nutrient deficiencies; weed and insect pests; and attack by birds (Assefa and Staggenborg, 2010).

Currently, sorghum hybrids are classified by maturity into three groups – early, medium, or late-maturing (Smith, 1995). The growing season ranges from as few as 60 days for early-maturing hybrids, to as many as 150 days for late/full-season hybrids. Sorghum is produced commercially as an annual cereal grain adapted to hot, semiarid tropical and dry temperate areas of the world (NRC, 1996). Based on temperature, three kinds of sorghum -- tropical lowland, temperate, and cool-tolerant tropical high altitude -- are grown in the world (Doggett, 1988). Temperate sorghums are grown throughout the midwestern United States.

Since the 1920s, researchers and plant breeders in the United States have worked to improve sorghum by developing hybrids. In the 1950s, sorghum hybrids were produced to be shorter, higher yielding, and temperately adapted. The development and use of sorghum hybrids more than tripled in the United States from 1950-1954 to 1975-1979 (Jackson et al., 1980). Sorghum can tolerate some salinity and poorly drained soils with pH from 5.5 to 8.5.

Various pests attack sorghum. Major insect pests of sorghum in the United States include: Banks grass mite, *Oligonychus pratensis* (Banks); chinch bug, *Blissus leucopterus leucopterus* (Say); corn earworm, *Helicoverpa zea* (Boddie); fall armyworm, *Spodoptera frugiperda* (J.E. Smith); greenbug, *Schizaphis graminum* (Rondani); sugarcane aphid, *Melanaphis sacchari* (Zehntner), sorghum midge, *Stenodiplosis sorghicola* (Coquillett); sorghum webworm, *Nola sorghiella* Riley; stink bugs, family Pentatomidae; white grubs, *Phyllophaga crinita* (Burmeister); and wireworms, families Elateridae and Tenebrionidae (Teetes et al., 1983; Teetes and Pendleton, 2000). Of the

major sorghum insect pests, greenbug and sorghum midge are considered the key pests of sorghum.  In 2013, the sugarcane aphid invaded sorghum in 38 counties and four states of the United States (Bowling et al., 2016).  The sugarcane aphid reproduces rapidly and damages sorghum by removing sap and covering plants with honeydew, causing general plant decline and yield loss ranging from 10 to 50%.

**Sorghum Water Requirements**

Challenges with the declining recharge of the Ogallala Aquifer in the Southern High Plains, coupled with rising energy costs to pump irrigation from the aquifer, has strained agricultural producers and resulted in the need for high-yielding crops that use less water.  Grain sorghum is adapted to the Southern and Central Great Plains, but water stress at the critical reproductive stage can sharply reduce grain yields of the crop under dryland conditions (Unger, 1988).  In contrast, forage sorghum does not require such timely rainfall to attain good yields and has no critical stage.  Sorghum requires 1/3 to 1/2 less water than maize and is better adapted to most regions of Texas (Butler and Bean, 2006).  Forage sorghum hybrids produce silage yield similar to that of maize, while using approximately 1/3 less water than is required by maize (Pederson and Rooney, 2004). Stone and Schlegel (2006) reported that grain sorghum began to produce grain at a threshold of approximately 175 mm and generally yielded approximately 230.3 kg m$^3$ above threshold (25.4 mm) while the minimum threshold for maize increased to 279.4 mm; however, maize can produce more kilograms per cubic meter (329.2) than sorghum above the threshold.  Spiegel (2015) was in agreement with the thresholds but reported that grain sorghum produced more grain per 25.4 mm of moisture to about 609.6 mm.

Staggenborg (2015) agreed with the thresholds but found grain sorghum more profitable when maize and sorghum prices were equal until maize yields exceeded 8,865 kg ha$^{-1}$. Less than 533.4 mm of water, grain sorghum was expected to out-yield maize by a slim margin, with the margin increasing as available water for production decreased (Stone, 2013; Staggenborg 2013, 2015). Sorghum requires less moisture for growth than other cereal crops; however, it is very dependent on environmental conditions: studies at Pradesh India, a semi-arid tropical environment, revealed that sorghum required 3.01 kg m$^3$ of water; maize required 2.72 kg m$^3$; barley 2.30 kg m$^3$; and wheat 1.96 kg m$^3$ (House, 1985). The water requirement of sorghum increases as the plant grows, reaching a peak during flowering (using 6-7 mm ha$^{-1}$ of water a day); after this time, the moisture consumption decreases (House, 1985).

Studies from Colby, KS, reported about 600-650 mm of water to complete the maize-growing season (Lamm et al., 2009). Other studies reported about 450-650 mm of water, depending on the maturity and environment, for maximum sorghum production (Assefa et al., 2010; Lemaire and Hebert, 1996). On the High Plains, evapotranspiration rates of sorghum and maize ranged from 535-628 to 667-789 mm, respectively (Tolk and Howell, 2008; Musick and Duesk, 1980). Howell et al. (1994) studied water use by three crops and reported an average of 578 and 771 mm evapotranspiration for sorghum and maize, respectively, which suggested relatively greater water use by maize than sorghum for maximum production (Assefa et al., 2013). A yield and water relationship curve by Stone and Schlegel (2006) in Tribune, KS, showed that the maximum yield of dryland sorghum (~8 Mg ha$^{-1}$) can be obtained from 300 mm of soil water at the beginning of

growing season, with an additional 300 mm of water (precipitation) from June to September.

In general, forage sorghum is more water-use efficient than maize and requires less water to produce dry matter (Martin et al., 1976).  Typically, maize requires 630 to 762 mm of irrigation in addition to annual precipitation to obtain silage yields of approximately 23 Mg ha$^{-1}$ (Marsalis et al., 2010).  In a two-year study in New Mexico comparing maize, conventional forage sorghum, and brown midrib forage sorghum, Marsalis et al. (2010) found that by reducing the amount of water by 30% (average water applied was 445 mm), average yields for maize and conventional forage sorghum were identical at 24.4 Mg ha$^{-1}$, while the 21.1 Mg ha$^{-1}$ yield of brown midrib forage sorghum was different.

Traditionally, grain sorghum has been shown to be superior to forage sorghum for silage.  In experiments in Kansas, only high grain-producing forage sorghum hybrids approached the feeding value of grain sorghum hybrids when they were fed as silage (White et. al., 1991).  Forage sorghum is considered to be a practical alternative to maize silage when water becomes limited in irrigation systems and when input costs associated with seed and fertilizer are obstacles (Marsalis, 2011).  In semi-arid environments, advantages of sorghum compared to maize include:  less production cost and greater drought tolerance (Lamm et al., 2007; Marsalis, 2011), slower wilting of leaves and stalks, lower transpiration ratios, and greater ability to recover from drought (Martin, 1930; Sanchez-Diaz and Kramer, 1971).  Lamm et al. (2007) compared irrigation rates for major irrigated crops, maize, grain sorghum, soybean (*Glycine max* L.), and

sunflower (*Helianthus annuus* L.), in Northwest Kansas and found less irrigation required and a smaller percentage of decrease in yield of grain sorghum and sunflower over maize and soybean when watered with 25 mm every six days.

Evapotranspiration (ET) is a combination of evaporation from surfaces and transpiration from plants. To date, few data exist comparing the ET of maize and forage sorghum on the Southern High Plains. Howell et al. (2008) showed that forage sorghum had 27% less ET than maize in a study at Bushland, TX, comparing maize and forage sorghum for silage. In circumstances where maize and forage sorghum water-use efficiencies (kg m$^3$) were similar, maize tended to use more water because of earlier planting and longer growing season (Howell et al., 1997). A study at the USDA-ARS Laboratory at Bushland, TX, compared the ET rates, leaf area index, and dry matter of wheat, maize, and sorghum. The sorghum hybrid was of medium maturity and grown under both irrigation and dryland conditions in 1988 and produced dry matter exceeding 1.4 kg m$^3$ with seasonal ET rates averaging 549 mm (Howell et al., 1996). In 1993, the sorghum hybrid was of longer maturity and planted earlier, which increased the maximum dry matter to more than 2.0 kg m$^3$ with seasonal average ET90 (90% of the ET for sorghum), respectively (Howell et al., 1997). Variable ET rates for maize were reported from 70 to 790 mm by Musick and Dusek (1980), for surface irrigation from 783 to 1,003 mm by Eck (1984), for sprinkler irrigation 883 mm by Howell et al. (1989), and for LEPA-irrigated maize from 786 to 973 mm by Howell et al. (1995).

Sorghum requires less water for cultivation compared to other crops grown in the hot, dry climate of the Texas Panhandle (Smith and Frederiksen, 2000). In general

sorghum requires 25% less water than maize (Martin et al., 1976). Maize has been used predominantly for dairy and beef production in the region; however, it requires large amounts of water (as much as 770 mm yr$^{-1}$, Al-Kaisi and Yin, 2003; New and Dusek, 2005; Gowda et al., 2007; Howell et al., 2008) to produce high yields and adequate nutrition for the dairy industry (Marsalis et al., 2010). Although sorghum like most crops responds to irrigation, sorghum has a significant advantage over maize as forage because of the lesser water requirement for plant growth. The Texas High Plains is a semiarid region with a high evaporation rate and limited and erratic precipitation (Stewart and Burnett, 1987). Higher yielding hybrids of sorghum because of drought tolerance and better water-use efficiency are a viable alternative to maize. Increasing the quality and yield of sorghum because of its drought tolerance and water-use efficiency has become important in semiarid regions (Marsalis, 2011). New improved breeding methods and higher yielding hybrids have improved the quality of sorghum. Bean and McCollum (2006) determined that some sorghum hybrids had comparable or better quality than maize with equivalent amounts of water.

**Economic Outlook of Sorghum**

In 2015, production of grain sorghum in the United States totaled 15.2 million Mg, an increase of 9.7 million kg or 64% and a 61% increase in value since 2011 (NASS, 2015). In 2011, less production was caused primarily by extreme drought in the primary sorghum-growing states of Kansas, Oklahoma, and Texas. In 2011, the value of the grain sorghum crop was $1.26 billion (NASS, 2012) while in 2015, the value was $2.1 billion (NASS, 2015). Predominantly produced on the southern Great Plains, sorghum is grown

in more than 30 states.  Historically, most sorghum has been produced in Kansas and Texas.  In 2011, the two states retained their ranking as leading producers, harvesting 78% of the sorghum crop in the United States.  Kansas produced 2.79 million tons valued at $671 million, while Texas produced 1.42 million tons valued at $331 million.  In 2015, Kansas produced 7.2 million Mg while Texas produced 3.8 million Mg.  Other states producing large quantities of grain sorghum, more than 40,000 ha harvested in 2015, were Arkansas, Colorado, Missouri, Nebraska, Oklahoma, and South Dakota.

In 2011, lead producers of sorghum in the world included:  United States (10.0%), Nigeria (12.6%), India (11.2%), and Mexico (11.2%) (FAS, 2012).  In 2015, lead producers in the world included:  United States (22.4%), Mexico (10.5%), Nigeria (9.1%), and Sudan and India (each 8.1%) (FAS, 2015).

The United States is the leading exporter of sorghum.  In 2011, the United States exported grain sorghum valued at $948.6 million, a 32% increase from 2010 (FAS, 2012).  In 2010, the United States exported grain sorghum valued at $720.8 million, a 13% increase from 2009.  Countries that purchased most of the grain sorghum from the United States were Mexico, Spain, and Japan.  Approximately half of the sorghum produced is fed to livestock, and half is consumed by humans and used for many other purposes.  In 2014-2015 (August-September), China (97%) was the leading importer of U.S. sorghum, followed by Japan (2%) (U.S. Grains, 2015).  In 2015-2016 (August-September), China (83%) continued to lead, followed by Mexico (7%), South Africa (1%), and China (0.8%) (U.S. Grains, 2016).

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**Sorghum Classification**

The ancestors of modern sorghums originated on the continent of Africa, associated with specific eco-geographical regions of sub-Saharan Africa, and consisted of five cultivated races of *S. bicolor* spp., including bicolor, caudatum, durra, guinea, and kafir. Murty and Govil (1967) proposed a system of working groups to classify cultivated races of sorghum. Harlan and DeWet (1972) proposed a simplified system of classification of cultivated sorghum in which five races: 1 = Bicolor (B), 2 = Guinea (G), 3 = Caudatum (C), 4 = Kafir (K), and 5 = Durra (D), and intermediates between the races, were described using 6-15 to include combinations of the basic races. The two approaches were revised to develop a modified numeric classification system by Dahlberg (2000), in which each working group was designated by a two- or three-digit number, the first digit indicating the race (Bicolor-1, Guinea-2, Caudatum-3, Kafir-4, and Durra-5). Various combinations of the races have numbers from 6 to 18, and 19, 20, and 21 are unclassified types. The last digit of a working group number indicated the subtype of the working group. A last digit '0' indicated the working group closest to the essential characteristics of the race, i.e., the actual sorghum Bicolor classification where the working group is most closely related to the actual is 10. Zera zera is a working group designated by the number 37, being a part of the race Caudatum, while understanding there are at least seven known subtypes. Understanding the genetics behind working groups and races would be useful for sorghum researchers by increasing diversity. Working groups such as Zera zeras contain useful sources of tan plant and white grain for use in food systems, while kafirs yield well.

**Introduction of Sorghum to U.S.**

Many sorghum varieties were introduced to the United States beginning in the 1850s. The kafirs came from South Africa in 1876, and shallu from India in 1890. In 1857, Peter Wray brought 16 cultivars of sorgo from Natal, South Africa (Snowden, 1936). J. H. Martin (1936) suggested that the first sorgo introduction was Chinese Amber introduced in 1853. Some suggest that Benjamin Franklin grew broomcorn, a sorghum relative, in the late 1700's. Most of the introductions were from the kafir and durra races (milos). Many sorghum varieties, including Redlan and Martin, derived from the kafir and milo races, were developed during the early decades of the 20th Century. Martin variety was grown on 80% of the sorghum acreage in the U.S. from the early 1940s to 1955 (Duncan et al., 1991).

**History of Hybrid Production**

Until the early 1950s, hybrids were made by hand emasculation, or mechanical-sterilization methods such as hot water emasculation. The experimental hybrids documented the heterotic potential of sorghum but they also confirmed that economically viable production of hybrid seed was needed (Karper and Quinby, 1937). In the 1950s, a commercially feasible system for large-scale hybridization in sorghum was developed (Quinby and Martin, 1954; Stephens and Holland, 1954). In 1954, Stephens and Holland proposed a method for creating hybrids based on a cytoplasmic male-sterility system that used sterile cytoplasm from milo. Backcrossing kafir with milo, with kafir as the recurrent parent, would result in kafir nuclear genes in milo male-sterile cytoplasm, in effect making a male-sterile version of the kafir line. The male-sterile kafir line could be

crossed with a durra male or any of a large number of milo/kafir derivative lines, restoring its fertility. Within a few years, most of the sorghum production area in the United States was planted with kafir female x milo/kafir derivative male hybrids (Duncan et al., 1991). The system was used to such a wide extent that much of the hybrid sorghum in the 1960s in the United States had similar cytoplasm, as still is the case. In making hybrids, A-lines (male sterile) are used as the female parents. These A- or male-sterile lines are derived from B-lines, and each A-line is isogenic to its corresponding B-line, from which it was derived, i.e., it is genetically identical to the B-line at all loci but the locus/loci for male sterility. An A-line is different from a B-line only because it is male sterile. This system from a practical standpoint of hybrid development works effectively and enables a sorghum breeder to classify a newly introduced genotype for use in a breeding program. However, research at Texas A&M University is characterizing elite U.S. sorghum lines, and results to date suggest a genetic grouping of lines into five broad groups: Kafir-Milo derivative males, Kafir type females, Zera zera derivative males, Zera zera derivative females, and Feterita derivative males (Menz et al., 2004).

**Sorghum Conversion Program**

Soon after hybrid sorghums were developed, sorghum breeders realized that the genetic base in the United States was limited, in large part because of difficulty in using tropical, tall, photoperiod-sensitive sorghums in the temperate United States. This concern led to the development of the TAES-USDA Sorghum Conversion Program, initiated in 1963. The purpose of the Sorghum Conversion Program was to convert

exotic tropical photoperiod-sensitive sorghum lines into temperate-adapted photoperiod-insensitive lines suitable for breeding programs in the United States, which enabled diversification of available germplasm (Stephens et al., 1967). The Sorghum Conversion Program has had a dramatic impact on sorghum improvement; it is difficult to find hybrids grown today that do not have sorghum conversion germplasm in their pedigrees.

Another reason for the narrow genetic base was that most hybrid sorghum production was (and is still) based on the same cytoplasm system (known as A1 sterile cytoplasm). Different male-sterility inducing systems, such as A2 and A3 cytoplasm, have been discovered in the last few decades, and hold promise for widening the genetic variability of elite lines. The A2 cytoplasm was reported from IS12662C (Schertz, 1977; Schertz and Ritchey, 1978), belonging to the caudatum-nigricans group. Quinby (1980) reported the sterility-inducing cytoplasm from the line IS1112C and designated it A3 cytoplasm whose limited sources of fertility-restorer genes have precluded widespread utilization (Rooney, 2000). Other cytoplasmic sterile systems also have been reported (Schertz and Pring, 1982). Apart from different cytoplasmic sterility sources, the conversion program has made available agronomically desirable lines with resistance to such economically significant diseases as anthracnose (*Collectotrichum graminicola* (Ces.) G.W. Wils) and downy mildew (*Sclerospora sorgi* (Kulk) Weston & Uppal). Sources of resistance to insect pests such as greenbug and sorghum midge, and to pre- and post-flowering stress, have been found in converted materials (Rosenow and Dahlberg, 2000).

The USDA-TAES Sorghum Conversion Program made available diverse sorghum germplasm, and different male sterility-inducing systems have been introduced. The Sorghum Conversion Program continues to serve as a major source of new germplasm for many breeding programs throughout the world (Smith and Frederiksen, 2000). It is a crucial component for increasing diversity in sorghum breeding programs.

## Combining Ability

Combining ability is useful for plant breeders to better understand genetic variance and inbred lines important in identifying hybrids for commercial production. Research on combining ability helps plant breeders to select the best parents for development of hybrids or varieties. The concept of general- and specific-combining ability was conceived by Spraque and Tatum (1942) who designated general-combining ability (GCA) as the average performance of a line in hybrid combination, and the term specific-combining ability (SCA) was applied to cases where certain hybrid combinations did relatively better or worse than would be expected on the basis of the average performance of the lines. GCA measures the average performance of an inbred when crossed with a series of other inbreds. GCA indicates the worth of an inbred as a parent of multiple hybrids. Estimates of GCA are useful for choosing a few key inbreds to use as testers. SCA is because of genetic effects specific to a hybrid combination and not accounted for by GCA effects. SCA measures genetic effects that are specific to a hybrid combination. As a general rule, GCA is the result of additive gene effects, while SCA is the result of non-allelic interactions (Jinks, 1954), is assumed to be a deviation from

additivity (Bernardo, 2014), or is attributed primarily to deviations from the additive gene action caused by dominance and epistasis.

Crossing a plant line with several others provides the mean performance of the line in all its crosses.  Mean performance, when expressed as a deviation from the mean of all crosses, is the GCA of the line.  Any particular cross, then, has an expected value which is the sum of the GCA of its two parental lines.  The cross might, however, deviate by a greater or lesser extent from the expected value.  The deviation is the SCA of the two lines in combination.  In statistical terms, the GCA is the main effect while the SCA is an interaction (Bernardo, 2014).  The SCA will be of interest because it will indicate the degree of heterosis expressed in each cross while representing the dominance deviation value in the simplest case but ignoring epistatic deviation.  Therefore, a cross between sorghums with greater combining ability, if from genetically divergent backgrounds, is more likely to result in a hybrid with a greater degree of heterosis, which will also be manifested in a greater SCA for one of the lines in specific combination with the other.

Green (1948b) studied $F_2$ generations of maize derived from crosses of high x high, high x low, and low x low combining inbred lines and found that combining ability was an inherited character.  Comstock and Robinson (1948) and Kempthorne (1957) introduced a method to study combining ability of inbred lines as the line x tester method. In this design, a set of female parents (n) are crossed with a genetically different set of male parents (m) in all possible combinations, resulting in a total of nm progenies.  The advantage of this method allows the breeder to test at one time a larger number of inbred

lines.  The focus of the research will be narrowed to include only the line-by-tester method.

Griffing (1956) showed that for homozygous parents (inbreeding coefficient F = 1), the genetic variance $\sigma^2 G$ (variance among hybrids) could be expressed in terms of combining ability variance as:

$$\sigma^2 G = \sigma^2 GCA + \sigma^2 SCA$$

where $\sigma^2 GCA$ and $\sigma 2SCA$ are the variances for general- and specific-combining ability effects, respectively.  Components of combining ability variance might reflect additive effects and additive interactions, while SCA variance components might reflect dominance and epistasis, and components of additive epistasis (Rojas and Sprague, 1952).

Kambal and Webster (1965) estimated the components of variance caused by GCA and SCA and their interaction with years for five traits in split-plot design and reported that both GCA and SCA were important in determining yield and other characters, but the GCA effects were more important and more stable over years.  Beil and Atkins et al. (1967) observed that variances for GCA were three times more than specific effects and found similar ratios with such traits as the number of kernels per panicle, number of panicles per plant, and weight of 100 kernels.  They reported that SCA effects were more stable than GCA effects in various environments particularly for the grain yield and number of kernels per panicle.

The concept of a good plant tester has been another question for most of the breeding programs to date. Matzinger (1953) defined a desirable tester as one that combined the greatest simplicity in use with maximum information on the performance to be expected from the tested lines. However, Allison and Curnow (1966) assessed that the best tester was the one that maximized the expected mean yield of the variety produced by random mating the selected genotypes. Green (1948a) compared maize progenies from crosses using two testers and found that the average performance was a better estimate of combining ability than was the top cross performance of either tester alone. Top cross refers to the estimation of combining ability of testers based on matings with specific single lines or a cross between an inbred line and an open-pollinated variety. For heterogeneous populations, Cress (1966) concluded that testers could be selected based on average performance of a test cross, i.e., the tester with the greatest average cross performance was chosen. However, if the selected genotypes are not to be used immediately in hybrid combination with the tester, emphasis on heterotic response is misplaced because it reveals little concerning the genetic potential and nothing concerning the expected rate of progress from selection.

Giriraj and Goud (1982) found that both additive and non-additive gene actions were important for grain yield, panicle length, number of primary branches, length of the primary branch, 100-kernel weight and number of grains per panicle, and number of leaves in grain sorghum. Nayeem and Bapat (1984) reported that the estimates of the mean squares due to GCA were more than SCA for the traits studied, indicating the importance of additive gene action for those traits. Kishan and Borikar et al. (1989)

analyzed a line x tester involving diverse cytoplasmic lines in sorghum and reported that restorers IS 12567C, IS 12662C, and SPV 650 had desirable GCA effects, and the cross (A [SUB2]T x 398) x IS 12662C had the greatest mean yield coupled with good SCA effects. Patel et al. (1991) studied the combining ability of 36 genotypes for seven traits in different environments, indicated the importance of additive and non-additive gene effects in the inheritance of the traits, and concluded that most genetic variation was additive. Reddy and Joshi (1993) studied combining ability for grain yield and its five components from $F_1$ to $F_4$ generations. The best parent identified was CSV 10 which was a good combiner for grain yield and 1000-kernel weight. They also reported that the magnitude of SCA variance decreased in $F_2$ and later generations and identified the best cross combinations as SPV 451 x SPV 474, SPV 474 x IS 508, CSV 10 x SPV 451, and CSV 10 x SPV 474 that can be exploited to improve yield of sorghum grain. Badhe and Patil (1997) found that additive gene action for plant height and non-additive gene action were dominant for grain yield and other attributes. They identified female MS 2077A and male SPV 386 as the best combiners for almost all traits except plant height and 1000-kernel weight. The cross MS 2077A X SPV-245 involving high x low combiners showed significant positive SCA effect for all the panicle traits, suggesting a dominant role of non-additive gene action for panicle traits. Can et al. (1997) studied combining ability in a diallel mating system in early maturing grain sorghum by sowing in spring and summer, observed that GCA and SCA effects were significant for all the traits, and identified some parents having large positive GCA for grain yield and small or negative for culm length and days to panicle emergence.

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Biradar et al. (2000) revealed significant variances due to GCA and SCA, suggesting the importance of additive and non-additive gene effects in inheritance of grain yield and other component traits. They identified that females 104A and P2A were good general combiners for grain yield per plant that had positive and significant GCA effects, and they also showed good average performance indicating strong relationship between GCA effects and *per se* performance (the individual performance of the line or tester). Hovny (2000) reported that ICSR-112 was a good combiner for grain yield per plant, and the cross ICSA-1 x ICSR-112 gave large grain yield per plant because it had high SCA. Hovny et al. (2001) reported that the female line ICSA-40 and the restorer ICSR-138 had significant positive GCA for grain yield, and the crosses ICSA-1 x ICSR-93002 and ICSA-40 x ICSR-89037 yielded more grain than the check. Iyanar et al. (2001) studied combining ability for grain yield and its components in sorghum and observed that non-additive gene action was dominant for all characters. The lines 2077A and 88005A expressed superior *per se* performance and GCA effects on grain yield, while testers such as CO 26, SPV 1192, and SPV 881 showed high *per se* performance for days to 50% flowering, panicle length, panicle weight, and grain yield. Kanawade et al. (2001) reported that additive gene effects were important in the inheritance of panicle breadth, 1000-kernel weight, and grain yield per plant, while plant height, days to 50% flowering, days to maturity, number of leaves per plant, and panicle length were under the control of non-additive gene effects. Siddiqui and Baig (2001) reported the ratio of GCA to SCA variances was less than unity for all the characters except days to flowering which indicated dominance of non-additive gene action for the characters.

El-Mottaleb and Asran (2004) analyzed a line x tester and indicated that lines ISCA-88003, ICSR-237, and ICSR-92003 had the most significant GCA effects for grain yield and that SCA variance was more important for all the traits studied except plant height.  Kenga et al. (2004) studied combining ability in tropical sorghum and reported significant GCA effects of males for all the traits and detected significant SCA in all traits except inflorescence length.  From the ratio of GCA to SCA variances, they concluded that non-additive gene action was dominant for most of the traits.  El-Menshawi (2005) studied combining ability in eight environments and observed that non-additive effects were two times greater than additive effects.  Kenga et al. (2005) observed that the ratio for GCA to SCA variances ranged from unity to a high of 10, indicating dominance of additive gene effects for most yield-contributing traits in sorghum.  Chaudhary et al. (2006) analyzed a line x tester for combining ability and observed non-additive gene action for all the traits and identified the lines 116A and 117A and testers RSLG 112, SPV 1090, SPV 839, and SPV 1167 as good general combiners for yield and its contributing characters.  Both GCA and SCA effects were present among the crosses and involved at least one of the parents with large GCA effect. They also exhibited significant SCA effects for most of the traits.  Kulakarni et al. (2006) did line x tester analysis using 33 hybrids along with parents and indicated the importance of additive gene effects in the inheritance of days to 50% flowering and fodder yield per plant, while non-additive gene action was important for 1000-kernel weight, plant height, number of leaves per plant, days to maturity, panicle weight, number of primary branches per panicle, and grain yield per plant.  Premalatha et al. (2006) studied heterosis and combining ability for grain yield and its components and

revealed non-additive gene action for all the traits and also reported that parents that performed well for *per se* performance and GCA effects could be considered good parents. Salini et al. (2008) did line x tester analysis in dual-purpose sorghum and reported that grain yield and crude protein content of leaves were affected by additive gene action, while green forage yield at 50% flowering, 1000-kernel weight, protein content of grain, and leaf breadth were under the control of additive and non-additive gene action, and the other traits were under the control of non-additive gene action. They also found that the lines SPV 1782, SPV 1714, SPV 1754, and SPV 1616 and tester CSV 15 were good general combiners. SPV 1782 x HC 308, SPV 1730 x HC 308, and SPV 1616 x CSH 16 were good specific combiners. Tadesse et al. (2008) reported that GCA for plant height, panicle exsertion, panicle length, grain yield, and kernel weight was significant among male parents, indicating the prevalence of additive gene action in determining the traits while the male x female interaction and SCA effect for all the parameters considered was non-significant, indicating little importance of non-additive genetic effects in expression of the traits.

Degu et al. (2009) did line x tester analysis for yield-related traits in grain sorghum in three low-moisture areas in Ethiopia and observed dominance of additive components in inheritance of most of the developmental, panicle, and grain traits. Aruna et al. (2010) reported that additive and non-additive gene actions were equally important for controlling such traits as the number of kernels per primary branch, number of primary branches, number of secondary branches, and kernels per unit length of primary

branch, while non-additive gene action was particularly important for panicle weight, yield per plant, and number of leaves.

Indhubala et al. (2010) reported the preponderance of non-additive gene action for all the characters studied in sweet sorghum, and based on GCA effects, the lines BJ 3A, CK 60A, and AKMS 22A and the testers RSSV 9, SSV 84, and ASV 9401 were identified as good combiners for most of the characters. The hybrid combinations AKMS 22A x RSSV 9, BJ 3A x VMS 98001, BJ 3A x RSSV 9, AKMS14A x RSSV 9, and CK 60 A x VMS 98001 were the best specific combiners. Makanda et al. (2010) studied combining ability for sorghum grain yield in different tropical low and mid-altitude environments and reported that GCA and SCA effects were significant for all the traits, implying both additive and non-additive gene actions were important in controlling inheritance of the traits. Kanbar et al. (2011) observed that varieties Baladi-1, Baladi-2, and Ezraa-7 had significant positive GCA for grain yield. Mahdy et al. (2011) reported that GCA variance components for days to flowering, plant height, and 1000-kernel weight were larger than those of SCA in different environments, while SCA variance for grain yield was larger than that of GCA. Variance components of GCA and SCA varied greatly from location to location and early to late planting for days to flowering, plant height, and 1000-kernel weight.

Tariq et al. (2014) studied heterosis and combining ability for quantitative traits in sorghum by evaluating nine crosses and six parents in Pakistan during 2009-2010. They found the mean squares for genotype, GCA, and SCA were significant for all the traits studied; however, the phenotypic component of variance was greater than the genotypic

component of variance for all the traits.  Similarly, the estimation of GCA variance was less than that of SCA variance for all traits.  The studies revealed significant mean squares for GCA and SCA which led to the existence of both additive and non-additive types of gene action.  Numerous studies also reported significant variability for genotype, GCA, and SCA for different components in sorghum (Mohammed et al., 2008; Kamdi et al., 2009; Prakash et al., 2010).  Tariq et al. (2014) discovered that the dominance variance was greater than the additive variance for all the parameters evaluated, with a degree of dominance greater than unity.  The ratio of GCA to SCA is an indicator of the dominance of additive gene effects.  Mohammed et al. (2015) researched combining insect resistance with desirable agronomic and morphological traits to increase sorghum productivity and found a larger ratio of $\sigma^2(GCA)/\sigma^2(SCA)$ for 100-kernel weight in the post-rainy season, indicating the dominance of additive gene action, whereas both additive and non-additive gene actions were observed during the rainy season.  Grain yield had greater SCA variance, suggesting dominance of dominance (non-additive) type of gene action (Wilson et al, 1978; Singhania, 1980; Hovny et al., 2000; Girma et al., 2010).

Hallauer and Miranda (1981) reported that some form of early generation testing is included in most breeding programs.  However, this does not imply that perfect relationship exists between initial and later generations for inbreeding, because early testing was designed to separate the population of lines into groups of good and poor combining ability.  According to Sprague (1946), early testing was based on two assumptions:  (i) there are marked differences in combining ability among open-

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pollinated plants, and (ii) selected samples based on tests of combining ability of S0 (variety) or S1 (advanced generations of a hybrid) plants offer a larger proportion of superior lines upon inbreeding, and then selection does a more nearly random sampling of combining abilities from the same population than on the basis of visual selection alone.

Kambal and Webster (1965) studied data collected during two years from a set of 190 sorghum hybrids obtained by crossing 10 male-sterile lines and 19 restorers. They concluded that both $\sigma^2$GCA and $\sigma^2$SCA were important and stable over years for grain yield. Beil and Atkins (1967) studied the performance of 40 $F_1$ hybrids obtained by crossing five male-sterile lines with eight restorers at three locations during two years and found that GCA variances for grain yield, number of kernels per panicle, number of panicles per plant, and 100-kernel weight were much larger than SCA variances. Malm (1968) studied eight fertility restorer lines developed from African introductions crossed with four male-sterile lines to produce 32 hybrids. The data reported indicated that parents with large kernels produced hybrids that yielded most; however, all sets of exotic hybrids produced larger kernels than the checks while some exotic hybrids produced 50% more protein than the checks. Malm (1968) concluded that for grain yield, kernel size, and protein content, additive gene action was more important than non-additive gene action. Mattei (1974) working in Venezuela with a line x tester cross of eight male-sterile lines and four restorers evaluated at three locations observed that variance caused by additive effects was several times greater than variance caused by non-additive effects for grain yield and concluded that evaluating parents based on GCA should be effective.

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Shankaregouda et al. (1972) used a line x tester study to show that plant height and days to flowering were mostly controlled by additive gene effects, whereas, yield and number of kernels per panicle were mostly controlled by non-additive gene effects, which was supported by results of Goud et al. (1973), Shahane and Bapat (1981), Shinde and Sudewad (1981), and Rao et al. (1982).

**Heterosis**

Plant breeders rely on genetic variability to select plants with traits of interest in a population. Plant breeders for almost two centuries observed expression of hybrid vigor, but it was not until the early part of the 20th Century that the modern concept of hybrid vigor was described. Heterosis is defined as the difference between a hybrid and the mean of the two parents for numerous agronomic traits that can be evaluated (Falconer and Mackay, 1996; Bernardo, 2014). Heterosis is expressed as the percentage increase or decrease of an $F_1$ hybrid over the mid-parental value. Exploitation of heterosis began in the United States in the 1950s, resulting in large increases in yields of sorghum and maize (USDA National Agricultural Statistics Service, 2007; Troyer and Wellin, 2009). The more genetically divergent a hybrid is, based on genetic relatedness of the parental lines, the greater the degree of heterosis that might exist.

The characteristically superior performance of hybrid sorghums was because of a phenomenon known as "heterosis" or "hybrid vigor", in which hybrids demonstrated markedly vigorous growth and yield when compared with their parents (Bernardo, 2014). In 1914, Shull proposed the term "heterosis" to describe developmental stimulation resulting from union of different gametes that caused superiority of hybrids over their

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parents (Shull, 1952). The terms heterosis and hybrid vigor are synonymous and often used interchangeably. A large degree of heterosis occurs when the parents are genetically divergent or unrelated, resulting in a heterozygous hybrid. Therefore, development of superior high-yielding sorghum hybrids requires a system by which genotypes can be crossed on the basis of the degree of 'unrelatedness' between them. Beil and Atkins et al. (1967) observed greatest heterosis for grain yield, suggesting that non-additive effects might be proportionately greater for grain yield than for any of its individual components. Quinby (1974) proposed a complementary interaction between recessive and dominant alleles as a possible cause of heterosis.

Blum et al. (1977) defined heterosis as "the advantage of the hybrid over the best parent." "Midparent heterosis", which is used in quantitative genetics, is defined as the superiority of a hybrid over the mean of its parents (Bernardo, 2014). The reason for the phenomenon is not understood, but two principal explanations are the concepts of dominance and overdominance (Crow, 1948, 1952). Davenport (1908) proposed the dominance theory, supported by Bruce (1910), Jones (1917), and Collins (1921) that cites the effect of dominant favorable alleles masking unfavorable recessive alleles as the reason for the superiority of a hybrid (Bernardo, 2014). East (1908) and Shull (1908) independently proposed the overdominance theory, which suggests that the heterozygous condition is responsible for heterosis; it is the inherent superiority of a heterozygote over either homozygote (Bernardo, 2014). Franca et al. (1986) reported midparent heterosis for grain yield per plant, with negative heterosis observed for days to 50% flowering and 1000-kernel weight. Berenji (1988) found that heterosis over the mid-parental value was

greater for number of kernels per panicle in grain sorghum, and the hybrids were taller

and yielded more than the parents. Nimbalkar et al. (1988) reported positive and

significant relative heterosis for panicle length, 1000-kernel weight, and grain yield per

plant. Patel et al. (1990) observed negative heterosis for plant height and significant

positive heterosis for panicle length, 1000-kernel weight, and grain yield per plant.

Nandanwankar (1990) reported that the number of grains per panicle was the major

contributor to heterosis for grain yield in sorghum and among the remaining components,

the number of primary branches per panicle exhibited maximum heterosis followed by

the number of whorls per panicle, panicle length, and 1000-kernel weight. Rao et al.

(1993) reported that hybrids had a large degree of heterosis over their parents in days to

50% flowering, panicle length, and grain yield per plant, and limited heterosis for 1000-

kernel weight. Ganesh et al. (1996) noticed midparent heterosis for days to 50%

flowering and grain yield per plant, better parent heterosis for plant height and panicle

length, and all three types of heterosis for 1000-kernel weight. Madhusudhana and Patil

(1996) crossed a random sample of 97 $F_3$ sorghum segregates from the cross 3660B x

MR-75 with a sterile tester and observed that as many as 21 derived $F_1$ plants showed

heterosis for yield, and some derived $F_1$ plants were superior over a commercial check.

Can et al. (1997) reported great positive heterosis in grain yield for more than half of the

hybrids, and several cross combinations had high heterosis for grain yield but negative

for days to panicle emergence. Lokapur (1997) noticed heterosis over the better parent in

the positive direction for plant height, significant positive heterosis for 1000-kernel

weight, and negative heterosis for days to 50% flowering. Salunke and Deore (1998)

reported that low heterosis was observed for days to 50% flowering and moderate

heterosis for 1000-kernel weight, while for plant height, and significant positive heterosis over a standard check was observed.  Iyanar et al. (2001) reported that the preponderance of non-additive gene action for the traits indicated the scope for exploitation of heterosis in improving yield in sorghum.  El-Mottaleb and Asran (2004) reported that better parent heterosis was generally manifested for plant height, panicle length, panicle width, and grain yield per plant; heterosis for 1000-kernel weight was observed for few of the crosses; and greatest positive significant heterosis for grain yield (87.88%) was manifested by the cross ICSA-37 x ICSR-93023.  Kenga et al. (2005) observed high positive heterosis for sorghum grain yield and its components including days to anthesis and plant height for most of the hybrids in different environments.  Premalatha et al. (2006) found that the hybrid CSV 15 x SPV 1521 yielded most grain with 90.00, 86.89, and 33.45% heterosis over the midparent, better parent, and standard check, respectively. The hybrid also was superior in terms of days to 50% flowering, plant height, number of kernels per panicle, and grain yield per plant, but hybrids that exhibited heterosis for grain yield were not heterotic for all the traits.  Sharma and Sharma (2006) reported that crosses SPV 1518 x IS 18580, IS 18580 x Raj 13, and SPV 1514 x Raj 36 had high heterosis over the midparent and better parent for grain yield per plant, panicle weight, and panicle length.  Salini et al. (2008) reported that high significant mean performance of hybrids with that of parents suggested the existence of heterosis for all the traits and the importance of non-additive gene effects in determining the traits.  Makanda et al. (2010) found that hybrids were dominant for grain yield and displayed as much as 285% standard heterosis, and overall hybrid mean yield was significantly greater than that of parents and standard check varieties, which was attributed to high levels of average

heterosis and standard heterosis, respectively.  El-Dardeer et al. (2011) studied heterosis

under normal and water-stress conditions and reported the better parent heterosis was

generally manifested for plant height, panicle length, panicle width, and grain yield per

plant, and crosses *viz.,* ICSA-364 x ICSR- 66, ICSA-364 x ICSR-102, and ICSA-490 x

ICSR-66 had significant standard heterosis for grain yield over the check.  Kanbar et al.

(2011) observed that hybrids Baladi-4 x SPL-10A and Baladi-3 x ATX-629 had large

significant positive values of heterosis, and high levels of mid- and better-parent heterosis

were recorded for grain yield in all hybrids except Ezraa-3 x SPL10-A and Ezraa-5 x

ATX-629.  Mahdy et al. (2011) reported positive heterosis for grain yield and 1000-

kernel weight and negative heterosis for days to 50% flowering in different

environments.

The phenomenon of heterosis between genetically distant or unrelated genotypes

has been widely reported, and the idea of defining genetic relatedness of genotypes has

spurred research to determine genetic distance between lines, based on the degree of

similarity in molecular markers shared.  An estimate of genetic distance can be used as an

index of relatedness, and therefore as a tool for defining the potential for diversity.  This

approach has been used in development of numerous crop plants.

In rice, good correlations between molecular marker-based distance and hybrid

performance, using diallel analysis, were reported by Saghai-Maroof et al. (1997), and

between specific marker heterozygosity (solely considering markers exhibiting

significant effects on the traits being studied) and heterosis by Zhang et al. (1994, 1995)

who also, however, reported low correlations with general heterozygosity based on all the

markers. Xiao et al. (1995) and Hua et al. (2003), using molecular marker techniques for rice, concluded that dominance was the major basis of heterosis. Charlesworth and Charlesworth (1999) concluded that overdominance effects were unimportant in most cases.

In alfalfa (*Medicago sativa* L.), Riday et al. (2003) observed no correlation of SCA or midparent heterosis with genetic distance. They theorized that estimates of genetic distance based on neutral molecular markers (not linked with genes controlling traits of interest) did not reflect heterotic potential between genotypes.

Bernardo (1992) suggested a set of conditions, including large heritability and strong dominance effects, for effective prediction of hybrid performance based on marker heterozygosity. Several studies based on molecular markers in crops such as maize (Stuber et al., 1992; Cockerham and Zeng, 1996), and rice (Yu et al., 1997; Li et al., 2001; Luo et al., 2001) found overdominance to be important. However, the possibility of pseudodominance effects could not be eliminated, while epistasis was shown to play a considerable role in the phenomenon of heterosis (Carr and Dudash, 2003).

Grain yield is a complex trait controlled by polygenes and has low heritability especially in stressful environments. For example, selection for grain yield under severe drought stress has often been considered inefficient because the estimate of heritability of yield has been observed to decrease with reduced yield (Bolaños and Edmeades, 1993). Quinby (1963) reported heterosis of sorghum in the forms of increased grain and forage yields, hastened flowering and maturity, increased height, and larger stalks and panicles.

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Enhanced grain yield was reported by Kambal and Webster (1966) and Blum (1969) to be the product of more kernels per panicle and increased kernel weight.

Heritability is a key component of plant breeding programs, because a trait needs to be heritable if any breeding progress is to be made. Defining and calculating heritability depends on how the plant breeder considered the trait, because it can be measured based on single plants or a group of offspring. Heritability is a measure of the relative influence of genetic versus non-genetic effects on the expression of a trait. It can explain the variation that is transferred from parents to offspring.

If a phenotype is determined, in part, by the genotype, the heritability is known as broad-sense heritability (Bernardo, 2014). Broad-sense heritability is the ratio of genotypic to phenotypic variance and is usually denoted by H. A trait considered heritable, in the sense of it being transmitted from a parent to its offspring, would be defined as having narrow-sense heritability. Narrow-sense heritability is denoted by $h_2$ and is the ratio of additive to phenotypic variance (Bernardo, 2012, 2014). The variance of the additive effect of alleles rather than genotypic variance is considered. Additive variance is because of the average effects of alleles and replaces genotypic variance in the narrow-sense heritability formula.

Both definitions have meaning and application when considering the germplasm and environment in which the plants are grown. Broad-sense heritability is expressed when a plant breeder is trying to exploit all types of genetic variance. Epistatic, dominant, and additive variance can all be exploited among clones in asexually propagated species (Bernardo, 2014). Narrow-sense heredity is expressed when a

breeder uses selection to determine the change or increase in the trait of interest. Selection involves identifying the best individuals in a population and using the selected plants as parents to produce the next generation. The goal of the plant breeder is to produce offspring with a larger quantitative or qualitative mean than that of the previous generation.

Govil and Murty (1973) reported high heritability estimates for days to flowering, length of the primary branch, plant height, and number of leaves and also reported that heritability estimates for protein and lysine were 9 and 14%, respectively, which were similar to the heritability estimates of grain yield. They also indicated that selection for grain quality did not seem to be more difficult than for grain yield. Nayeem (1992) said additive gene action was important in controlling such traits as protein, lysine, and sugar contents. Desai and Shukla (1995) reported that additive and non-additive gene effects controlled the inheritance of most of the traits, with the latter being more important in sorghum and grain yield. Panicle components were under the control of dominance gene action, and the exploitation of hybrid vigor seemed to be beneficial. Sankarapandian et al. (1996) found that heritability was greatest (90%) for all the traits except kernel density and panicle breadth. High heritability of 99.87% was observed for the number of grains per panicle, followed by grain yield and 1000-kernel weight. They also observed that the genetic advance as a percentage of the mean was greatest for grain yield, 1000-kernel weight, number of rachis branches, peduncle length, and panicle length.

Hoshmand and Rezai (1997) used generation mean analysis to study the heritability estimates and type of gene action involved for grain yield per plant, mean

panicle weight, panicle length, plant height, and number of days to flowering in 17

families and reported great genetic potentials among the lines studied. Different

heritability estimates were observed in different families, and their averages ranged from

50.99% for panicle length to 77.54% for plant height. Can et al. (1998) reported that high

heritability estimates coupled with high genetic advance were observed for dry weight of

leaves, plant height, and 100-kernel weight, indicating the traits were controlled by

additive gene action. Audilakshmi and Aruna (2005) reported that grain size was

controlled by dominant genes that were polygenic. Predominance of dominance and

epistatic interactions in crosses indicated that selection for larger grain size would be

more effective if the dominance and epistatic effects were first reduced by a few

generations of selfing. Aruna et al. (2010) studied the use of different germplasm lines in

developing sorghum varieties and hybrids and reported that genetic improvement of grain

yield per plant would be easier through indirect selection because many yield components

showed significant positive correlation with yield along with high heritability value.

**Correlation**

Correlation studies provide information on the association of yield with its

component characters and help formulate phenotypic selection to discard the bulk of the

segregating base population and select desirable types phenotypically. Improvement of

yield is possible through the associated characters. Beil and Atkins et al. (1967) reported

that the correlation of grain yield with its components revealed that the number of kernels

per panicle was related to yield. Expressions for yield were not affected appreciably by

100-kernel weight, and significant negative association for the number of panicles per

plant with grain yield was observed for hybrids and parental lines. Badwal (1970) observed no association of grain yield with days to 50% flowering, plant height, span of maturity, or 100-kernel weight in sorghum. Goud and Asawa (1978) studied correlation and found that yield was positively and significantly correlated with plant height and significantly correlated with the number of days to 70% maturity, and yield was more correlated with plant height in the parental population than in $F_1$ plants. However, panicle length and grain yield were negatively correlated. Bohra et al. (1985) reported that grain yield per plant had significant and positive correlation with harvest index and panicle length in sorghum grown in limited moisture or irrigated conditions and also with flag-leaf area in the irrigated condition. The relationship between grain yield and protein content was negative. Sugar content was negatively correlated with panicle length; however, it did not show any association with protein content. Nimbalkar (1988) observed significant positive correlation coefficients between grain yield per plant and panicle weight, panicle breadth, and 1000-kernel weight. Raut et al. (1992) observed that among 20 sorghum genotypes, the number of leaves per plant and panicle weight were positively and significantly associated with yield. Veerbadhiran et al. (1994) noticed that grain yield was positively correlated with the number of days to 50% flowering and panicle weight. Sankarapandian et al. (1996) found no correlation of grain yield with most of the component characters except 1000-kernel weight and the number of kernels per rachis that might be because of elimination effects of one or other characters contributing for grain yield in *rabi* sorghum. Jeyaprakash et al. (1997) reported grain yield was significantly and positively correlated with panicle weight, panicle length, and dry fodder yield, and plant height had a positive significant association with grain yield.

Taurchi and Rezai (1997) observed that plant height, panicle length, and 100-kernel weight were significantly positively correlated with grain yield. Can et al. (1998) found that harvest index and its components were positively correlated with grain yield and suggested that harvest index could be used as a selection criterion for high yield and short-plant genotypes. Iyanar et al. (2001) analyzed correlations of 54 genotypes of sorghum and reported that grain yield was significantly and positively correlated with panicle weight and length. Sunku et al. (2002) reported that correlations were significant and high among yield of dry matter, content of dry matter, yield of green fodder, plant height, number of leaves, leaf length, and leaf width in grain sorghum. Tiwari et al. (2003) noticed that panicle length was an important trait contributing to yield because it was significantly positively correlated with grain yield. Ezeaku and Mohammed (2006) revealed significant and positive correlation between grain yield and panicle weight, grain yield and 1000-kernel weight, and 1000-kernel weight and panicle weight, and similarly, significant but negative correlation between the number of panicles and panicle length. Plant height had high positive phenotypic and genotypic correlation coefficients with panicle weight and grain yield in sorghum. Makanda et al. (2010) observed that grain yield was positively and significantly correlated with panicle length and the number of leaves per plant, suggesting improvement in grain yield potential as the number of leaves and panicle size increased. Prakash et al. (2010) reported that yield of green fodder per plant was significantly and positively correlated with plant height, number of tillers, leaf length, leaf breadth, stalk diameter, hydrocyanic acid content, and crude fiber. The number of days to 50% flowering, crude protein, and in vitro dry matter digestibility were negatively associated with the yield of green fodder per sorghum plant. Warkad et

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al. (2010) found that only one character, 1000-kernel weight, was significantly correlated with grain yield per plant at and among the yield components themselves. The number of days to 50% flowering was significantly positively associated with the number of days to maturity, plant height, dry fodder weight per plant, and number of leaves per plant. Chavan et al. (2011) reported improvement in component traits including panicle length, number of grains per panicle, panicle width, test weight (a measure of bulk density, or the weight of a specified volume of sorghum), number of primary branches per panicle, and harvest index through simple selection methods in sorghum, and the traits had positive and significant association with grain yield per panicle. Mahajan et al. (2011) stated that grain yield per panicle showed positive significant correlation with panicle length, panicle width, plant height, branches per panicle, grains per panicle, test weight, and harvest index in sorghum.

**Harvest Index**

Harvest index is defined as the ratio of grain yield to dry matter yield (Donald, 1962) or total biomass. Gardner and Gardner (1983) argued that as plants increased in size, a larger portion of the dry matter was grain. Prihar and Stewart (1990) presented evidence from the literature showing that harvest index was independent of the size of mature plants and in some cases, harvest index was observed to increase with decrease in plant size.

Crop simulation models are difficult to develop and often deficient in their predictions of grain growth. Hammer and Muchow (1994) developed a crop model for sorghum that accounted for 94% of the variation in total biomass, but only 64% of the

variation in grain yield when tested using data sets from a broad range of environments. The harvest index approach used a linear increase in harvest index with time from shortly after anthesis until two-thirds of the time between anthesis and physiological maturity had elapsed or a maximum harvest index of 0.55 had been reached (Hammer and Muchow, 1994). Hammer and Broad (2003) studied different maturity sorghum hybrids with contrasting phenology (early, medium, and late) and found that grain yield varied from 4,700 to 9,400 kg ha$^{-1}$. There was large and significant variation in yield among experiments, despite all being grown under non-limiting water and nutrient conditions. Grain yield is the product of total biomass and harvest index. Hammer and Broad (2003) found large yields were associated with great biomass production (14.3-17.6 t ha$^{-1}$) and harvest index (0.47-0.57). The harvest index values were close to the maximum harvest index of 0.55 reported as reflecting the genetic potential of most current sorghum hybrids (Hammer and Muchow, 1994). Hammer and Broad (2003) reported low yield associated with low biomass production (10.3 and 13.3 t ha$^{-1}$) and lower values of harvest index (0.42-0.46) that also contributed to substantially less yield. Hammer and Broad (2003) found differences in grain yield manifested through the difference in total biomass and harvest index; differences in total biomass and yield at maturity can be explained by differences in assimilation during grain-filling which was associated with greater incident radiation, warmer temperature, and slightly greater leaf area index. This reflected the enhanced amounts of light interception and growth between initiation and anthesis, which is known to influence kernel number in sorghum (Rosenthal et al., 1989) and other cereals (Fisher, 1985; Hammer and Broad, 1994).

Harvest index had a negative correlation with plant height and a positive correlation with grain yield, both phenotypically and genotypically (Can and Yoshida, 1999). Mohammad et. al. (1993) studied 54 genotypes of sorghum and found greater forage yield was associated with tallness, late maturity, greater tiller retention, and greater stover yield, but low crude protein and harvest index. High grain yield was associated with high harvest index, greater kernel number and size, but short height while crude protein was associated with high harvest index and short height; however, late maturity and taller plant height were associated with high harvest index (Mohammad et al., 1993). Performance of sorghum under rainfed conditions was significantly associated with retention of green leaf area, plant height, and maturity (Habyarimana et al., 2004). Like harvest index, green fodder and dry matter yield varied by cultivar (Gampawar et al., 2002). Also, grain yield and physiological traits related to development and vegetative growth were significantly negatively correlated in genotypes of *S. bicolor* (Soltani et al., 2001). However, there were significant positive correlations for growth rate, grain filling rate, and harvest index. According to Briggs and Knowles (1967), the heritability of quantitative characters was usually high, because breeding behavior could be predicted. High heritability coupled with genetic advance indicated that additive gene effects were operating, and selection for superior genotype was possible (Arunkumar et al., 2004). In addition to correlation and heritability, knowledge of genetic variability among different parameters contributing to yield was an important criterion for yield enhancement. Khan et al. (2005) observed that estimates of genetic variance were smaller than the respective phenotypic variance. Harvest index might be affected by environment and cultivar (Phihar and Stewart, 1991).

# Chapter III

# Materials and Methods

## Germplasm

The study used sorghum conversion materials selected from extremes, high or low percentage of genome recovery, from $F_{2:3}$ and $BC_1 F_{2:3}$ progeny to determine combining ability for early testing. The experiments consisted of 44 parents (four female testers and four male lines in each of the 10 Reinstated Sorghum Conversion (RSC) families which produced 160 $F_1$ hybrids. It will determine yield potential based on converted lines and whether a relationship between combining ability and yield exists between various sorghum conversion populations and progeny.

In 2009-2011, populations from the RSC collections were developed at Puerto Vallarta, Mexico (a short-day sorghum nursery), under the direction of Dr. Fred Miller, using standard techniques to emasculate by hand, selected sorghum accessions and B.Tx406 as the female parent (Klein et al., 2016). The $F_1$ plants were self-pollinated at Puerto Vallarta, resulting in $F_2$ populations. Phenotypic self-pollinated selections were made based on plant height (<75 cm) and early flowering (<65 days) from the $F_2$ populations grown at Richardson Seeds LTD at Vega, TX. Twenty selections of early-maturing, dwarf $F_2$ progeny from each cross were genotyped with restriction-site-associated DNA sequencing technology developed by Morishige et al. (2013) and subsequently reported by Klein et al. (2013, 2016). Sorghum selections were grown at

USDA-ARS at College Station, TX, and seedling tissue was collected and evaluated via Illumina by Dr. Bob Klein.

Single nucleotide polymorphism (SNPs) across all 10 chromosomes was examined to identify $F_2$ descendants that recovered the greatest percentage of the tropical (exotic) parental genome and showed the least linkage disequilibrium (linkage drag) around loci under intense selection pressure (height and flowering time) (Klein et al., 2016). The $F_2$ progeny that showed the high percentage of whole-genome SNPs from the exotic parent were classified as having the high percentage of the tropical genome, and one genomic and phenotypically chosen $F_2$ descendant from each population was advanced by backcrossing to the tropical introduction parent.

The resulting $BC_1F_1$ was grown, self-pollinated, and subjected to the same rigorous phenotypic selection process. The resulting $BC_1F_2$ was grown, subjected to the same phenotypic and genomic selection processes to identify part of the whole based on the high or low percentage of exotic genome recovery. One $BC_1F_2$ plant from each population that showed the high proportion of the tropical genome was identified as described previously and self-pollinated. Grain from each of the $F_{2:3}$ and $BC_1F_{2:3}$ progeny rows were bulked for distribution and made available for the study. Table 1 shows the selected taxonomic groups based on the high or low percentage of genomic recovery in this study, along with the country of origin, sorghum race, and working group. The exotic male parent lines included several race and working group combinations; however, not all taxonomic classes were represented.

Table 1. Sorghum from the Reinstated Sorghum Conversion Program (RSC) with country of origin, race, working group, and percentage of exotic genome recovery value.

| | Classification | | | % Recovery | | |
|---|---|---|---|---|---|---|
| RSC | Country of origin | Race | Working group | RSC | Recovery | Value |
| | | | | 73 | $F_2$ High | 0.489 |
| | | | | 73 | $BC_1F_2$ High | 0.660 |
| | | | | 73 | $F_2$ Low | 0.171 |
| RSC73-0 | Sudan | C | C | 73 | $BC_1F_2$ Low | 0.530 |
| | | | | 83 | $F_2$ High | 0.468 |
| | | | | 83 | $BC_1F_2$ High | 0.650 |
| | | | | 83 | $F_2$ Low | 0.116 |
| RSC83-0 | Sudan | C | C | 83 | $BC_1F_2$ Low | 0.550 |
| | | | | 112 | $F_2$ High | 0.464 |
| | | | | 112 | $BC_1F_2$ High | 0.720 |
| | | | | 112 | $F_2$ Low | 0.111 |
| RSC112-0 | Ethiopia | D | Nandyal | 112 | $BC_1F_2$ Low | 0.470 |
| | | | | 76 | $F_2$ High | 0.463 |
| | | | | 76 | $BC_1F_2$ High | 0.840 |
| | | | | 76 | $F_2$ Low | 0.113 |
| RSC76-0 | Sudan | CD | CD | 76 | $BC_1F_2$ Low | 0.690 |
| | | | | 38 | $F_2$ High | 0.445 |
| | | | | 38 | $BC_1F_2$ High | 0.750 |
| | | | | 38 | $F_2$ Low | 0.178 |
| RSC38-0 | Mali | DB | D-B | 38 | $BC_1F_2$ Low | 0.590 |
| | | | | 37 | $F_2$ High | 0.280 |
| | | | | 37 | $BC_1F_2$ High | 0.720 |
| | | | | 37 | $F_2$ Low | 0.160 |
| RSC37-0 | Sudan | C | C-Nigr | 37 | $BC_1F_2$ Low | 0.510 |
| | | | | 15 | $F_2$ High | 0.274 |
| | | | | 15 | $BC_1F_2$ High | 0.710 |
| | | | | 15 | $F_2$ Low | 0.081 |
| RSC15-0 | Sudan | CG | CG | 15 | $BC_1F_2$ Low | 0.530 |
| | | | | 124 | $F_2$ High | 0.261 |
| | | | | 124 | $BC_1F_2$ High | 0.710 |
| | | | | 124 | $F_2$ Low | 0.116 |
| RSC124-0 | Ethiopia | DK | D-K | 124 | $BC_1F_2$ Low | 0.480 |
| | | | | 117 | $F_2$ High | 0.257 |
| | | | | 117 | $BC_1F_2$ High | 0.680 |
| | | | | 117 | $F_2$ Low | 0.117 |
| RSC117-0 | Ethiopia | D | Nandyal | 117 | $BC_1F_2$ Low | 0.440 |
| | | | | 19 | $F_2$ High | 0.201 |
| | | | | 19 | $BC_1F_2$ High | 0.560 |
| | | | | 19 | $F_2$ Low | 0.083 |
| RSC19-0 | USA | B | C-Nigr | 19 | $BC_1F_2$ Low | 0.300 |

Two $F_{2:3}$ progeny and two $BC_1F_{2:3}$ progeny from the $F_2$ populations of 10 RSC families were chosen based on the extremes of high to low percentage of genome recovery of the exotic parent. The A- (female) and B- (maintainer) lines were provided by Richardson Seeds LTD., and all were kafir types, 301 a four-dwarf early maturing Wheatland Redlan derivative kafir-Martin, 319 a three-dwarf medium early maturity red kafir-kafir, Tx3197 a public three-dwarf medium maturity Std kafir (standard check), and 338 a three-dwarf medium late maturity kafir-modified (unique/elite females with great combining ability). Parental crosses between the selected lines from the Sorghum Conversion Program and the four elite females, previously referenced, were made in the summer of 2014 and 2015 at Vega, TX, and during the winter of 2014 at Bucerias, Mexico. To achieve good synchrony (best "nick") in flowering time of the male and female parents, all 44 parents were planted twice (15 days apart) in two-row plots (0.762 m spacing) 5.18 m long with 1.5 m borders at Vega, TX. Best agronomic practices were used across years for each location of the parental crossing. The panicles of female lines were bagged before stigmas were visible while unbagged RSC male parents were allowed to reach anthesis. For each combination of crosses, multiple panicles were pollinated to achieve an adequate quantity of kernels. Care was taken to use the most uniform $F_{2:3}$ and $BC_1F_{2:3}$ plants because of the heterozygous nature of the $F_2$ selections.

**Experimental Procedures - Evaluation in Field**

Research in the summers of 2015 and 2016 was at various locations (Table 2). In 2015, the 160 $F_1$ hybrids and four B-line parents corresponding to the A-line used in hybridization were evaluated at two locations, with two replications per location at Vega,

TX (latitude 35.12922 N, longitude -102.51716 E; 1241.9 m above sea level) on Pullman clay loam, and at Hutchinson, KS (latitude 38.13003 N, longitude -97.71266; 437.9 m above sea level) on Crete silt loam.

During the same summer, the 160 $F_1$ hybrids were planted at Taylor, TX (latitude 30.51867 N, longitude -97.49257 E; 189.1 m above sea level) on Branyon clay, and at Perryton, TX (latitude 36.32269 N, longitude -100.86301 E; 905.1 m above sea level) on Sherman clay loam (NRCS web soil survey) to evaluate and increase the environmental effect against commercial checks.  Two groups of commercial checks with three maturity classes in each group consisting of early maturity and low yield, medium maturity and medium yield, and late maturity and high yield were provided by Richardson Seeds, Inc. and used for the research.  In 2016, the same 160 $F_1$ hybrids, checks, and parents were planted at Vega and Dumas, TX (latitude 35.96557 N, longitude-l01.93120 E; 1092.8 m above sea level) on Sherm silty clay loam (NRCS web soil survey) while the $F_1$ hybrids and checks were planted only at Hutchinson, KS.  The sorghums, other than the checks, were grown in a completely randomized augmented spilt-block design with two replications at each location.  The hybrids were blocked by female and the RSC family with checks arranged into two groups represented in each female block.

Table 2. Agronomic, environmental, and soil characteristics during two years in seven environments used to grow $F_1$ sorghum hybrids and parents to measure combining ability and heterosis.

| Location | Soil type | Altitude -m- | Latitude -N- | Longitude -E- | Plot length -m- | Row spacing -m- | Date planted | Date harvested | Rainfall* -mm- |
|---|---|---|---|---|---|---|---|---|---|
| Vega Texas (2015) | Pullman clay loam | 1241.9 | 35.12923 | -102.51716 | 5.18 | 0.762 | 7 June | 4-5 November | 538.9 |
| Perryton Texas (2015) | Sherman clay loam | 905.1 | 36.32269 | -100.86301 | 7.92 | 0.762 | 3 June | NA | 940.8 |
| Hutchinson Kansas (2015) | Crete silt loam | 437.9 | 38.13003 | -97.71266 | 5.18 | 0.762 | 26-27 June | 7 November | 404.6 |
| Taylor Texas (2015) | Branyon clay | 189.1 | 30.51867 | -97.49257 | 5.18 | 0.762 | 1 April | 4 September | 538.7 |
| Vega Texas (2016) | Pullman clay loam | 1242.7 | 35.13222 | -102.52174 | 5.18 | 0.762 | 12 May | 17-18 October | 215.1 |
| Dumas Texas (2016) | Sherm silty clay loam | 1092.8 | 35.96557 | -101.93120 | 5.18 | 0.762 | 5-6 May | 13-14 October | 245.6 |
| Hutchinson Kansas (2016) | Crete silt loam | 437.9 | 38.13002 | -97.71265 | 5.18 | 0.762 | 17 June | 7 November | 746.5 |

*Rainfall is the amount from 1 January until harvest.

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At each location, an experimental unit was designated as two rows, with row length varying with location. Dependent upon location, the genotypes were evaluated for the following agronomic traits:

1. Days to mid-anthesis: number of days from the date of planting to the date when half the plants in a plot reached mid-anthesis.

2. Plant height: average distance in centimeters from the ground to the tip of the panicle at maturity.

3. Flag leaf height: average distance in centimeters from the ground to the flag leaf.

4. Panicle exsertion: distance in centimeters from the ligule of the flag leaf to the base of the lowest panicle branch at maturity.

5. Panicle length: distance in centimeters from the lowest panicle branch to the tip of the panicle at maturity.

6. 1000-kernel weight: weight of 1000 kernels, measured in grams, from grain samples of three panicles hand harvested per plot, before harvesting by a combine.

7. Grain yield: weight of grain harvested per plot, expressed in kilograms per hectare ($kg\ ha^{-1}$)

8. NIR was estimated by Dr. William Rooney at College Station/Bryan, TX, measuring grain protein, starch, fiber, and fat concentration (%), and moisture for calibration. Grain ash concentration was calculated but not analyzed.

**Harvest and Grain Yield**

In 2015 and 2016, the plots were harvested with an Allis-Chalmers Gleaner K2 combine harvester at Vega, Taylor, and Dumas, TX.  The plots at Hutchinson, KS, were harvested with a Kincaid 8XP using a Harvest master Classic Grain Gage for plot weight. The plot yield was converted to Mg ha$^{-1}$ after adjusting for 14% moisture, and a conversion factor based on row width and plot length was used, which differed across environments.  In some environments, not all traits could be evaluated.  Data on the number of days to anthesis were not collected at Perryton (2015), and no yield data were obtained because of the wet year.  Data on panicle height, exsertion, and length, and 1000-kernel weight were not collected at Hutchinson in 2015 and 2016 or Taylor in 2015. Data on total plant and flag leaf height, including panicle sampling for 1000-kernel weight were collected on both replications at Perryton and Vega in 2015 and at Dumas and Vega in 2016.  Numbers of days to anthesis were determined at Vega during both years.  Best agronomic practices were used at each location during both years.

**Three-panicle Weight and 1000-kernel Weight**

The three panicles harvested from each two-row plot were fully dried, threshed, weighed, and expressed to the nearest tenth of a gram.  A key-mat seed counter (Model 946, St. Charles, IL) was used to determine 1000-kernel weight to thousandths of a gram of the kernels from the same three panicles.

**Plant Height and Panicle Length**

Plant heights were measured for each plot by randomly selecting three uniform plants from the two rows in each plot at Vega and Perryton in 2015 and at Vega and

Dumas in 2016.  The length from the base of the plant to the tallest point of the tip of the panicle was measured, and the average of three plants was recorded per two-row plot. The heights to the flag leaf on the same three plants were measured from the base of the plant to the tallest point of the collar of the flag leaf.  Three uniform panicles were randomly selected and harvested by hand, and panicle length was measured from the tip to the base of each panicle and averaged.  Exsertion was extrapolated from the difference between the base of the panicle and the tip of the collar of the flag leaf and averaged for all three panicles.

**Near-infrared Spectroscopy**

Cereal grains are predominantly composed of carbohydrates, mostly in the form of starch, with considerable but variable amounts of protein as well as some lipids, vitamins, and minerals.  Genetic and environmental effects create significant variation in the amount and quality of each constituent.  Near-infrared spectroscopy (NIR) is widely applied in agriculture for determining the quality of forage, grain, grain products, and other products.  It is much used to quantify the composition of agricultural products because it meets the criteria of being accurate, reliable, rapid, non-destructive, and inexpensive (Burns, 2007).  Organic molecules have specific absorption patterns in the near-infrared region that can be used to estimate the chemical composition of the material being analyzed (Williams and Norris, 2001).  Bulk whole-grain samples can be evaluated rapidly, require no sample preparation, and preserve the kernels after measurement for further analysis or for propagation (Velasco et al., 1999; Baye and Becker, 2004).

## Statistical Analysis

The class of augmented experimental design was first introduced by Walter T. Federer in 1955 (Federer, 1961). An augmented experimental design is any standard design augmented with additional treatments in a complete or incomplete block. Mejza (1998) presented a class of split-block experimental designs wherein a check treatment represented one of the treatments for either or both of the two factors involved. The designs of Mejza had similarities to augmented experimental designs (Federer, 1993, 2002, 2004) and gave rise to a new class of augmented split-block experimental designs (Federer, 2004).

The sorghums, other than the checks, were grown in a completely randomized spilt-block design with two replications at each location. The hybrids were blocked by female and the RSC family, with checks arranged into two groups randomly represented in each female block. At each location, an experimental unit was designated as two rows, with row length varying with location (Table 2). In each environment, data were analyzed as a randomized complete block design with two replications per environment. Genotypes were considered fixed effects, while replications and environments were considered random effects.

The model used was $Y_{ijl} = \mu + e_l + r_{il} + g_j + (gl)_{jl} + e_{ijl}$

where $Y_{ijl}$ = value of the $ijl^{th}$ plot,

$\mu$ = grand mean,

$e_l$ = effect of l-th environment, $l = 1, 2, 3, 4, 5$

$r_{il}$ = effect of i-th replication at $l^{-th}$ environment, $i = 1, 2$

$g_j$ = effect of j-th genotype, $j$ = 1, 2, …, 211

$(ge)_{jl}$ = effect of interaction of $j^{-th}$ genotype with $l^{-th}$ environment

$e_{ijl}$ = error associated with the $ijl^{-th}$ observation

Variation due to genotype was partitioned into variation within hybrids, parental lines, and check hybrids. Contrasts were analyzed between hybrids, parents, RSC families, and selections by percentage of exotic genome recovery using highest and lowest $BC_1F_{2:3}$ and $F_{2:3}$ generations. The percentage of exotic genome recovery was previously calculated for each exotic parent in the Sorghum Conversion Program used in the study (Table 1). Analysis of variance (ANOVA) across environments and for individual environments was done using PROC GLM 2002-2012 by SAS Institute Inc., Cary, NC, using line x tester design by Singh and Chaudhary (1985). Contrasts were analyzed to evaluate differences in combining abilities and heterosis between lines, testers, RSC families, and the generation to aid sorghum breeders in early detection of potential new hybrids. Bartlett's test for heterogeneity of error variances assessed the validity of combining the data from individual environments for a combined analysis (Little and Hills, 1978; Steel and Torrie, 1980). Heterogeneous error variances were calculated for all traits evaluated in the seven environments. Because there were no egregious problems with the data, the data from individual environments were combined for analysis in addition to the individual analysis.

Evaluation of the materials for heterosis and combining ability should provide sorghum breeders the information necessary to determine the impact on early testing based on the proportion of genetic recovery. The additional benefit is to determine if

there is a difference between sorghum conversion populations and their combining ability and genetic recovery.  This will provide insight into early testing for sorghum breeders worldwide.

**Line x Tester Analysis**

The data recorded on the material generated as per the line x tester model of Kempthorne (1957) were subjected to analysis of variance as per the line x tester model by Singh and Chaudhary (1985).

**Combining Ability Analysis and Heterosis**

GCA effects of parents, SCA effects of $BC_1F_1$ and $F_1$ hybrids, the corresponding standard errors, and their mean squares were estimated using R Studio (R version 3.2.2 (2015-08-14) © 2015 The R Foundation for Statistical Computing Platform: x86_64_w64-mingw32/x64 (64 bit).  Percentage of heterosis of all hybrids over the mid-parental value (midparent heterosis) was calculated using the following formulas:

Midparent heterosis (MPH) = ($F_1$ – MP)/ MP x 100

Bestparent heterosis (BPH) = ($F_1$ – BP)/ BP x 100

Rex Bernardo formula for combining ability.

General Combining Ability was calculated as GCAi = (Yi - Y../ Y..) x 100

 GCAj = (Yj - Y../ Y..) x 100

Specific Combining Ability as SCAij = ((Yij - Yi. - Y.j + Y..)/ Y..) x 100

where Yi = mean of ith male

Yj = mean of jth female

Yij = mean of j x i hybrid

Y.. = mean of all hybrids

R-studio model for combining ability.

The additive model used to estimate GCA and SCA effects of the ijk observation follows:

$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$

where

$X_{ijk}$ = any character measured of the cross (i x j) in the kth replication

$\mu$ = population mean

$g_i$ = *gca* effect of ith line

$g_j$ = *gca* effect of jth tester

$s_{ij}$ = *sca* effect of (i x j)th cross

$e_{ijk}$ = error associated with observation $Y_{ijk}$

i = number of lines

j = number of testers

k = number of replications

The variances for GCA and SCA were tested against their respective error variances, derived from the analysis of variance of the different traits based on Fellahi et al. (2013):

Covariance of half-sib of line

= Cov.H.S.(line)

$= \dfrac{Ml - Ml \times t}{rt}$

Covariance of half-sib of tester

= Cov.H.S.(tester)

$= \dfrac{Mt - Ml \times t}{rl}$

Covariance of full sib

= Cov.F.S.

$$= \frac{(Ml - Me) + (Mt - Me) + (Ml{\times}t - Me)}{3r}$$
$$+ \frac{6r\text{Cov.H.S.} - r\,(l+t)\,\text{Cov.H.S.}}{3r}$$

while Cov. H.S. (average) was calculated by the formula

Cov. H.S. (average) = $1/r\,(2lt - l - t)\,[(l - 1)\,(Ml) + (t - 1)\,(Mt)/l + t - 2 - Ml{\times}t]$

Assuming no epistasis, variance caused by GCA ($\sigma 2$gca) and variance caused by SCA ($\sigma 2$sca) were calculated by:

$\sigma 2$ gca = Cov. H.S. = $(1 + F/4)\,\sigma 2A$

$\sigma 2$sca = $(1 + F/2)2D$

Additive and dominance genetic variance ($\sigma 2_A$ and $\sigma 2_D$) were calculated by taking inbreeding coefficient $F$ equal to 1; that is, F = 1 because both lines and testers were considered inbred (Fellahi et al., 2013). Significance for GCA and SCA effects were determined by using a *t*-test. Midparent heterosis was estimated from mean values, and its significance was determined using a *t*-test.

**Correlation Estimates**

Pearson's correlation coefficients between all the traits were estimated using SAS statistical software. Correlations were estimated separately for parents, for hybrids, and for all the genotypes combined. Correlations were also estimated between indices of heterosis – SCA and midparent heterosis.

# Chapter IV

# Results and Discussion

## Means of Genotypes

Means for the traits evaluated – number of days to anthesis, height to the flag leaf, total plant height, panicle exsertion, panicle length, three-panicle weight, 1000-kernel weight, and grain yield – varied across environments (Table 3).  The means are averages over the seven environments analyzed, barring a few traits for which data were not available in particular environments, as mentioned in the previous chapter.  The two high grain yield averages of 8.52 and 8.24 Mg ha$^{-1}$ were for the commercial check hybrids 304/5 and 319/54, respectively.  Testers included in the top 20 were A.319 with (seven) crosses, followed by A.301 (four), A.338 (two), and A.Tx3197 (one) crosses.  Lines in the top 20 were RSC83-1 $BC_1F_{2:3}$ selected as the low percentage of exotic genome recovered (low), followed by RSC83-14 $BC_1F_{2:3}$ that appeared twice and was selected as the high percentage of exotic genome recovered (high).  RSC117-4 $BC_1F_{2:3}$ and RSC112-9 $BC_1F_{2:3}$ also appeared twice, and both were selected for high percentage of exotic genome recovery (high).  The hybrids required slightly fewer mean days to anthesis (74.3) compared to lines (76.3) and testers (74.5), but slightly more than checks (72.5).

Table 3. Means for 12 traits of 160 sorghum hybrids, 44 parental lines, and seven hybrid checks ranked by yield in seven environments - Vega, Perryton, and Taylor, TX, and Hutchinson, KS, in 2015, and Vega and Dumas, TX, and Hutchinson, KS, in 2016.

| Yield rank | Genotype | Grain yield (Mg ha⁻¹) | DTF | Flag leaf height (cm) | Total height (cm) | Panicle length (cm) | Exs† (cm) | 3-panicle weight (g) | 1000-kernel weight (g) | Fat (%) | Fiber (%) | Protein (%) | Starch (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 304/5 | 8.52 | 75.0 | 97.9 | 140.6 | 30.4 | 12.2 | 214.0 | 27.8 | 3.20 | 1.82 | 8.20 | 68.62 |
| 2 | 319/54 | 8.24 | 68.9 | 93.6 | 132.8 | 29.7 | 9.5 | 207.6 | 24.1 | 2.91 | 1.85 | 8.22 | 69.03 |
| 3 | A.319*((RSC83)RSC83)-1 | 8.21 | 72.2 | 121.8 | 153.0 | 23.3 | 7.9 | 191.9 | 26.5 | 2.80 | 1.78 | 8.94 | 67.68 |
| 4 | 302/29 | 8.17 | 71.5 | 85.6 | 127.4 | 30.7 | 11.0 | 176.7 | 28.6 | 3.03 | 1.82 | 8.62 | 69.62 |
| 5 | A.338*((RSC117)RSC117)-4 | 8.06 | 75.8 | 104.6 | 135.8 | 26.8 | 4.4 | 195.1 | 33.4 | 3.12 | 1.82 | 8.80 | 68.39 |
| 6 | 338/4 | 7.66 | 74.3 | 111.4 | 146.6 | 26.8 | 8.5 | 208.2 | 30.5 | 3.40 | 1.90 | 9.07 | 68.47 |
| 7 | 319/22 | 7.52 | 69.7 | 87.1 | 130.1 | 29.9 | 13.1 | 159.2 | 22.9 | 2.06 | 1.78 | 7.73 | 68.83 |
| 8 | A.301*((RSC83)RSC83)-14 | 7.47 | 67.3 | 98.9 | 127.5 | 23.4 | 5.2 | 182.3 | 29.1 | 2.29 | 1.77 | 8.76 | 68.02 |
| 9 | 301/41 | 7.39 | 67.0 | 85.6 | 120.7 | 27.8 | 7.3 | 153.5 | 25.4 | 1.80 | 1.70 | 8.08 | 68.80 |
| 10 | A.319*((RSC19)RSC19)-10 | 7.35 | 71.3 | 150.9 | 185.0 | 24.4 | 9.7 | 188.1 | 25.2 | 2.82 | 1.81 | 9.18 | 67.81 |
| 11 | A.301*((RSC112)RSC112)-19 | 7.22 | 71.2 | 82.0 | 116.1 | 27.6 | 6.5 | 167.9 | 28.0 | 2.75 | 1.86 | 9.24 | 68.03 |
| 12 | A.319*((RSC83)RSC83)-14 | 7.21 | 72.0 | 131.1 | 160.0 | 25.5 | 3.5 | 232.8 | 25.7 | 2.64 | 1.76 | 8.88 | 67.85 |
| 13 | A.319*((RSC117)RSC117)-4 | 7.16 | 73.0 | 87.6 | 120.7 | 29.6 | 3.5 | 168.5 | 29.3 | 3.09 | 1.84 | 8.83 | 68.64 |
| 14 | A.301*((RSC19)RSC19)-10 | 7.14 | 68.3 | 102.4 | 136.5 | 25.5 | 8.6 | 187.4 | 26.0 | 2.36 | 1.79 | 8.56 | 68.36 |
| 15 | A.319*((RSC112)RSC112)-19 | 7.10 | 72.2 | 96.8 | 131.9 | 25.6 | 9.5 | 184.1 | 27.3 | 2.99 | 1.80 | 8.49 | 68.38 |
| 16 | A.Tx3197*(RSC112)-5 | 7.00 | 71.3 | 119.2 | 160.8 | 27.6 | 14.0 | 188.6 | 29.2 | 2.36 | 1.61 | 8.22 | 69.13 |
| 17 | A.301*((RSC37)RSC37)-12 | 6.99 | 67.7 | 117.5 | 149.7 | 22.7 | 9.5 | 195.0 | 29.5 | 2.55 | 1.88 | 9.27 | 67.22 |
| 18 | A.338*(RSC117)-2 | 6.91 | 77.0 | 114.4 | 146.5 | 26.9 | 5.1 | 177.9 | 27.5 | 2.84 | 1.76 | 8.32 | 68.65 |
| 19 | A.319*((RSC37)RSC37)-8 | 6.87 | 70.5 | 125.6 | 162.1 | 28.1 | 8.5 | 204.9 | 22.0 | 2.60 | 1.85 | 8.52 | 67.73 |
| 20 | A.319*(RSC37)-12 | 6.86 | 74.0 | 135.5 | 169.8 | 24.3 | 10.1 | 207.4 | 26.2 | 3.01 | 1.77 | 9.27 | 67.39 |
| 21 | A.301*((RSC37)RSC37)-8 | 6.81 | 65.2 | 87.6 | 123.8 | 23.5 | 12.7 | 150.4 | 26.2 | 2.43 | 1.87 | 8.65 | 67.86 |
| 22 | A.301*((RSC19)RSC19)-17 | 6.81 | 67.5 | 120.3 | 152.9 | 25.7 | 6.9 | 183.4 | 27.4 | 3.01 | 1.82 | 9.81 | 67.21 |
| 23 | A.Tx3197*((RSC117)RSC117)-4 | 6.80 | 69.0 | 90.1 | 128.4 | 29.1 | 9.1 | 199.7 | 34.1 | 2.98 | 1.72 | 8.75 | 68.62 |
| 24 | A.319*((RSC37)RSC37)-12 | 6.79 | 71.0 | 126.7 | 158.9 | 26.0 | 6.2 | 231.3 | 24.3 | 2.74 | 1.89 | 9.10 | 67.53 |
| 25 | A.338*((RSC117)RSC117)-3 | 6.72 | 79.0 | 106.8 | 137.4 | 25.3 | 5.4 | 172.3 | 31.5 | 2.93 | 1.74 | 8.59 | 68.42 |
| 26 | A.301*(RSC112)-5 | 6.70 | 71.0 | 95.7 | 132.4 | 28.1 | 8.6 | 228.7 | 27.1 | 2.55 | 1.77 | 8.11 | 68.71 |
| 27 | A.Tx3197*(RSC124)-9 | 6.69 | 70.2 | 91.3 | 128.3 | 29.1 | 7.9 | 165.4 | 24.9 | 2.40 | 1.65 | 8.33 | 68.66 |
| 28 | A.338*((RSC83)RSC83)-14 | 6.66 | 75.7 | 153.1 | 185.3 | 22.6 | 9.6 | 217.8 | 30.0 | 2.69 | 1.69 | 8.79 | 67.99 |
| 29 | A.Tx3197*((RSC112)RSC112)-19 | 6.66 | 70.8 | 110.5 | 146.5 | 25.2 | 10.8 | 191.0 | 29.2 | 2.64 | 1.61 | 7.89 | 69.59 |

| 30 | A.301*((RSC124)RSC83RSC124)-16 | 6.62 | 72.2 | 88.7 | 128.0 | 28.3 | 11.1 | 199.6 | 25.9 | 2.57 | 1.77 | 8.09 | 68.49 |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 31 | A.Tx3197*((RSC83)RSC83)-1 | 6.61 | 69.5 | 142.8 | 175.4 | 23.1 | 9.5 | 216.1 | 31.6 | 2.59 | 1.73 | 8.73 | 67.94 |
| 32 | A.301*((RSC76)RSC76)-2 | 6.59 | 71.2 | 145.9 | 175.3 | 22.5 | 6.9 | 221.9 | 37.1 | 1.76 | 1.72 | 7.33 | 69.56 |
| 33 | A.301*((RSC83)RSC83)-1 | 6.57 | 66.7 | 97.4 | 127.7 | 22.3 | 7.9 | 163.4 | 30.7 | 2.17 | 1.76 | 8.63 | 68.38 |
| 34 | A.Tx3197**((RSC112)RSC112)-15 | 6.53 | 70.5 | 105.7 | 144.6 | 27.1 | 11.9 | 190.7 | 29.1 | 2.64 | 1.63 | 8.29 | 69.01 |
| 35 | A.319*(RSC73)-9 | 6.52 | 70.5 | 122.6 | 159.4 | 25.0 | 11.8 | 171.2 | 24.0 | 2.98 | 1.78 | 8.53 | 67.96 |
| 36 | A.338**((RSC112)RSC112)-15 | 6.51 | 77.2 | 123.3 | 160.4 | 25.2 | 12.0 | 234.5 | 27.7 | 3.12 | 1.75 | 8.54 | 68.04 |
| 37 | A.319*(RSC124)-9 | 6.50 | 69.2 | 87.5 | 126.8 | 30.8 | 8.5 | 149.8 | 23.5 | 2.51 | 1.76 | 8.27 | 68.42 |
| 38 | B.Tx3197 | 6.49 | 70.7 | 86.4 | 112.3 | 23.8 | 2.2 | 128.6 | 27.9 | 2.39 | 1.72 | 7.84 | 69.51 |
| 39 | (RSC19)-12 | 6.48 | 71.8 | 59.6 | 94.7 | 22.3 | 12.8 | 129.2 | 22.0 | 2.89 | 1.86 | 9.71 | 67.13 |
| 40 | A.319*(RSC112)-5 | 6.45 | 72.3 | 106.8 | 144.6 | 28.2 | 9.6 | 191.3 | 28.0 | 2.63 | 1.75 | 7.96 | 68.75 |
| 41 | A.319*((RSC73)RSC73)-6 | 6.41 | 71.2 | 117.6 | 149.6 | 23.4 | 8.6 | 156.5 | 23.6 | 2.80 | 1.76 | 8.56 | 67.87 |
| 42 | A.301*((RSC124)(RSC124)-4 | 6.41 | 69.5 | 82.8 | 113.5 | 25.7 | 4.9 | 180.6 | 27.9 | 2.37 | 1.74 | 8.90 | 68.04 |
| 43 | A.319*((RSC117)RSC117)-3 | 6.39 | 72.2 | 73.1 | 113.5 | 28.2 | 12.2 | 212.6 | 25.6 | 2.99 | 1.76 | 8.75 | 68.58 |
| 44 | A.319*(RSC38)-5 | 6.35 | 72.0 | 82.8 | 121.4 | 31.2 | 7.4 | 160.8 | 20.8 | 2.90 | 1.74 | 9.04 | 67.49 |
| 45 | A.301*(RSC124)-9 | 6.34 | 68.0 | 71.8 | 109.0 | 28.6 | 8.6 | 159.0 | 27.6 | 2.25 | 1.74 | 8.84 | 68.13 |
| 46 | A.Tx3197*((RSC124)RSC124)-16 | 6.30 | 70.5 | 131.9 | 168.2 | 27.1 | 9.2 | 193.8 | 25.6 | 2.36 | 1.56 | 8.24 | 68.91 |
| 47 | A.338*(RSC124)-9 | 6.30 | 78.5 | 108.2 | 139.1 | 25.9 | 4.9 | 182.7 | 26.6 | 2.67 | 1.68 | 8.62 | 67.99 |
| 48 | A.301*((RSC73)RSC73)-5 | 6.28 | 66.2 | 113.2 | 146.8 | 22.1 | 11.5 | 185.6 | 30.9 | 2.01 | 1.76 | 8.05 | 68.59 |
| 49 | B.MMR338 | 6.23 | 78.0 | 99.5 | 128.6 | 22.0 | 7.1 | 153.7 | 25.4 | 2.88 | 1.83 | 8.40 | 68.74 |
| 50 | A.301*((RSC38)RSC38)-15 | 6.23 | 65.0 | 116.1 | 143.4 | 23.3 | 4.0 | 179.5 | 28.1 | 2.76 | 1.76 | 9.27 | 67.20 |
| 51 | A.319*(RSC117)-2 | 6.22 | 71.2 | 81.0 | 115.0 | 28.5 | 5.5 | 168.8 | 23.9 | 2.89 | 1.83 | 8.41 | 68.73 |
| 52 | A.319*((RSC124)RSC124)-16 | 6.21 | 72.0 | 122.8 | 163.5 | 28.8 | 11.8 | 224.1 | 25.4 | 2.55 | 1.74 | 7.93 | 68.61 |
| 53 | A.338*((RSC112)RSC112)-19 | 6.20 | 75.5 | 128.0 | 157.8 | 24.5 | 5.3 | 188.1 | 25.7 | 3.13 | 1.70 | 8.44 | 68.19 |
| 54 | (RSC124)-9(RSC124)-4 | 6.20 | 83.2 | 86.9 | 127.4 | 26.6 | 13.9 | 119.6 | 22.8 | 2.84 | 1.66 | 9.08 | 67.63 |
| 55 | A.Tx3197*((RSC15)RSC15)-15 | 6.19 | 67.8 | 99.2 | 141.5 | 27.8 | 14.6 | 159.6 | 28.8 | 3.02 | 1.73 | 9.55 | 68.47 |
| 56 | A.301*(RSC73)-9 | 6.19 | 65.8 | 94.2 | 127.1 | 23.5 | 9.4 | 113.0 | 24.8 | 2.59 | 1.78 | 8.62 | 67.82 |
| 57 | A.Tx3197*((RSC83)RSC83)-14 | 6.18 | 69.0 | 139.1 | 166.5 | 23.1 | 4.3 | 228.9 | 30.3 | 2.64 | 1.68 | 8.41 | 68.21 |
| 58 | A.319*(RSC37)-7 | 6.18 | 71.7 | 138.8 | 178.7 | 25.4 | 14.5 | 208.3 | 25.0 | 2.79 | 1.80 | 8.55 | 67.73 |
| 59 | A.319*(RSC83)-1 | 6.17 | 72.7 | 123.6 | 158.3 | 26.5 | 8.2 | 160.0 | 27.0 | 2.56 | 1.79 | 8.60 | 68.10 |
| 60 | A.301*((RSC73)RSC73)-6 | 6.16 | 65.8 | 95.4 | 128.0 | 22.8 | 9.9 | 164.0 | 26.4 | 2.46 | 1.77 | 8.50 | 68.04 |
| 61 | A.301*((RSC117)RSC117)-4 | 6.16 | 67.5 | 69.5 | 102.6 | 29.1 | 4.0 | 179.7 | 29.9 | 2.73 | 1.89 | 9.46 | 68.40 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 62 | A.301*(RSC19)-3 | 6.15 | 65.5 | 93.4 | 136.9 | 26.9 | 16.5 | 155.2 | 25.3 | 2.67 | 1.86 | 9.36 | 67.64 |
| 63 | A.301*((RSC112)RSC112)-15 | 6.14 | 66.7 | 70.2 | 103.8 | 25.8 | 7.7 | 184.4 | 31.1 | 2.79 | 1.84 | 9.36 | 67.81 |
| 64 | A.Tx3197*(RSC73)-9 | 6.13 | 67.7 | 134.2 | 170.5 | 22.4 | 13.8 | 153.1 | 28.6 | 2.75 | 1.74 | 7.87 | 68.02 |
| 65 | (RSC112)-5(RSC112)-15 | 6.12 | 74.0 | 91.4 | 130.5 | 26.5 | 12.6 | 124.5 | 29.4 | 2.50 | 1.76 | 9.17 | 68.34 |
| 66 | (RSC19)-8(RSC19)-7 | 6.12 | 68.8 | 133.1 | 169.0 | 24.8 | 11.2 | 126.7 | 21.6 | 2.91 | 1.68 | 9.56 | 68.34 |
| 67 | A.301*(RSC15)-13 | 6.12 | 65.5 | 113.2 | 144.5 | 22.4 | 9.0 | 122.6 | 29.1 | 2.90 | 1.77 | 9.90 | 68.30 |
| 68 | A.301*(RSC76)-4 | 6.11 | 68.3 | 140.6 | 167.3 | 20.5 | 6.2 | 198.3 | 37.0 | 1.78 | 1.67 | 7.73 | 69.05 |
| 69 | A.319**((RSC112)RSC112)-15 | 6.10 | 71.3 | 96.1 | 134.5 | 27.5 | 10.9 | 164.7 | 27.8 | 2.81 | 1.82 | 8.61 | 68.45 |
| 70 | A.338*((RSC83)RSC83)-1 | 6.09 | 76.2 | 154.7 | 185.4 | 21.1 | 9.6 | 218.1 | 29.2 | 2.50 | 1.75 | 8.28 | 68.37 |
| 71 | A.301*((RSC117)RSC117)-3 | 6.09 | 68.3 | 91.0 | 127.2 | 26.3 | 10.0 | 160.6 | 29.3 | 2.87 | 1.86 | 9.81 | 67.56 |
| 72 | A.301*(RSC117)-2 | 6.06 | 66.3 | 71.7 | 104.1 | 29.0 | 3.4 | 164.7 | 27.8 | 2.37 | 1.82 | 8.96 | 68.55 |
| 73 | A.338*(RSC83)-10-10 | 6.06 | 76.5 | 110.1 | 144.9 | 24.5 | 10.3 | 163.6 | 28.9 | 3.07 | 1.82 | 9.11 | 67.65 |
| 74 | A.Tx3197*((RSC124)RSC124)-4 | 6.06 | 70.5 | 104.9 | 138.4 | 24.8 | 8.8 | 150.0 | 26.5 | 2.46 | 1.67 | 8.05 | 68.67 |
| 75 | A.319*(RSC117)-10-10 | 6.04 | 71.3 | 74.7 | 115.4 | 27.7 | 13.1 | 164.9 | 23.0 | 2.89 | 1.76 | 8.82 | 67.92 |
| 76 | A.301*((RSC76)RSC76)-16 | 6.03 | 71.3 | 141.3 | 173.6 | 21.7 | 10.7 | 213.4 | 37.2 | 1.80 | 1.73 | 7.76 | 69.37 |
| 77 | (RSC37)-2(RSC37)-12 | 6.01 | 77.0 | 94.4 | 117.1 | 24.3 | -1.6 | 124.2 | 25.0 | 2.30 | 1.78 | 8.32 | 67.81 |
| 78 | A.338*(RSC112)-5 | 6.00 | 73.3 | 103.3 | 140.1 | 23.1 | 13.7 | 159.4 | 32.2 | 2.68 | 1.78 | 8.37 | 68.34 |
| 79 | A.338*(RSC83)-1 | 5.99 | 76.0 | 163.8 | 194.5 | 22.7 | 8.0 | 224.4 | 30.2 | 2.55 | 1.73 | 8.31 | 68.13 |
| 80 | B.MMR319 | 5.99 | 68.7 | 70.7 | 104.3 | 26.0 | 7.6 | 132.3 | 20.8 | 2.41 | 1.96 | 8.20 | 68.80 |
| 81 | A.319*((RSC73)RSC73)-5 | 5.99 | 74.7 | 154.5 | 189.8 | 23.7 | 11.6 | 163.6 | 27.7 | 2.31 | 1.79 | 8.13 | 68.40 |
| 82 | A.338*((RSC37)RSC37)-8 | 5.98 | 75.7 | 165.8 | 194.6 | 23.2 | 5.6 | 248.6 | 25.2 | 2.68 | 1.82 | 8.25 | 68.02 |
| 83 | A.338*(RSC19)-3 | 5.97 | 74.8 | 141.2 | 184.7 | 26.4 | 17.2 | 211.4 | 28.4 | 2.73 | 1.81 | 8.89 | 67.71 |
| 84 | A.319*((RSC124)RSC124)-4 | 5.95 | 76.3 | 92.5 | 131.1 | 28.8 | 9.8 | 155.1 | 21.6 | 2.55 | 1.81 | 8.27 | 68.45 |
| 85 | A.301*(RSC38)-8 | 5.91 | 65.3 | 93.6 | 130.1 | 22.3 | 14.3 | 152.6 | 28.2 | 2.23 | 1.69 | 8.40 | 68.59 |
| 86 | A.319*((RSC76)RSC76)-16 | 5.90 | 74.0 | 174.7 | 212.5 | 23.9 | 13.9 | 262.4 | 33.1 | 2.26 | 1.79 | 8.29 | 68.49 |
| 87 | A.338*((RSC124)RSC124)-4 | 5.90 | 76.0 | 155.9 | 190.9 | 23.8 | 11.2 | 162.7 | 28.4 | 2.72 | 1.73 | 8.71 | 68.13 |
| 88 | A.319*(RSC15)-11 | 5.89 | 72.0 | 134.3 | 174.8 | 26.4 | 14.1 | 138.7 | 23.3 | 3.21 | 1.86 | 9.25 | 68.49 |
| 89 | A.301*(RSC83)-1 | 5.89 | 67.5 | 96.2 | 123.3 | 22.6 | 4.5 | 149.4 | 28.0 | 2.21 | 1.79 | 8.70 | 68.26 |
| 90 | A.301*(RSC37)-12 | 5.88 | 64.0 | 82.0 | 117.9 | 25.4 | 10.5 | 152.4 | 27.2 | 2.62 | 1.82 | 9.00 | 67.51 |
| 91 | (RSC76)-4(RSC76)-2 | 5.87 | 81.2 | 149.0 | 175.8 | 20.0 | 6.8 | 184.7 | 34.8 | 1.41 | 1.57 | 7.38 | 70.42 |
| 92 | A.319*(RSC38)-8 | 5.87 | 70.2 | 138.2 | 172.9 | 24.5 | 10.1 | 207.7 | 25.7 | 2.71 | 1.77 | 8.19 | 68.29 |

| # | Entry | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 93 | A.Tx3197*((RSC37)RSC37)-12 | 5.86 | 68.8 | 151.8 | 189.7 | 23.6 | 14.2 | 208.9 | 28.7 | 2.68 | 1.76 | 7.65 | 68.12 |
| 94 | A.338*((RSC124)-RSC124)-16 | 5.82 | 76.5 | 163.8 | 200.1 | 27.1 | 9.1 | 233.5 | 28.6 | 2.83 | 1.70 | 8.21 | 68.28 |
| 95 | A.319*(RSC124)-3 | 5.81 | 69.2 | 102.2 | 144.4 | 30.0 | 12.2 | 139.6 | 24.9 | 2.52 | 1.78 | 8.96 | 68.16 |
| 96 | A.338*(RSC117)-10 | 5.78 | 76.0 | 97.2 | 131.5 | 25.7 | 8.6 | 185.0 | 27.3 | 2.75 | 1.72 | 8.42 | 68.31 |
| 97 | (RSC19)-8(RSC19)-10 | 5.78 | 76.3 | 122.1 | 154.7 | 22.6 | 10.0 | 109.6 | 18.8 | 2.16 | 1.73 | 8.98 | 68.83 |
| 98 | A.319*(RSC19)-12-1 | 5.77 | 74.3 | 75.6 | 112.6 | 27.8 | 9.2 | 140.9 | 20.9 | 2.96 | 1.86 | 8.91 | 67.96 |
| 99 | A.Tx3197*(RSC112)-8 | 5.75 | 70.8 | 92.9 | 130.2 | 24.4 | 13.0 | 146.9 | 29.1 | 2.02 | 1.62 | 7.89 | 69.50 |
| 100 | (RSC117)-2(RSC117)-4 | 5.72 | 75.5 | 80.3 | 104.6 | 28.0 | -3.6 | 143.0 | 35.2 | 3.12 | 1.86 | 10.07 | 67.95 |
| 101* | A.338*(RSC37)-12 | 5.72 | 71.5 | 129.8 | 166.0 | 23.8 | 12.3 | 175.7 | 26.2 | 2.73 | 1.85 | 8.56 | 67.83 |
| 102 | A.301*((RSC15)RSC15)-15 | 5.72 | 66.7 | 78.2 | 113.6 | 26.8 | 8.6 | 150.8 | 27.7 | 2.83 | 1.84 | 10.00 | 68.25 |
| 103 | A.Tx3197*((RSC117)RSC117)-3 | 5.72 | 70.7 | 100.6 | 130.2 | 26.3 | 3.3 | 209.3 | 29.9 | 3.08 | 1.70 | 8.58 | 68.14 |
| 104 | A.319*((RSC38)RSC38)-15 | 5.71 | 70.5 | 155.1 | 188.1 | 24.7 | 8.4 | 189.7 | 25.5 | 3.05 | 1.68 | 8.89 | 67.50 |
| 105 | A.338*(RSC15)-13 | 5.71 | 74.2 | 163.9 | 194.4 | 22.6 | 7.8 | 164.6 | 32.5 | 3.27 | 1.76 | 10.15 | 67.72 |
| 106 | (RSC73)-9(RSC73)-6 | 5.70 | 68.3 | 66.0 | 81.9 | 19.9 | -4.1 | 58.2 | 21.4 | 2.03 | 1.61 | 8.38 | 68.97 |
| 107 | A.319*(RSC112)-8 | 5.69 | 72.2 | 87.1 | 121.0 | 26.8 | 7.1 | 150.8 | 25.9 | 2.56 | 1.80 | 8.40 | 68.75 |
| 108 | A.301*(RSC15)-11 | 5.68 | 65.3 | 142.4 | 180.6 | 24.5 | 13.8 | 135.5 | 27.6 | 3.04 | 1.83 | 10.63 | 67.70 |
| 109 | A.301*(RSC76)-13 | 5.67 | 68.0 | 135.7 | 169.7 | 22.2 | 11.8 | 148.4 | 32.8 | 2.09 | 1.77 | 8.67 | 68.65 |
| 110 | A.Tx3197*(RSC19)-3-3 | 5.65 | 69.8 | 125.2 | 169.8 | 27.3 | 17.3 | 173.2 | 27.2 | 2.53 | 1.77 | 8.16 | 68.26 |
| 111 | A.319*(RSC15)-13 | 5.64 | 68.0 | 93.0 | 134.1 | 27.6 | 13.5 | 142.9 | 27.0 | 2.94 | 1.78 | 9.53 | 68.68 |
| 112 | A.Tx3197*(RSC37)-12 | 5.64 | 67.8 | 131.9 | 167.4 | 22.4 | 13.0 | 130.9 | 25.8 | 2.60 | 1.79 | 7.93 | 68.38 |
| 113 | A.338*(RSC15)-11 | 5.64 | 73.8 | 171.9 | 202.9 | 23.8 | 7.2 | 181.3 | 29.0 | 3.50 | 1.86 | 10.24 | 67.31 |
| 114 | A.Tx3197*(RSC117)-2-2 | 5.62 | 69.2 | 98.6 | 132.0 | 23.1 | 10.3 | 140.6 | 31.5 | 2.64 | 1.69 | 8.54 | 68.77 |
| 115 | A.Tx3197*((RSC38)RSC38)-9 | 5.59 | 66.3 | 134.5 | 166.9 | 26.1 | 6.4 | 159.1 | 28.6 | 2.67 | 1.74 | 8.36 | 67.58 |
| 116 | A.338*((RSC19)RSC19)-10 | 5.59 | 76.8 | 173.7 | 202.5 | 20.9 | 7.9 | 152.6 | 28.2 | 2.61 | 1.80 | 9.08 | 67.74 |
| 117 | A.338*((RSC15)RSC15)-14 | 5.58 | 73.7 | 163.2 | 194.9 | 22.6 | 9.1 | 190.3 | 32.7 | 3.13 | 1.80 | 10.22 | 67.82 |
| 118 | A.338*(RSC112)-8 | 5.57 | 77.5 | 106.5 | 139.3 | 24.8 | 7.9 | 165.7 | 26.2 | 2.88 | 1.76 | 8.39 | 68.32 |
| 119 | A.319*(RSC76)-13 | 5.57 | 71.0 | 162.7 | 198.4 | 23.8 | 11.9 | 187.0 | 32.1 | 2.25 | 1.74 | 8.65 | 68.34 |
| 120 | A.319*((RSC38)RSC38)-9 | 5.57 | 66.7 | 118.1 | 158.5 | 30.7 | 9.7 | 179.1 | 24.0 | 2.94 | 1.81 | 9.02 | 67.36 |
| 121 | A.338*((RSC73)RSC73)-6 | 5.54 | 74.0 | 152.7 | 182.9 | 20.8 | 9.4 | 213.4 | 30.9 | 2.74 | 1.73 | 8.14 | 68.32 |
| 122 | A.301*(RSC124)-3 | 5.52 | 67.7 | 86.1 | 123.5 | 28.0 | 9.5 | 135.8 | 30.8 | 2.12 | 1.70 | 8.88 | 68.55 |
| 123 | A.319*(RSC83)-10 | 5.52 | 73.2 | 87.2 | 120.4 | 27.9 | 5.4 | 170.2 | 22.6 | 3.11 | 1.85 | 9.54 | 67.44 |
| 124 | A.301*(RSC19)-12 | 5.49 | 66.5 | 64.5 | 104.7 | 24.0 | 16.2 | 143.8 | 25.2 | 2.48 | 1.84 | 9.08 | 68.04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 125 | A.Tx3197*((RSC37)RSC37)-8 | 5.48 | 67.0 | 137.4 | 174.0 | 24.4 | 12.2 | 223.1 | 25.8 | 2.60 | 1.72 | 7.32 | 68.90 |
| 126 | (RSC37)-7 | 5.47 | 73.2 | 94.7 | 129.5 | 23.6 | 11.2 | 123.4 | 24.9 | 2.73 | 1.64 | 8.45 | 67.48 |
| 127 | A.319*(RSC19)-3 | 5.46 | 71.8 | 117.0 | 161.6 | 29.2 | 15.4 | 131.7 | 23.4 | 2.95 | 1.88 | 9.33 | 67.49 |
| 128 | A.Tx3197*(RSC117)-10-10 | 5.46 | 68.2 | 83.5 | 120.4 | 25.9 | 11.0 | 162.7 | 28.9 | 2.49 | 1.64 | 8.32 | 68.74 |
| 129 | A.Tx3197*((RSC73)RSC73)-6 | 5.46 | 67.3 | 127.9 | 156.9 | 22.6 | 6.5 | 160.4 | 27.7 | 2.70 | 1.71 | 7.60 | 68.43 |
| 130 | A.301*(RSC117)-10 | 5.46 | 67.8 | 59.7 | 92.6 | 25.5 | 7.4 | 155.3 | 28.1 | 2.28 | 1.75 | 8.78 | 68.52 |
| 131 | A.301*(RSC83)-10 | 5.44 | 67.7 | 70.1 | 105.8 | 26.1 | 9.6 | 150.4 | 29.4 | 2.47 | 1.85 | 9.52 | 67.83 |
| 132 | (RSC83)-1 | 5.44 | 75.5 | 85.0 | 112.8 | 22.4 | 5.5 | 132.9 | 29.8 | 2.42 | 1.75 | 8.80 | 68.12 |
| 133 | A.Tx3197*(RSC38)-5 | 5.42 | 68.7 | 88.5 | 125.9 | 26.8 | 10.7 | 156.3 | 25.8 | 2.75 | 1.63 | 8.53 | 67.63 |
| 134 | A.319*((RSC19)RSC19)-7 | 5.40 | 71.7 | 167.8 | 205.9 | 25.7 | 12.4 | 159.8 | 25.0 | 3.23 | 1.78 | 10.09 | 67.56 |
| 135 | A.338*((RSC15)RSC15)-15 | 5.40 | 74.7 | 119.4 | 156.2 | 27.8 | 9.1 | 197.7 | 28.7 | 3.18 | 1.84 | 9.31 | 68.09 |
| 136 | 344?79 | 5.40 | 58.2 | 75.5 | 116.2 | 26.9 | 13.9 | 132.2 | 27.5 | 2.45 | 1.69 | 9.25 | 69.36 |
| 137 | A.301*((RSC15)RSC15)-14 | 5.39 | 66.0 | 106.5 | 140.3 | 24.1 | 9.6 | 155.0 | 29.7 | 2.79 | 1.80 | 9.71 | 68.90 |
| 138 | A.Tx3197*((RSC73)RSC73)-5 | 5.38 | 70.8 | 170.8 | 209.1 | 21.9 | 16.5 | 166.1 | 30.1 | 1.85 | 1.72 | 8.29 | 68.92 |
| 139 | A.319*((RSC15)RSC15)-14 | 5.37 | 68.8 | 141.8 | 177.1 | 24.0 | 11.3 | 139.8 | 28.3 | 3.13 | 1.82 | 9.51 | 68.79 |
| 140 | (RSC124)-9(RSC124)-16 | 5.37 | 79.2 | 132.9 | 168.8 | 27.6 | 8.2 | 181.6 | 27.2 | 2.35 | 1.62 | 9.11 | 67.97 |
| 141 | (RSC117)-2(RSC117)-3 | 5.32 | 76.8 | 72.5 | 100.8 | 26.2 | 2.0 | 107.3 | 30.4 | 2.98 | 1.80 | 10.28 | 66.92 |
| 142 | A.301*((RSC38)RSC38)-9 | 5.32 | 65.2 | 86.2 | 122.4 | 27.8 | 8.4 | 158.5 | 27.5 | 2.62 | 1.76 | 8.99 | 67.67 |
| 143 | (RSC38)-5(RSC38)-15 | 5.32 | 71.8 | 124.0 | 151.8 | 23.0 | 4.7 | 119.0 | 22.6 | 2.72 | 1.61 | 9.31 | 67.52 |
| 144 | A.319*(RSC73)-1 | 5.29 | 72.3 | 128.8 | 161.2 | 23.4 | 8.9 | 179.2 | 26.8 | 2.49 | 1.81 | 8.74 | 67.99 |
| 145 | A.338*(RSC73)-9 | 5.28 | 74.8 | 157.2 | 193.0 | 21.7 | 14.2 | 212.1 | 29.7 | 2.73 | 1.70 | 8.47 | 67.93 |
| 146 | A.338*((RSC37)RSC37)-12 | 5.28 | 74.5 | 171.5 | 203.9 | 23.2 | 9.2 | 231.9 | 27.8 | 2.70 | 1.78 | 8.30 | 68.05 |
| 147 | (RSC19)-3 | 5.28 | 69.7 | 103.2 | 138.4 | 23.0 | 12.2 | 123.5 | 24.9 | 2.28 | 1.85 | 9.34 | 67.79 |
| 148 | A.Tx3197*(RSC38)-8-8 | 5.27 | 68.2 | 146.9 | 182.9 | 23.3 | 12.7 | 154.7 | 29.6 | 2.47 | 1.68 | 8.51 | 68.44 |
| 149 | (RSC38)-8 | 5.27 | 72.5 | 116.0 | 146.2 | 22.1 | 8.1 | 141.9 | 23.2 | 2.53 | 1.65 | 8.79 | 68.05 |
| 150 | (RSC112)-8 | 5.26 | 77.5 | 78.0 | 113.7 | 24.0 | 11.7 | 111.5 | 26.1 | 2.77 | 1.70 | 8.74 | 68.09 |
| 151 | (RSC112)-5 | 5.19 | 77.5 | 88.8 | 134.3 | 28.7 | 16.9 | 124.2 | 26.1 | 2.24 | 1.61 | 8.84 | 68.19 |
| 152 | B.MMR301 | 5.19 | 64.0 | 59.6 | 92.0 | 23.6 | 8.8 | 132.6 | 27.1 | 2.33 | 1.85 | 8.59 | 68.91 |
| 153 | A.301*(RSC112)-8 | 5.18 | 66.7 | 69.8 | 104.6 | 26.4 | 8.4 | 186.1 | 28.0 | 2.44 | 1.81 | 8.94 | 68.95 |
| 154 | A.319*((RSC15)RSC15)-15 | 5.18 | 70.5 | 94.7 | 129.2 | 29.1 | 5.4 | 162.2 | 24.2 | 3.04 | 1.89 | 8.85 | 68.66 |
| 155 | (RSC73)-1 | 5.18 | 67.3 | 91.2 | 119.7 | 23.8 | 4.8 | 111.4 | 25.6 | 1.88 | 1.68 | 8.76 | 68.56 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 156 | A.338*(RSC19)-12-1 | 5.18 | 75.2 | 89.0 | 127.3 | 24.2 | 14.1 | 148.7 | 24.8 | 2.98 | 1.81 | 8.90 | 67.89 |
| 157 | (RSC37)-2(RSC37)-8 | 5.17 | 72.8 | 81.3 | 102.2 | 25.6 | -4.7 | 127.6 | 24.1 | 2.18 | 1.72 | 7.97 | 68.36 |
| 158 | A.Tx3197*((RSC15)RSC15)-14 | 5.17 | 67.8 | 141.6 | 177.0 | 25.8 | 9.6 | 117.9 | 29.5 | 2.96 | 1.70 | 9.83 | 68.33 |
| 159 | A.301*(RSC73)-1 | 5.16 | 65.2 | 85.0 | 119.4 | 23.7 | 10.7 | 140.1 | 27.2 | 2.35 | 1.75 | 8.57 | 68.52 |
| 160 | (RSC112)-5(RSC112)-19 | 5.14 | 81.8 | 91.6 | 125.4 | 22.8 | 11.1 | 148.0 | 29.9 | 2.86 | 1.65 | 9.38 | 67.71 |
| 161 | A.Tx3197*(RSC73)-1 | 5.10 | 72.0 | 143.1 | 173.9 | 22.8 | 8.0 | 164.5 | 29.3 | 2.35 | 1.73 | 8.35 | 68.33 |
| 162 | (RSC38)-5 | 5.10 | 71.0 | 65.8 | 99.0 | 27.4 | 5.8 | 87.4 | 19.7 | 2.67 | 1.59 | 8.74 | 67.56 |
| 163 | A.Tx3197*(RSC83)-10 | 5.09 | 72.3 | 92.9 | 128.0 | 26.3 | 8.8 | 125.7 | 30.4 | 2.64 | 1.76 | 9.00 | 68.22 |
| 164 | (RSC117)-2 | 5.08 | 70.7 | 71.0 | 104.1 | 25.4 | 7.8 | 103.5 | 27.0 | 2.52 | 1.77 | 9.03 | 68.64 |
| 165 | A.319*(RSC76)-4 | 5.08 | 73.7 | 178.4 | 211.8 | 22.6 | 10.8 | 225.4 | 32.4 | 1.97 | 1.72 | 7.98 | 68.42 |
| 166 | A.301*(RSC37)-7 | 5.07 | 64.5 | 69.1 | 101.0 | 23.9 | 8.0 | 142.2 | 24.9 | 2.36 | 1.75 | 8.65 | 68.13 |
| 167 | (RSC15)-13(RSC15)-14 | 5.07 | 74.2 | 103.3 | 135.1 | 20.2 | 11.6 | 86.2 | 26.9 | 2.80 | 1.83 | 10.12 | 68.06 |
| 168 | (RSC76)-13 | 5.06 | 70.0 | 139.7 | 162.6 | 18.8 | 4.1 | 107.5 | 30.3 | 1.93 | 1.67 | 8.11 | 69.01 |
| 169 | A.338*(RSC73)-1-1 | 5.01 | 75.5 | 165.5 | 198.1 | 20.5 | 12.1 | 162.2 | 30.5 | 2.79 | 1.77 | 8.59 | 68.07 |
| 170 | A.338*(RSC37)-7-7 | 5.00 | 76.8 | 177.7 | 210.4 | 22.0 | 10.7 | 220.1 | 28.6 | 2.74 | 1.73 | 8.28 | 68.02 |
| 171 | (RSC124)-3 | 5.00 | 72.3 | 140.8 | 184.2 | 26.7 | 16.7 | 94.0 | 25.7 | 2.38 | 1.66 | 9.58 | 67.72 |
| 172 | (RSC76)-4(RSC76)-16 | 4.98 | 77.3 | 167.4 | 204.9 | 18.3 | 19.2 | 163.2 | 33.6 | 1.65 | 1.68 | 7.59 | 70.28 |
| 173 | (RSC83)-1(RSC83)-14 | 4.98 | 74.3 | 65.8 | 85.9 | 18.2 | 2.0 | 121.8 | 25.1 | 1.89 | 1.59 | 8.78 | 68.54 |
| 174 | (RSC37)-12 | 4.95 | 69.0 | 59.2 | 85.2 | 23.5 | 2.5 | 88.9 | 23.7 | 2.36 | 1.69 | 9.08 | 67.59 |
| 175 | (RSC15)-13 | 4.92 | 68.5 | 103.7 | 135.2 | 22.9 | 8.6 | 93.9 | 27.5 | 2.61 | 1.65 | 10.38 | 68.39 |
| 176 | (RSC83)-10 | 4.88 | 77.8 | 80.3 | 117.3 | 26.1 | 10.9 | 126.0 | 20.8 | 2.69 | 1.83 | 8.76 | 68.12 |
| 177 | A.338*((RSC19)RSC19)-7 | 4.87 | 74.2 | 188.5 | 222.0 | 23.5 | 10.0 | 209.5 | 26.1 | 3.60 | 1.74 | 9.56 | 67.67 |
| 178 | A.338*((RSC73)RSC73)-5 | 4.87 | 77.2 | 200.0 | 235.9 | 21.9 | 14.1 | 215.2 | 29.0 | 2.29 | 1.74 | 7.92 | 68.44 |
| 179 | (RSC117)-10 | 4.85 | 72.8 | 63.8 | 97.4 | 24.4 | 9.1 | 110.8 | 23.0 | 2.84 | 1.64 | 9.01 | 67.23 |
| 180 | A.Tx3197*((RSC76)RSC76)-2 | 4.85 | 71.2 | 204.8 | 242.0 | 23.2 | 14.1 | 263.7 | 35.1 | 1.86 | 1.65 | 7.82 | 69.63 |
| 181 | (RSC15)-13(RSC15)-15 | 4.81 | 75.7 | 84.0 | 120.5 | 28.3 | 8.3 | 94.7 | 27.8 | 3.18 | 1.99 | 10.99 | 66.47 |
| 182 | A.301*(RSC38)-5 | 4.78 | 64.3 | 61.4 | 95.5 | 28.2 | 6.0 | 136.2 | 24.3 | 2.45 | 1.75 | 9.30 | 67.71 |
| 183 | A.338*(RSC124)-3 | 4.77 | 76.8 | 140.4 | 182.9 | 25.2 | 17.3 | 166.5 | 28.5 | 2.59 | 1.74 | 8.40 | 68.34 |
| 184 | A.Tx3197*(RSC37)-7 | 4.75 | 68.8 | 142.8 | 181.9 | 23.4 | 15.7 | 170.1 | 29.7 | 2.54 | 1.74 | 8.16 | 68.22 |
| 185 | (RSC38)-5(RSC38)-9 | 4.70 | 65.0 | 101.6 | 128.5 | 26.6 | 0.3 | 126.8 | 25.5 | 2.40 | 1.64 | 8.74 | 67.78 |
| 186 | A.319*((RSC76)RSC76)-2 | 4.68 | 75.2 | 178.1 | 219.9 | 25.0 | 16.7 | 267.1 | 30.7 | 1.91 | 1.72 | 7.49 | 68.91 |

| 187 | A.338*((RSC38)RSC38)-15 | 4.66 | 76.3 | 215.9 | 241.3 | 22.5 | 2.9 | 193.7 | 28.9 | 3.06 | 1.64 | 8.77 | 67.26 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 188 | A.Tx3197*(RSC19)-12-1 | 4.65 | 69.8 | 80.2 | 116.3 | 24.5 | 11.6 | 135.1 | 26.0 | 2.47 | 1.76 | 8.45 | 68.50 |
| 189 | A.Tx3197*(RSC76)-4 | 4.58 | 72.7 | 194.2 | 227.9 | 21.7 | 12.0 | 199.0 | 34.4 | 1.71 | 1.66 | 8.34 | 68.96 |
| 190 | (RSC73)-9(RSC73)-5 | 4.58 | 76.5 | 100.6 | 122.8 | 18.3 | 3.9 | 126.1 | 24.1 | 1.63 | 1.68 | 8.18 | 68.80 |
| 191 | A.Tx3197*((RSC19)RSC19)-10 | 4.52 | 70.7 | 159.7 | 189.3 | 22.5 | 7.1 | 184.8 | 27.5 | 2.51 | 1.72 | 8.57 | 68.88 |
| 192 | A.Tx3197*((RSC38)RSC38)-15 | 4.50 | 67.2 | 167.6 | 200.5 | 21.6 | 11.3 | 169.6 | 29.1 | 2.79 | 1.65 | 9.17 | 67.05 |
| 193 | (RSC76)-4 | 4.48 | 76.8 | 146.3 | 167.4 | 19.7 | 1.4 | 140.8 | 32.4 | 1.52 | 1.54 | 7.59 | 69.66 |
| 194 | A.Tx3197*((RSC19)RSC19)-7 | 4.46 | 72.8 | 164.7 | 204.3 | 24.2 | 15.4 | 184.5 | 28.4 | 3.29 | 1.77 | 9.06 | 67.82 |
| 195 | A.Tx3197*(RSC124)-3 | 4.40 | 69.3 | 125.6 | 164.5 | 25.7 | 13.3 | 126.4 | 29.3 | 2.16 | 1.66 | 8.72 | 68.48 |
| 196 | A.338*(RSC38)-8 | 4.39 | 76.8 | 179.6 | 212.2 | 22.6 | 10.0 | 270.8 | 29.9 | 2.69 | 1.70 | 8.43 | 68.17 |
| 197 | A.Tx3197*((RSC76)RSC76)-16 | 4.35 | 71.3 | 198.3 | 240.7 | 22.5 | 20.0 | 236.9 | 34.9 | 1.76 | 1.68 | 7.87 | 69.75 |
| 198 | A.Tx3197*(RSC83)-1 | 4.25 | 74.7 | 130.5 | 164.4 | 25.0 | 8.8 | 182.6 | 30.9 | 2.58 | 1.71 | 8.50 | 68.11 |
| 199 | A.338*((RSC38)RSC38)-9 | 4.14 | 75.8 | 167.9 | 199.3 | 24.4 | 6.9 | 169.2 | 28.5 | 2.93 | 1.75 | 8.72 | 67.47 |
| 200 | (RSC73)-9 | 4.14 | 66.7 | 74.2 | 95.7 | 23.0 | -1.6 | 95.6 | 17.8 | 2.55 | 1.66 | 8.23 | 68.05 |
| 201 | A.338*(RSC76)-13 | 4.07 | 75.5 | 189.4 | 220.3 | 22.0 | 8.9 | 188.3 | 34.2 | 2.46 | 1.76 | 8.68 | 68.07 |
| 202 | (RSC83)-1(RSC83)-1 | 4.06 | 71.8 | 65.1 | 80.4 | 19.3 | -4.0 | 96.9 | 26.6 | 2.10 | 1.64 | 9.28 | 68.06 |
| 203 | A.338*((RSC76)RSC76)-2 | 4.01 | 77.8 | 217.0 | 252.9 | 23.4 | 12.4 | 305.0 | 35.4 | 1.94 | 1.67 | 7.54 | 69.14 |
| 204 | A.Tx3197*(RSC15)-13 | 4.01 | 66.7 | 146.8 | 185.6 | 22.8 | 16.0 | 106.4 | 30.1 | 2.94 | 1.65 | 10.12 | 68.07 |
| 205 | A.Tx3197*(RSC15)-11 | 3.92 | 68.3 | 154.8 | 194.5 | 24.6 | 15.1 | 147.1 | 27.4 | 3.13 | 1.73 | 9.51 | 68.34 |
| 206 | A.Tx3197*(RSC76)-13 | 3.77 | 71.2 | 180.9 | 213.1 | 23.1 | 9.1 | 158.7 | 31.7 | 2.12 | 1.71 | 8.38 | 68.90 |
| 207 | A.338*(RSC38)-5 | 3.54 | 75.0 | 179.6 | 212.8 | 25.0 | 8.2 | 192.7 | 26.7 | 3.01 | 1.70 | 9.08 | 67.26 |
| 208 | (RSC15)-11 | 3.50 | 67.7 | 160.4 | 200.4 | 21.2 | 18.8 | 83.0 | 21.8 | 3.23 | 1.80 | 11.22 | 67.09 |
| 209 | A.338*(RSC76)-4 | 3.34 | 75.3 | 221.1 | 251.6 | 21.3 | 9.2 | 219.5 | 36.2 | 1.71 | 1.68 | 7.60 | 69.00 |
| 210 | (RSC124)-9 | 3.30 | 77.2 | 84.8 | 121.1 | 28.1 | 8.3 | 90.7 | 23.6 | 2.53 | 1.64 | 8.69 | 67.71 |
| 211 | A.338*((RSC76)RSC76)-16 | 3.07 | 77.2 | 221.0 | 255.6 | 22.0 | 12.6 | 234.3 | 37.2 | 2.13 | 1.70 | 7.86 | 68.77 |

DTF = days to flowering

†Exs = plant exsertion

## Analysis of Variance

In the combined analysis, differences among levels of effects were detected for most sources of variation (Table 4). Grain yield was obtained for six environments; 2015 was a very wet year at Perryton, and the grain could not be harvested; however, this was the only common dependent variable among the six environments, and removing parents and checks allowed for an overall grain yield ANOVA. Of that, only four environments had parents, and traits could not be evaluated in every environment (number of days to anthesis, height to the flag leaf, total plant height, panicle length, three-panicle weight, 1000-kernel weight, and quality data), for which reason, degrees of freedom were modified for those traits in the analysis of variance across environments with parents. This also was reflected in the ANOVA tables for individual environments. By removing parents and checks, a combined mean squared analysis showed significant differences for environment, replication (environment), hybrids, lines, testers, RSC, selections, the interaction between hybrids, lines, tester x environment, and line x tester interaction ($P < 0.01$) for almost every trait considered. Line x tester x environment interaction was significant ($P < 0.01$) for grain yield, whereas total plant height, height to the flag leaf, panicle length, and percentage of fat concentration in grain had significant interaction at $P < 0.05$. The interaction between RSC x environment showed significant differences ($P < 0.01$) for grain yield, total plant height, height to the flag leaf, number of days to anthesis, and percentage of starch, fiber, and fat concentration in grain, but only significant differences at the $P < 0.05$ for plant exsertion, panicle length, three-panicle weight, 1000-kernel weight, and the percentage of concentration of protein in grain. RSC

Table 4. Mean squares of grain yield and agronomic traits of sorghum hybrids in seven environments – Vega, Perryton, and Taylor, TX, and Hutchinson, KS, in 2015, and Vega and Dumas, TX, and Hutchinson, KS, in 2016. Ten hybrids and yield results from Perryton (2015) and NIR data of one hybrid sorghum at Vega (2016) are missing.

| Source of variation | Df† | Grain yield Mg ha⁻¹ | Df | Total height cm | Flag leaf height cm | Plant exsertion cm | Panicle length cm | 3-panicle weight g | 1000-kernel weight g | Df | Days to anthesis | Df | Protein¶ % | Starch¶ % | Fiber¶ % | Fat¶ % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Environment (E) | 5 | 1095.5** | 3 | 146003.3** | 83577.8** | 5682.3** | 1598.6** | 1009747.3** | 13.9 | 2 | 11343.3** | 3 | 4.45** | 4.87** | 0.48** | 7.39** |
| Rep (E) | 6 | 13.6** | 4 | 523.8* | 834.6** | 853.6** | 39.1** | 17229.4** | 95.9** | 3 | 42.6** | 3 | 7.47** | 6.65** | 0.03** | 0.50** |
| Hybrids (H) | 159 | 9.2** | 159 | 11715.8** | 12200.1** | 84.5** | 48.9** | 10070.1** | 78.5** | 159 | 79.5** | 159 | 2.38** | 1.92** | 0.02** | 0.81** |
| H X E | 795 | 3.3** | 467 | 441.7** | 433.4** | 39.4** | 4.9** | 2630.6** | 7.9* | 318 | 17.8** | 466 | 0.32* | 0.35* | 0.00** | 0.07** |
| Lines (L) | 39 | 18.2** | 39 | 28079.0** | 29718.4** | 186.1** | 138.3** | 22644.4** | 221.8** | 39 | 41.8** | 39 | 7.46** | 5.66** | 0.04** | 2.65** |
| Testers (T) | 3 | 73.7** | 3 | 205521.7** | 211615.2** | 457.2** | 455.7** | 95806.2** | 782.3 | 3 | 3140.1** | 3 | 6.77** | 5.82** | 0.35** | 5.92** |
| L X T | 117 | 4.5** | 117 | 1151.3** | 1150.6** | 40.0 | 8.3** | 3340.7** | 12.3** | 117 | 12.8** | 117 | 0.63** | 0.58** | 0.01** | 0.07** |
| L X E | 195 | 5.2** | 117 | 900.6** | 919.8** | 44.4* | 6.9** | 3394.2** | 9.8** | 78 | 10.2* | 117 | 0.44** | 0.60** | 0.00** | 0.10** |
| T X E | 15 | 11.6** | 9 | 2668.3** | 3021.9** | 174.3** | 16.0** | 7862.9** | 25.4** | 6 | 548.8** | 9 | 2.68** | 2.02** | 0.05** | 0.23** |
| L X T X E | 585 | 2.5** | 341 | 227.0* | 201.2* | 34.2 | 4.1* | 2247.0 | 6.9 | 234 | 6.6 | 340 | 0.21 | 0.21 | 0.00 | 0.06* |
| RSC‡ | 9 | 45.0** | 9 | 82873.1** | 86108.5** | 391.6** | 376.6** | 41364.6** | 751.6** | 9 | 122.1** | 9 | 23.85** | 18.04** | 0.12** | 8.03** |
| RSC X E | 45 | 7.6** | 27 | 2663.3** | 2744.4** | 61.0* | 11.8* | 5337.2* | 16.4* | 18 | 23.0** | 27 | 0.66* | 1.33** | 0.01** | 0.26** |
| RSC X T | 27 | 10.1** | 27 | 2808.8** | 2817.8** | 42.8 | 12.7* | 3837.3 | 20.7** | 27 | 17.0* | 27 | 1.39** | 1.41** | 0.01** | 0.14* |
| RSC X T X E | 135 | 3.8** | 81 | 428.5 | 398.9 | 47.9* | 5.9 | 2695.9 | 9.1 | 54 | 9.8 | 81 | 0.19 | 0.30 | 0.00 | 0.08 |
| Selections (S)δ | 3 | 47.8** | 3 | 18400.2** | 24354.3** | 486.6** | 18.0 | 69201.5** | 55.6* | 3 | 13.5 | 3 | 0.87 | 1.09 | 0.00 | 1.62** |
| S X E | 15 | 6.3* | 9 | 348.4 | 436.6 | 65.0 | 6.9 | 2012.1 | 6.4 | 6 | 9.3 | 9 | 0.70 | 0.50 | 0.00 | 0.25 |
| S X T | 9 | 2.2 | 9 | 376.7 | 360.0 | 49.8 | 4.4 | 812.0 | 9.1 | 9 | 17.9 | 9 | 0.09 | 0.40 | 0.00 | 0.05 |
| S X T X E | 45 | 3.3 | 27 | 126.2 | 109.3 | 30.1 | 3.7 | 2342.3 | 9.4 | 18 | 7.9 | 27 | 0.23 | 0.24 | 0.00 | 0.06 |
| Error | 947 | 1.99 | 615 | 168.04 | 158.41 | 34.2 | 3.45 | 1915.8 | 6.01 | 473 | 7.57 | 456 | 0.27 | 0.26 | 0.00 | 0.05 |

DTF = days to flowering.
*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.
†Separate columns for degrees of freedom for particular traits are because of differences in the number of replications or environments from which data were collected for the traits.
‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.
δSelections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F₂:₃, BC₁F₂:₃, and the Low F₂:₃, BC₁F₂:₃.
¶Content in grain

x tester interaction showed significance ($P < 0.01$) for grain yield, total plant height, height to the flag leaf, 1000-kernel weight, and percentage of concentration of protein, starch, and fiber in grain but also showed significance at $P < 0.05$ for panicle length, number of days to anthesis, and percentage of concentration of fat in grain. RSC x tester x site interaction was significant at $P < 0.01$ for grain yield but only $P < 0.05$ for plant exsertion. The sorghum selections, which represent generations with high or low percentage of exotic genome recovery, were significant at $P < 0.01$ for grain yield, total plant height, height to the flag leaf, plant exsertion, three-panicle weight, and percentage of concentration of fat in grain, but significantly different only at $P < 0.05$ for 1000-kernel weight and interaction between selection x environment for grain yield. No significant differences were found for selection x tester or selection x tester x site. The significant differences indicated sufficient genetic variability among the hybrids and will be further partitioned into a line x tester analysis of variance with parents and checks.

In the combined line x tester analysis of variance with parents and checks, differences among levels of effects were detected for most sources of variation (Table 5). Environment, genotypes, hybrids, lines, testers, RSC, parents, and checks were significant ($P < 0.01$) for almost all the traits evaluated. Genotype x environment interaction was significant for all traits with at least a $P < 0.05$ difference. Replication (environment) showed significant differences at $P < 0.01$ for the height to the flag leaf, plant exsertion, panicle length, 1000-kernel weight, number of days to anthesis, and percentage of concentration of protein, starch, fiber, and fat in grain, and a significant difference at $P < 0.05$ was found for three-panicle weight. Hybrid x environment

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Table 5. Mean squares of grain yield and agronomic traits of sorghum hybrids, including parents and checks, in four environments - Vega, TX, and Hutchinson, KS, in 2015, and Vega and Dumas, TX, in 2016.

| Source of variation | Df† | Grain yield (Mg ha⁻¹) | Df | Total height (cm) | Flag leaf height (cm) | Plant exsertion (cm) | Panicle length (cm) | 3-panicle weight (g) | Df | 1000-kernel weight (g) | Df | Days to anthesis | Df | Protein¶ (%) | Starch¶ (%) | Fiber¶ (%) | Fat¶ (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Environment (E) | 3 | 510.5*** | 3 | 187012.2*** | 106502.8** | 7421.4** | 2813.4** | 1652954.2*** | 2 | 9.1 | 2 | 14496.1** | 2 | 9.82** | 0.51 | 0.33** | 17.22** |
| Rep (E) | 4 | 9.1* | 3 | 352.9 | 834.5** | 1433.3*** | 70.4*** | 5584.7* | 3 | 154.3*** | 3 | 70.4*** | 2 | 2.51** | 2.78 | 0.01** | 0.37** |
| Genotypes (G) | 210 | 11.9*** | 210 | 8886.9** | 8803.0** | 111.6*** | 51.7*** | 10298.8*** | 210 | 77.7*** | 210 | 115.9*** | 210 | 2.03** | 1.66** | 0.03** | 0.71** |
| G X E | 630 | 4.3** | 420 | 465.5** | 446.2** | 42.2* | 5.4** | 2048.8* | 420 | 9.9** | 420 | 22.2** | 419 | 0.33* | 0.40** | 0.00** | 0.08* |
| Hybrids (H) | 159 | 8.7** | 159 | 8192.8** | 8387.6** | 68.4** | 34.5*** | 6953.9** | 159 | 61.3*** | 159 | 79.5*** | 159 | 1.68** | 1.26** | 0.02** | 0.60** |
| H X E | 477 | 4.0** | 318 | 465.5** | 446.5** | 42.1 | 4.8 | 2278.4 | 318 | 8.5* | 318 | 17.8** | 317 | 0.31* | 0.32* | 0.00* | 0.07* |
| Lines (L) | 39 | 16.2*** | 39 | 19630.0** | 20344.5** | 144.9** | 94.8*** | 16719.0*** | 39 | 163.2*** | 39 | 41.8** | 39 | 5.00** | 3.39** | 0.03** | 1.89** |
| Testers (T) | 3 | 69.5*** | 3 | 142479.9** | 144569.9** | 266.5** | 350.0** | 48360.3*** | 3 | 705.8*** | 3 | 3140.1** | 3 | 6.90** | 6.56** | 0.37** | 4.63** |
| L X T | 117 | 4.5*** | 117 | 929.3** | 914.6** | 37.6 | 6.5*** | 2589.8* | 117 | 11.3** | 117 | 12.8** | 117 | 0.46** | 0.40** | 0.01** | 0.07 |
| L X E | 117 | 6.2*** | 78 | 1045.5** | 1063.0** | 40.8 | 6.3*** | 3143.8*** | 78 | 10.6* | 78 | 10.2* | 78 | 0.39* | 0.52** | 0.00* | 0.09* |
| T X E | 9 | 15.5*** | 6 | 2617.3** | 2908.5** | 195.8** | 21.8** | 2865.2 | 6 | 28.0** | 6 | 548.8** | 6 | 3.64** | 2.13** | 0.05** | 0.32** |
| L X T X E | 351 | 3.0* | 234 | 217.3* | 178.9 | 38.6 | 3.9 | 1958.5 | 234 | 7.3 | 233 | 6.6 | 233 | 0.20 | 0.20 | 0.00 | 0.06 |
| RSC‡ | 9 | 39.0*** | 9 | 57951.3** | 59150.2** | 275.8** | 257.1** | 32796.4*** | 9 | 556.7*** | 9 | 122.1** | 9 | 16.47** | 10.30** | 0.09** | 5.95** |
| RSC X E | 27 | 8.5** | 18 | 3132.4** | 3105.2** | 56.3 | 10.5* | 4845.3* | 18 | 17.0* | 18 | 23.0** | 18 | 0.59* | 1.16** | 0.00* | 0.18* |
| RSC X T | 27 | 10.7** | 27 | 1978.6** | 1976.4** | 38.4 | 7.4 | 3438.8 | 27 | 17.2* | 27 | 17.0* | 27 | 0.98** | 0.93** | 0.01** | 0.11 |
| RSC X T X E | 81 | 4.2* | 54 | 370.0 | 273.1 | 58.4* | 5.3 | 2148.3 | 54 | 9.0 | 54 | 9.8 | 54 | 0.20 | 0.32 | 0.00 | 0.09 |
| Selections (S)δ | 3 | 38.6*** | 3 | 12037.6** | 15224.4** | 190.3* | 29.2* | 57132.7*** | 3 | 50.2* | 3 | 13.5 | 3 | 0.92 | 0.62 | 0.00 | 1.17** |
| S X E | 9 | 7.7** | 6 | 278.2 | 297.95 | 38.7 | 4.1 | 2657.9 | 6 | 5.4 | 6 | 9.3 | 6 | 0.70 | 0.59 | 0.00 | 0.32 |
| S X T | 9 | 2.2 | 9 | 227.7 | 209.7 | 50.6 | 4.1 | 1186.1 | 9 | 9.3 | 9 | 17.9 | 9 | 0.07 | 0.28 | 0.01 | 0.12 |
| S X T X E | 27 | 4.6 | 18 | 128.2 | 104.0 | 34.9 | 4.4 | 1654.6 | 18 | 9.9 | 18 | 8.0 | 18 | 0.25 | 0.24 | 0.00 | 0.05 |
| Parents (P) | 43 | 4.0* | 43 | 5749.9** | 5034.3** | 223.0** | 52.7** | 3822.1** | 43 | 96.9** | 43 | 122.4** | 43 | 3.17** | 2.96** | 0.05** | 0.86** |
| P X E | 129 | 3.0** | 86 | 339.9** | 296.7** | 41.8 | 5.6 | 969.9 | 86 | 12.2* | 86 | 31.6** | 86 | 0.43 | 0.64* | 0.01** | 0.11 |
| Checks (C) | 6 | 33.0** | 6 | 2697.4** | 3122.0** | 139.0** | 66.8** | 22289.5*** | 6 | 154.4*** | 6 | 765.1** | 6 | 1.44** | 0.78* | 0.03** | 1.73** |
| C vs P vs H | 2 | 370.2** | 2 | 147959.7** | 140200.6** | 1078.2** | 1364.6** | 377713.7** | 2 | 746.2** | 2 | 925.2** | 2 | 6.84** | 8.38** | 0.18** | 2.83** |
| C vs P vs H X E | 6 | 45.3** | 4 | 4266.9* | 4616.6* | 88.5 | 39.2* | 10303.3* | 4 | 32.4 | 4 | 36.6 | 4 | 0.48 | 2.59* | 0.01 | 0.59* |
| P vs H | 1 | 468.7** | 1 | 227198.7** | 172145.4** | 1822.5** | 363.3** | 743383.6*** | 1 | 1397.9** | 1 | 1096.0** | 1 | 10.66** | 0.21 | 0.29** | 5.44** |
| P vs H X E | 3 | 49.9** | 2 | 4433.4 | 3143.1 | 80.2 | 59.6* | 13614.4 | 2 | 15.3 | 2 | 55.0 | 2 | 0.66 | 3.47* | 0.02 | 0.78* |
| C vs H | 1 | 154.5** | 1 | 116151.8** | 156801.4** | 111.5 | 1989.3** | 1755.6 | 1 | 256.3** | 1 | 453.8** | 1 | 1.97 | 15.97** | 0.05* | 0.06 |
| Error | 987 | 2.21 | 737 | 149.1 | 129.89 | 32.4 | 3.55 | 1556.5 | 744 | 6.43 | 418 | 6.9 | 418 | 0.28 | 0.26 | 0.00 | 0.06 |

*and** Significant at the 0.05 and 0.01 probability level

†Separate columns for degrees of freedom for particular traits are because of differences in the number of replications or environments from which data were collected for the traits.

‡RSC represents the different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δ Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, $BC_1F_2$: and the Low $F_{2:3}$, $BC_1F_{2:3}$,

¶ Content in grain

interaction was significant at $P < 0.01$ for grain yield, total plant height, height to the flag leaf, and number of days to anthesis; 1000-kernel weight and percentage of grain of protein, starch, fiber, and fat in grain were significant at $P < 0.05$. Line x tester interaction was significant at $P < 0.01$ for all traits evaluated except percentage of concentration of fat in grain. Line x environment interaction was significant at $P < 0.01$ for grain yield, total plant height, height to the flag leaf, panicle length, three-panicle weight, and percentage of concentration of starch in grain, while 1000-kernel weight, number of days to anthesis, and percentage of concentration of protein, fiber, and fat in grain showed significance at $P < 0.05$. Tester x environment interaction was significant at $P < 0.01$ for all traits except three-panicle weight that was not significant. Line x tester x environment was significant ($P < 0.05$) only for grain yield and total plant height. RSC x environment was significant at $P < 0.01$ for grain yield, total plant height, height to the flag leaf, number of days to anthesis, and percentage of concentration of starch in grain, while panicle length, three-panicle weight, 1000-kernel weight, and percentage of concentration of protein, fiber, and fat in grain was significant at $P < 0.05$. RSC x tester interaction was significant at $P < 0.05$ for grain yield, total plant height, height to the flag leaf, and percentage of concentration of protein, starch, and fiber in grain. The 1000-kernel weight and number of days to anthesis were significant for RSC x tester at $P < 0.05$. RSC x tester x site interaction was significant at $P < 0.05$ for grain yield and plant exsertion. Grain yield, total plant height, height to the flag leaf, three-panicle weight, and percentage of concentration of fat in grain were significant at $P < 0.01$ for selections, while plant exsertion, panicle length, and 1000-kernel weight were significant at $P < 0.05$. Selection x environment was significant ($P < 0.05$) only for grain yield. There was

no interaction for selection x tester x environment. The sorghum parents were significant ($P < 0.01$) for all traits evaluated except grain yield that was significant at $P < 0.05$. Parent x environment was significant at $P < 0.01$ for total plant height, height to the flag leaf, and number of days to anthesis, with significance at $P < 0.05$ for grain yield, 1000-kernel weight, and percentage of concentration of starch in grain. Checks and checks versus parents versus hybrids were significant at $P < 0.01$ for all traits except percentage of concentration of fat in grain. Checks versus parents versus hybrid x environment interaction were significant at $P < 0.01$ only for grain; however, total plant height, height to the flag leaf, panicle length, three-panicle weight, and percentage of concentration of starch and fat in grain were significant at $P < 0.05$. Parent versus hybrid was significant ($P < 0.01$) for all traits except percentage of concentration of starch in grain. Parent versus hybrid x environment was significant ($P < 0.01$) for grain yield only with panicle length and with percentage of concentration of starch and fat in grain ($P < 0.05$). The check versus hybrid was significant at $P < 0.01$ for grain yield, total plant height, height to the flag leaf, panicle length, 1000-kernel weight, number of days to anthesis, and percentage of concentration of starch in grain, with fiber concentration significant only at $P < 0.05$. The significant differences in mean square between parents and hybrids for almost all traits indicated they were suitable for studies of combining ability. Significant mean squares of parent versus hybrid indicated good scope for manifestation of heterosis in all the studied traits except percentage of concentration of starch in grain. This provided evidence of the presence of sufficient genetic variability among lines, testers, and hybrids and allows further analysis of GCA and heterosis. The results coincided with

the findings of Jayasudha and Sharma (2009) and Rahimi et al. (2010) who also found significant difference among parents and hybrids.

The significant differences between the interaction of line x tester for the traits indicated SCA attributed in the expression of the traits and provide the importance of dominance or non-additive variance for all traits. Variation among parents, hybrids, parents versus hybrids, lines, testers, and line x tester also was observed in several other sorghum studies (Hovny and El-Dsouky, 2007; Abedel-Mottaleb, 2009; Essa, 2009; Mahdy et al., 2011).

Significant differences between genotypes including parents and checks were found for all traits in three of the four environments (Tables 6-10), while significant differences were found in all traits in the across-environment analysis for genotype (Table 5). No differences were found in NIR for sorghum at Vega in 2016 because of low kernel quantity and analysis of differences only between replications. Combined analysis of the various components of the genotype, hybrid, and line, and the interaction with genotype x environment showed significant differences for all traits, as was the case at Dumas, TX, in 2016. Significant differences between RSC families were recorded for all traits in all four environments (Tables 6-10), as was the case in the across-environment analysis (Table 5).

RSC x tester interaction showed various significant differences at individual locations, whereas in the combined location analysis (Table 5), RSC x tester and RSC * environment showed significant differences for grain yield, total plant height, height to

Table 6. Mean squares of grain yield and agronomic traits of sorghum hybrids at Vega, TX, in 2015, with means of various categories of experimental entries.

| Source of variation | Df† | Grain yield Mg ha⁻¹ | Days to anthesis | Total height cm | Flag leaf height cm | Plant exsertion cm | Panicle length cm | 3-panicle weight g | 1000-kernel weight g | Protein¶ % | Starch¶ % | Fiber¶ % | Fat¶ % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1 | 11.0* | 132.8*** | 0.6 | 2243.0* | 3924.4** | 210.7** | 1.6 | 458.2*** | 0.40 | 0.34 | 0.00 | 0.03 |
| Genotypes (G) | 210 | 6.8*** | 62.0*** | 3994.6*** | 3849.1*** | 100.2*** | 21.3*** | 5567.4*** | 35.5*** | 1.10*** | 1.66*** | 0.02*** | 0.39*** |
| Hybrids (H) | 159 | 5.6*** | 49.6*** | 3746.5*** | 3753.1*** | 80.9 | 13.6*** | 4893.6*** | 28.3*** | 0.94*** | 1.25*** | 0.01*** | 0.34*** |
| Lines (L) | 39 | 12.5*** | 14.5* | 8489.4*** | 8557.7*** | 98.3 | 31.7*** | 9447.1*** | 67.7*** | 2.44*** | 3.34*** | 0.02*** | 0.97*** |
| Testers (T) | 3 | 34.24*** | 2038.6*** | 64640.3*** | 67055.5*** | 382.3* | 116.2*** | 22744.1** | 257.6*** | 1.54* | 4.55*** | 0.10*** | 1.29*** |
| L X T | 117 | 2.5*** | 8.6 | 591.0*** | 524.1*** | 67.4 | 5.0 | 2817.9 | 9.6 | 0.44* | 0.47* | 0.00* | 0.10* |
| RSC‡ | 9 | 32.2*** | 36.9*** | 26595.1*** | 25913.7*** | 184.1* | 77.6*** | 16148.3*** | 206.4*** | 6.98*** | 10.01*** | 0.06*** | 2.88*** |
| RSC X T | 27 | 3.8* | 11.5 | 1069.6* | 921.1 | 111.1* | 5.9 | 3607.2 | 16.3* | 0.88*** | 1.09*** | 0.01* | 0.17* |
| Selections (S)δ | 3 | 11.5* | 6.3 | 6214.5 | 6787.8* | 34.4 | 5.5 | 21215.8* | 16.2 | 0.56 | 0.87 | 0.00 | 0.46 |
| S X T | 9 | 0.8 | 11.6 | 185.6 | 214.4 | 74.2 | 7.7 | 1953.2 | 10.2 | 0.26 | 0.42 | 0.00 | 0.10 |
| Parents (P) | 43 | 2.62** | 57.5*** | 2555.5*** | 2138.3*** | 141.5** | 18.0*** | 1392.8 | 47.3*** | 1.65** | 2.94*** | 0.03*** | 0.53*** |
| Checks (C) | 6 | 14.4*** | 347.7*** | 859.1*** | 1383.4*** | 130.1 | 43.0*** | 9302.8*** | 46.2*** | 0.92* | 0.59 | 0.00 | 0.29*** |
| C vs P vs H | 2 | 171.3*** | 291.5*** | 64059.8*** | 55660.8*** | 654.1*** | 637.4*** | 137683.7*** | 318.5*** | 2.57* | 10.08*** | 0.15*** | 1.98*** |
| P vs H | 1 | 110.4*** | 162.2* | 104009.3*** | 72285.2*** | 1149.9*** | 389.5*** | 260135.3*** | 631.1*** | 2.05 | 2.42 | 0.27*** | 3.73*** |
| C vs H | 1 | 172.8*** | 321.9*** | 43878.9*** | 58420.6*** | 40.9 | 667.3*** | 1044.9 | 4.4 | 2.60* | 18.85*** | 0.01 | 0.42 |
| Error | 242/206 | 1.19 | 10.19 | 198.79 | 178.85 | 54.19 | 4.62 | 2036.95 | 7.27 | 0.29 | 0.31 | 0.00 | 0.06 |
| | | | | | | | | | | | | | |
| Mean of genotypes | | 5.50 | 72.5 | 162.1 | 121.1 | 14.3 | 26.8 | 170.9 | 27.6 | 8.5 | 68.22 | 1.71 | 2.34 |
| Mean of hybrids | | 5.52 | 72.5 | 173.2 | 131.4 | 15.0 | 26.8 | 182.2 | 28.2 | 8.5 | 68.14 | 1.72 | 2.40 |
| Mean of parents | | 4.25 | 74.0 | 134.3 | 99.0 | 10.8 | 24.4 | 120.7 | 25.2 | 8.7 | 68.33 | 1.66 | 2.16 |
| Mean of checks | | 7.48 | 69.8 | 141.8 | 95.3 | 15.8 | 30.7 | 170.9 | 27.9 | 8.1 | 69.33 | 1.76 | 2.22 |
| Mean of lines | | 4.08 | 74.2 | 135.5 | 100.4 | 10.8 | 24.4 | 120.0 | 25.3 | 8.8 | 68.25 | 1.65 | 2.40 |
| Mean of testers | | 5.93 | 72.5 | 122.6 | 85.9 | 10.8 | 25.9 | 127.7 | 23.9 | 7.8 | 69.08 | 1.79 | 2.40 |

*and** Significant at the 0.05 and 0.01 probability levels.

†Df separated for NIR quality analysis (protein, starch, fiber, and ash) because only one replication was analyzed: difference = checks plus one entry missing.

‡RSC represents the different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δ Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F2:3, BC1F2:3, and the Low F2:3, BC1F2:3.

¶ Content in grain

Table 7. Mean squares of grain yield and agronomic traits of sorghum hybrids at Vega, TX, in 2016, with means of various categories of experimental entries.

| Source of variation | Df† | Grain yield Mg ha⁻¹ | Days to anthesis | Total height cm | Flag leaf height cm | Plant exsertion cm | Panicle length cm | 3-panicle weight g | 1000-kernel weight g | Protein¶ % | Starch¶ % | Fiber¶ % | Fat¶ % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1/0 | 3.6 | 78.5** | 1039.3* | 186.9 | 352.1** | 0.04 | 16439.0** | 2.9 | N/A | N/A | N/A | N/A |
| Genotypes (G) | 210/209 | 3.7** | 70.0** | 1582.9** | 1483.0** | 43.4** | 15.5** | 3080.8** | 26.5** | 0.68 | 0.45 | 0.01 | 0.23 |
| Hybrids (H) | 159/158 | 2.7** | 55.3** | 1442.5** | 1406.4** | 35.7* | 11.2** | 2571.6** | 20.4** | 0.61 | 0.36 | 0.01 | 0.19 |
|   Lines (L) | 39 | 4.1** | 34.9** | 2697.4** | 2770.1** | 58.9** | 24.7** | 4805.1** | 47.8** | 1.43 | 0.66 | 0.01 | 0.46 |
|   Testers (T) | 3 | 10.5** | 2123.2** | 31469.9** | 29833.7** | 131.8** | 120.1** | 14148.8** | 161.4** | 6.23** | 3.20** | 0.16** | 2.24** |
|   L X T | 117/116 | 2.0 | 8.9* | 254.3** | 222.9** | 25.5 | 3.9* | 1530.3** | 7.6* | 0.19 | 0.18 | 0.00 | 0.04 |
| RSC‡ | 9 | 7.2** | 102.2** | 6483.5** | 6923.4** | 73.2** | 66.3** | 10068.2** | 152.9** | 4.88** | 2.07** | 0.02** | 1.50** |
|   RSC X T | 27 | 2.9** | 15.4* | 507.3** | 8498.9* | 23.9 | 5.7 | 1517.8 | 9.0 | 0.19 | 0.31* | 0.00 | 0.06 |
| Selections (S)δ | 3 | 9.1** | 13.8 | 2297.8* | 2806.3** | 41.8 | 13.4 | 8825.3* | 36.9* | 0.69 | 0.17 | 0.00 | 0.30 |
|   S X T | 9 | 4.5* | 6.3 | 66.1 | 34.7 | 33.4 | 1.6 | 1042.3 | 6.8 | 0.07 | 0.20 | 0.00 | 0.08 |
| Parents (P) | 43 | 2.2* | 57.5** | 1168.2** | 936.5** | 71.5** | 17.7** | 1410.4** | 35.9** | 0.99 | 0.81 | 0.02 | 0.28 |
| Checks (C) | 6 | 11.0** | 490.0** | 947.7** | 825.4** | 19.4 | 15.4** | 4392.9** | 68.9** | 0.37 | 0.22 | 0.01 | 0.66 |
| C vs P vs H | 2 | 95.4** | 252.9** | 23563.5** | 21299.2** | 129.3** | 305.5** | 75530.9** | 183.2** | 1.12 | 0.87 | 0.02 | 1.50* |
|   P vs H | 1 | 147.7** | 300.7** | 394.9** | 30629.8** | 258.6** | 66.5* | 141053.4** | 302.9** | 2.10 | 0.05 | 0.03 | 2.60** |
|   C vs H | 1 | 18.9* | 123.0 | 14278.8** | 19079.4** | 8.6 | 465.0** | 1109.5 | 118.0* | 0.05 | 1.62 | 0.01 | 0.23 |
| Error | 248/N/A | 1.4 | 4.68 | 98.83 | 72.40 | 24.50 | 2.53 | 659.24 | 1.28 | N/A | N/A | N/A | N/A |
| | | | | | | | | | | | | | |
| Mean of genotypes | | 5.65 | 76.4 | 127.1 | 98.9 | 6.0 | 22.1 | 104.8 | 27.7 | 8.9 | 68.26 | 1.77 | 2.75 |
| Mean of hybrids | | 5.85 | 76.2 | 133.7 | 105.3 | 6.4 | 22.0 | 112.9 | 28.3 | 8.8 | 68.25 | 1.77 | 2.79 |
| Mean of parents | | 4.39 | 78.3 | 109.7 | 84.2 | 4.5 | 21.0 | 67.7 | 26.2 | 9.1 | 68.21 | 1.75 | 2.52 |
| Mean of checks | | 6.50 | 74.5 | 115.8 | 84.6 | 6.0 | 25.2 | 117.9 | 26.7 | 8.7 | 67.74 | 1.82 | 2.98 |
| Mean of lines | | 4.38 | 78.5 | 111.2 | 85.7 | 4.6 | 21.0 | 67.1 | 26.2 | 9.1 | 68.13 | 1.73 | 2.80 |
| Mean of testers | | 4.54 | 76.5 | 94.2 | 69.4 | 4.0 | 20.8 | 73.4 | 25.8 | 8.5 | 69.02 | 1.88 | 2.74 |

*and** Significant at the 0.05 and 0.01 probability levels.

†Df separated for NIR quality analysis (protein, starch, fiber, and ash) because only one replication was analyzed: difference = checks plus one entry missing.

‡RSC represents the different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δ Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, and the Low $F_{2:3}$, $BC_1F_{2:3}$.

¶ Content in grain

Table 8. Mean squares of grain yield and agronomic traits of sorghum hybrids at Dumas, TX, in 2016, with means of various categories of experimental entries.

| Source of variation | Df† | Grain yield Mg ha⁻¹ | Total height cm | Flag leaf height cm | Plant exsertion cm | Panicle length cm | 3-panicle weight g | 1000-kernel weight g | Protein¶ % | Starch¶ % | Fiber¶ % | Fat¶ % |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1 | 0.01 | 18.8 | 73.7 | 23.3 | 0.3 | 313.6 | 1.8 | 4.63** | 5.22** | 0.01* | 0.71** |
| Genotypes (G) | 210 | 5.07** | 4242.3** | 4365.3*** | 52.3** | 25.9** | 5747.3** | 35.8*** | 1.10** | 0.63** | 0.01** | 0.31** |
| Hybrids (H) | 159 | 5.48** | 3939.9*** | 4124.7*** | 35.9** | 19.4** | 4067.7** | 29.8*** | 0.00** | 0.50** | 0.01** | 0.27** |
| Lines (L) | 39 | 4.76* | 10511.9** | 11122.1** | 69.4** | 50.9** | 8759.5** | 68.9*** | 2.32** | 1.06** | 0.01** | 0.83** |
| Testers (T) | 3 | 51.97** | 51061.6** | 52828.6*** | 142.4** | 160.6** | 16945.9** | 343.6** | 5.37** | 3.98** | 0.21** | 1.31** |
| L X T | 117 | 4.49* | 519.4** | 526.2** | 21.9 | 5.3* | 2161.9 | 8.7 | 0.29* | 0.22* | 0.00* | 0.06 |
| RSC‡ | 9 | 10.84** | 31059.9*** | 32448.9*** | 130.7** | 133.8** | 16303.7** | 231.2** | 6.88** | 2.48** | 0.02** | 2.47** |
| RSC X T | 27 | 9.05** | 1131.7* | 1095.1 | 19.6 | 6.3 | 2542.5 | 9.9 | 0.56* | 0.41* | 0.01* | 0.07 |
| Selections (S)δ | 3 | 3.47 | 454.1 | 6197.4* | 191.7** | 18.5 | 32279.7** | 7.8 | 0.88 | 0.85* | 0.00 | 0.62* |
| S X T | 9 | 5.41 | 231.5 | 238.2 | 12.7 | 3.6 | 1508.4 | 12.1 | 0.24 | 0.14 | 0.00 | 0.03 |
| Parents (P) | 43 | 3.77 | 2806.0** | 2553.0** | 93.6** | 28.2** | 2958.1* | 38.0** | 1.74** | 0.97* | 0.03** | 0.33** |
| Checks (C) | 6 | 4.59 | 1131.9** | 1193.3** | 52.8** | 23.6** | 10371.3** | 91.2** | 0.71 | 0.24 | 0.03** | 1.03** |
| C vs P vs H | 2 | 1.53 | 68484.0** | 71943.6 | 468.4** | 497.3** | 185293.7** | 308.2** | 5.42** | 4.55** | 0.10** | 0.24 |
| P vs H | 1 | 3.00 | 92276.9** | 75464.7** | 573.1** | 26.1 | 369303.6** | 493.9*** | 9.30*** | 4.71* | 0.10** | 0.21 |
| C vs H | 1 | 0.02 | 67727.3** | 92856.2** | 215.5** | 887.3** | 18583.9* | 215.5* | 0.81 | 3.40* | 0.03* | 0.24 |
| Error | 245/212 | 3.03 | 150.51 | 139.32 | 18.68 | 3.52 | 1986.25 | 7.77 | 0.27 | 0.21 | 0.00 | 0.07 |
| | | | | | | | | | | | | |
| Mean of genotypes | | 6.53 | 162.0 | 127.2 | 8.3 | 26.4 | 226.8 | 27.6 | 8.78 | 68.29 | 1.76 | 2.69 |
| Mean of hybrids | | 6.57 | 173.3 | 138.6 | 8.6 | 26.1 | 243.2 | 28.4 | 8.71 | 68.32 | 1.76 | 2.70 |
| Mean of parents | | 6.36 | 136.7 | 105.5 | 5.7 | 25.5 | 170.0 | 25.7 | 9.08 | 68.07 | 1.73 | 2.65 |
| Mean of checks | | 6.55 | 133.7 | 92.3 | 10.9 | 30.6 | 222.4 | 26.1 | 8.47 | 68.81 | 1.81 | 2.81 |
| Mean of lines | | 6.33 | 139.3 | 107.9 | 5.9 | 25.1 | 166.0 | 25.6 | 9.14 | 67.98 | 1.71 | 2.70 |
| Mean of testers | | 6.73 | 111.3 | 82.1 | 4.5 | 24.8 | 209.3 | 26.2 | 8.46 | 68.90 | 1.86 | 2.70 |

*and** Significant at the 0.05 and 0.01 probability levels.

†Df separated for NIR quality analysis (protein, starch, fiber, and ash) because only two replications were analyzed: difference = checks.

‡RSC represents the different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δ Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F₂:₃, BC₁F₂:₃, and the Low F₂:₃, BC₁F₂:₃

¶ Content in grain

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Table 9. Mean squares of grain yield and agronomic traits of sorghum hybrids at Perryton, TX, in 2015, with means of various categories of experimental entries. Data missing 10 hybrids and no parents planted.

| Source of variation | Df† | Total height cm | Flag leaf height cm | Plant exsertion cm | Panicle length cm | 3-panicle weight g | 1000-kernel weight g | Protein¶ % | Starch¶ % | Fiber¶ % | Fat¶ % |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1 | 1807.5** | 1794.4** | 2.04 | 1.7 | 59356.6** | 22.1* | 18.16** | 39.20 | 0.07** | 0.25* |
| Genotypes (G) | 156 | 4569.3** | 4992.5** | 50.8** | 29.1** | 7385.9** | 26.7** | 1.13** | 9.74 | 0.01** | 0.34** |
| Hybrids (H) | 149 | 4165.3** | 4485.9** | 50.8** | 20.6** | 6572.9** | 25.1** | 1.14** | 1.21** | 0.01** | 0.31** |
| Lines (L) | 39 | 9300.2** | 10195.9** | 94.3** | 52.7** | 10101.7** | 67.5** | 3.14** | 3.33** | 0.02** | 0.94** |
| Testers (T) | 3 | 67720.7** | 71177.0** | 284.8** | 110.4** | 62726.6** | 105.3** | 0.92* | 1.01* | 0.02** | 1.43** |
| L X T | 107 | 481.7** | 497.0** | 27.2 | 6.3** | 3578.5* | 7.1* | 0.43* | 0.43 | 0.00** | 0.06** |
| RSC‡ | 9 | 26914.0** | 29133.4** | 179.3** | 139.7** | 16342.8** | 219.7** | 8.28** | 10.35** | 0.05** | 2.49** |
| RSC X T | 27 | 1238.9** | 1315.1** | 34.5 | 10.5* | 4225.4 | 13.6* | 0.59 | 0.70* | 0.01** | 1.51** |
| Selections (S)δ | 3 | 67524.5* | 9601.0* | 401.2** | 2.5 | 13276.4* | 14.4 | 0.70 | 0.87 | 0.00 | 0.49* |
| S X T | 9 | 262.3 | 196.5 | 20.0 | 2.4 | 3252.7 | 8.3 | 0.24 | 0.34 | 0.00 | 0.05 |
| Checks (C) | 6 | 1213.4** | 1170.7** | 54.3* | 41.7** | 27505.0** | 25.5** | 1.21* | 175.9 | 0.01* | 0.90** |
| C vs H | 1 | 84908.4** | 103417.0** | 23.2 | 1225.3** | 7749.5 | 264.0** | 0.05 | 165.4* | 0.01 | 0.21 |
| Error | 191/150 | 105.89 | 117.55 | 25.01 | 2.53 | 2207.18 | 3.99 | 0.30 | 19.6 | 0.00 | 0.03 |
| | | | | | | | | | | | |
| Mean of genotypes | | 177.2 | 135.5 | 14.8 | 26.9 | 217.9 | 28.5 | 8.8 | 68.28 | 1.68 | 2.59 |
| Mean of hybrids | | 183.9 | 142.9 | 14.9 | 26.1 | 215..8 | 28.8 | 8.5 | 68.44 | 1.68 | 2.59 |
| Mean of checks | | 141.2 | 95.7 | 14.2 | 31.2 | 229.0 | 26.4 | 8.6 | 65.01 | 1.70 | 2.47 |

DTF = days to 50% flowering; *and** Significant at the 0.05 and 0.01 probability levels.

†Separate columns for degrees of freedom for particular traits are because of differences in the number of replications or environments from which data were collected for the traits.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δSelections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F₂:₃, BC₁F₂:₃, and the Low F₂:₃, BC₁F₂:₃.

¶ Content in grain

Table 10. Mean squares of grain yield of sorghum hybrids at Taylor, TX, in 2015, and Hutchinson, KS, in 2015 and 2016, with means of various categories of experimental entries. Data on days to flowering (DTF) were collected only at Hutchinson, KS, in 2015.

| Source of variation | | Hutchinson | | | | | Taylor |
|---|---|---|---|---|---|---|---|
| | | 2015 | | | 2016 | | 2015 |
| | Df | Grain yield | DTF | Df | Grain yield | Df | Grain yield |
| | | Mg ha$^{-1}$ | | | Mg ha$^{-1}$ | | Mg ha$^{-1}$ |
| Replications | 1 | 21.79* | 0.01 | 1 | 42.19** | 1 | 084 |
| Genotypes (G) | 210 | 9.12** | 28.3** | 166 | 4.24** | . | |
| Hybrids (H) | 159 | 7.00** | 10.2 | 159 | 3.44* | 159 | 1.67* |
| Lines (L) | 39 | 13.44** | 13.12* | 39 | 6.71** | 39 | 2.43* |
| Testers (T) | 3 | 18.52* | 44.76* | 3 | 10.32* | 3 | 5.58** |
| L X T | 117 | 4.56 | 8.30 | 117 | 2.18 | 117 | 1.31** |
| RSC† | 9 | 13.81* | 29.61** | 9 | 13.72** | 9 | 4.99** |
| RSC X T | 27 | 8.64* | 13.13* | 27 | 3.93* | 27 | 1.69* |
| Selections (S)‡ | 3 | 37.81** | 11.96 | 3 | 16.32* | 3 | 1.13 |
| S X T | 9 | 5.24 | 15.81 | 9 | 0.54 | 9 | 1.95 |
| Parents (P) | 43 | 4.30 | 70.6** | . | . | . | . |
| Checks (C) | 6 | 22.18** | 63.6** | 6 | 9.51* | . | . |
| C vs P vs H | 2 | 241.91** | 454.0** | . | . | . | . |
| P vs H | 1 | 357.59** | 743.8** | . | . | . | . |
| C vs H | 1 | 58.74* | 59.6* | 1 | 99.35** | . | . |
| Error | 252 | 3.19 | 5.92 | 204 | 2.18 | 159 | 0.59 |
| | | | | | . | | . |
| Mean of genotypes | | 7.864 | 65.03 | | 6.11 | | . |
| Mean of hybrids | | 8.162 | 64.54 | | 5.90 | | . |
| Mean of parents | | 5.886 | 67.83 | | . | | 2.50 |
| Mean of checks | | 9.272 | 63.43 | | 7.39 | | . |
| Mean of lines | | 5.799 | 68.41 | | 5.897 | | . |
| Mean of testers | | 6.743 | 62.00 | | 5.897 | | . |

*Significant at the 0.05 probability level.
**Significant at the 0.01 probability level.
†RSC represents the different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.
‡Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, and Low F$_{2:3}$, BC$_1$F$_2$

the flag leaf, and percentage of concentration of starch in grain. The sorghum selections were significant at Vega, TX, in 2015 for grain yield, height to the flag leaf, and three-panicle weight that also were recorded for Vega in 2016, but with the inclusion of total plant height and 1000-kernel weight. Selections showing significant differences at Dumas, TX, in 2016 were height to the flag leaf, three-panicle weight, and concentrations of starch and fat in grain, with significance of only $P < 0.05$ for grain yield at Vega in 2015. In the combined analysis, sorghum selections showed significant differences for all traits except concentrations of protein, starch, and fiber in the grain. Parents showed

significant differences in individual locations with the exception of three-panicle weight at Vega in 2015; NIR data at Vega in 2016 as previously explained; and grain yield at Dumas in 2016. In the combined analysis, parents showed significant differences for all traits. The seven commercial check hybrids were significantly different in the across-environment analysis (Table 5); at Vega in 2015, there were significant differences among the checks for all traits except plant exsertion and starch concentration in grain, which also was found at Vega in 2016 with the exclusion of concentrations of protein, starch, fiber, and fat in grain. Commercial check sorghums at Dumas, TX, showed significant differences for all traits except grain yield and concentrations of protein and starch in grain. All seven commercial checks at Hutchinson, KS, in 2015 showed significant differences for grain yield and number of days to anthesis.

The greatest overall grain yield for genotypes and hybrids, 7.86 and 8.16 Mg ha$^{-1}$, respectively, were at Hutchinson in 2015, followed by Dumas, Vega (2016), and Vega (2015), with 6.53, 6.57; 5.65, 5.85; and 5.50, 5.52 Mg ha$^{-1}$, respectively. Mean grain yield of parents was greatest at Dumas in 2016, followed by Hutchinson in 2015, Vega in 2016, and Vega in 2015, with yields of 6.36, 5.89, 4.39, and 4.25 Mg ha$^{-1}$, respectively. The greatest overall mean yield was at Hutchinson in 2015, with 9.27 Mg ha$^{-1}$, followed by Vega in 2015, Dumas in 2016, and Vega in 2016, with 7.48, 6.55, and 6.50 Mg ha$^{-1}$, respectively. The greatest overall mean yield of lines was at Dumas in 2016, followed by Hutchinson in 2015, Vega in 2016, and Vega in 2015, with 6.33, 5.80, 4.38, and 4.08 Mg ha$^{-1}$, respectively. The testers yielded more than the lines at all four locations, with greatest yield at Hutchinson in 2015, followed by Dumas in 2016, Vega in 2015, and

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Vega in 2016, with mean yields of 6.73, 6.73, 5.93, and 4.54 Mg ha$^{-1}$, respectively. Sorghum at Vega was planted later than usual in 2015 because of increased rainfall during the planting season but still had 144 growing days, which might have affected yield. Sorghum at Hutchinson was planted 10 days earlier in 2015 than in 2016, with only 133-134 and 143 growing days, respectively; this might account for negative GCA for A.Tx3197 and A.338 because they were probably harvested too early. Sorghum at Vega in 2016 and Dumas in 2016 was planted during the target date for the season in the Texas Panhandle, with 159 and 162 growing days, respectively.

**General Combining Ability (GCA) Effects**

General combining ability (GCA) effects represent the fixable component of genetic variance, and are important for developing superior genotypes. Individual GCA estimates for Perryton in 2015 could not be obtained because of the absence of 10 experimental hybrids in the line x tester analysis, while individual NIR data could not be obtained for Vega in 2016 because of one missing hybrid. GCA estimates were variable for all traits measured at each location (Table 11). Standard errors were greater for lines than testers across all traits evaluated while both standard errors for lines and testers were one or less for all traits except total height, height to the flag leaf, and three-panicle weight, indicating more variability in lines than testers. The range of combined GCA effects for grain yield varied from -0.982 (RSC76-13 $F_{2:3}$ low) to 1.295 (RSC117-4 $BC_1F_{2:3}$ high) among the lines and from -0.359 (A.Tx3197) to 0.359 (A.319) among the testers (Table 12). The magnitude of variance due to specific combining ability (SCA) was greater than that of GCA for grain yield, number of days to anthesis, total plant

Table 11. Combined means of General Combining Ability (GCA) estimates for 12 traits for each parental line in a line x tester evaluated across environments.

| Parent RSCδ | Selections¶ | Grain yield | Days to anthesis | Total height | Height to flag leaf | Plant exsertion | Panicle length | 3-panicle weight | 1000-kernel weight | Protein‡ | Starch‡ | Fiber‡ | Fat‡ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Mg ha⁻¹ | | cm | cm | cm | cm | g | g | % | % | % | % |
| RSC73-9 | $F_{2:3}$ High | 0.28 | -1.38 | 1.75 | 2.38 | 1.20 | -1.90 | -22.48 | -1.35 | -0.32 | -0.08 | 0.00 | -0.05 |
| RSC73-6 | $BC_1F_{2:3}$ High | 0.14 | -1.50 | -7.08 | -2.49 | -1.83 | -2.72 | -11.30 | -1.62 | -0.08 | -0.11 | 0.01 | 0.10 |
| RSC73-1 | $F_{2:3}$ Low | -0.61 | 0.17 | 5.48 | 7.77 | 0.35 | -2.42 | -18.96 | 0.13 | -0.42 | 0.30 | -0.02 | -0.35 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -0.12 | 1.12 | 36.32 | 36.75 | 2.11 | -2.64 | 3.02 | 1.28 | -0.12 | 0.17 | 0.03 | -0.16 |
| RSC83-1 | $F_{2:3}$ High | -0.18 | 1.62 | 0.09 | 4.23 | -3.22 | -0.93 | 21.41 | 0.89 | -0.28 | 0.05 | -0.01 | -0.14 |
| RSC83-14 | $BC_1F_{2:3}$ High | 1.13 | -0.08 | 1.64 | 7.66 | -4.57 | -1.49 | 36.34 | 0.41 | 0.24 | -0.62 | -0.01 | 0.10 |
| RSC83-10 | $F_{2:3}$ Low | -0.22 | 1.33 | -35.86 | -36.33 | -1.43 | 1.82 | -25.71 | -1.06 | -0.03 | -0.06 | 0.03 | -0.05 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 1.12 | 0.04 | 1.01 | 4.74 | -1.93 | -1.82 | 17.98 | 0.71 | 0.25 | -0.46 | 0.00 | 0.11 |
| RSC112-5 | $F_{2:3}$ High | 0.79 | 0.92 | -22.30 | -25.40 | 1.66 | 1.34 | 4.47 | 1.40 | -0.53 | 0.68 | -0.01 | -0.14 |
| RSC112-19 | $BC_1F_{2:3}$ High | 1.05 | 1.29 | -22.34 | -20.93 | -2.08 | 0.72 | 15.59 | -0.52 | -0.11 | 0.39 | 0.01 | 0.13 |
| RSC112-8 | $F_{2:3}$ Low | -0.21 | 0.71 | -38.76 | -40.11 | 0.37 | 0.90 | -17.54 | -1.17 | -0.08 | 0.01 | 0.02 | -0.09 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 0.56 | 0.33 | -26.00 | -28.66 | 0.99 | 1.64 | 5.70 | 0.17 | -0.21 | 0.48 | 0.02 | 0.05 |
| RSC76-4 | $F_{2:3}$ High | -0.98 | 1.42 | 58.77 | 61.28 | 1.19 | -3.70 | 22.50 | 6.85 | -0.50 | 0.32 | -0.05 | -0.54 |
| RSC76-16 | $BC_1F_{2:3}$ High | -0.92 | 2.37 | 63.82 | 62.88 | 3.34 | -2.49 | 55.21 | 7.36 | -0.32 | 0.40 | 0.00 | -0.32 |
| RSC76-13 | $F_{2:3}$ Low | -0.98 | 0.33 | 44.27 | 45.63 | 1.38 | -2.64 | -11.02 | 4.72 | -0.23 | 0.14 | -0.02 | -0.28 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -0.72 | 2.75 | 64.64 | 64.89 | 1.41 | -1.58 | 90.48 | 6.54 | -0.27 | 0.20 | -0.02 | -0.24 |
| RSC38-5 | $F_{2:3}$ High | -0.73 | -1.08 | -26.29 | -27.11 | -2.15 | 2.98 | -20.89 | -3.71 | -0.01 | -0.21 | -0.05 | -0.12 |
| RSC38-15 | $BC_1F_{2:3}$ High | -0.48 | -1.33 | 32.56 | 37.36 | -2.52 | -2.07 | 1.76 | -0.45 | 0.54 | -0.21 | -0.04 | 0.32 |
| RSC38-8 | $F_{2:3}$ Low | -0.40 | -0.96 | 15.41 | 15.70 | 1.81 | -2.19 | 18.21 | -0.04 | -0.49 | 0.31 | -0.06 | -0.35 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -0.60 | -2.58 | 3.26 | 2.14 | -1.32 | 2.38 | -13.24 | -1.19 | 0.31 | -0.05 | 0.02 | 0.14 |
| RSC37-12 | $F_{2:3}$ High | 0.27 | -1.75 | -4.27 | -5.03 | 1.83 | -1.17 | -16.01 | -2.10 | -0.29 | -0.11 | 0.02 | -0.08 |
| RSC37-12 | $BC_1F_{2:3}$ High | 0.48 | -0.58 | 15.52 | 17.26 | -0.87 | -0.97 | 38.55 | -0.73 | 0.15 | -0.17 | 0.04 | 0.09 |
| RSC37-7 | $F_{2:3}$ Low | -0.50 | -0.63 | 9.10 | 8.07 | 2.46 | -1.52 | 10.96 | -0.91 | -0.36 | -0.01 | 0.00 | -0.13 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 0.53 | -1.50 | 3.44 | 4.56 | -1.02 | -0.19 | 24.27 | -3.08 | 0.13 | 0.00 | 0.03 | 0.15 |
| RSC15-13 | $F_{2:3}$ High | -0.38 | -2.50 | -1.07 | -0.97 | 0.81 | -1.00 | -39.35 | 1.28 | 0.72 | -0.38 | -0.02 | 0.24 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RSC15-15 | BC₁F₂:₃ High | -0.13 | -1.17 | -26.97 | -30.02 | -0.16 | 3.46 | -6.70 | -1.64 | 0.39 | 0.13 | -0.01 | 0.14 |
| RSC15-11 | F₂:₃ Low | -0.46 | -1.25 | 25.09 | 22.81 | 2.83 | -0.63 | -35.54 | -1.22 | 0.60 | -0.46 | 0.00 | 0.36 |
| RSC15-14 | BC₁F₂:₃ Low | -0.37 | -2.04 | 6.54 | 6.97 | 0.06 | -0.59 | -23.83 | 1.48 | 0.75 | 0.07 | 0.00 | 0.28 |
| RSC124-9 | F₂:₃ High | 0.70 | 0.37 | -36.98 | -37.18 | -3.08 | 3.32 | -18.51 | -2.62 | -0.21 | -0.17 | -0.04 | 0.00 |
| RSC124-16 | BC₁F₂:₃ High | 0.49 | 1.71 | 3.20 | 1.46 | -1.28 | 2.93 | 36.18 | -1.97 | -0.04 | 0.16 | 0.01 | 0.11 |
| RSC124-3 | F₂:₃ Low | -0.63 | -0.33 | -4.58 | -11.88 | 4.67 | 2.55 | -39.35 | 0.48 | 0.15 | -0.24 | -0.03 | -0.11 |
| RSC124-4 | BC₁F₂:₃ Low | 0.33 | 1.96 | -14.87 | -13.99 | -1.26 | 0.37 | -21.01 | -1.82 | 0.03 | 0.16 | 0.01 | 0.04 |
| RSC117-2 | F₂:₃ High | 0.45 | -0.17 | -33.28 | -32.01 | -2.97 | 1.89 | -12.33 | -0.57 | -0.15 | 0.03 | 0.01 | -0.02 |
| RSC117-4 | BC₁F₂:₃ High | 1.30 | 0.25 | -39.82 | -38.85 | -4.96 | 4.25 | 9.76 | 3.29 | 0.24 | 0.24 | 0.03 | 0.24 |
| RSC117-10 | F₂:₃ Low | -0.07 | -0.25 | -47.00 | -48.61 | -0.13 | 1.64 | -8.05 | -1.44 | -0.08 | -0.05 | 0.00 | -0.08 |
| RSC117-3 | BC₁F₂:₃ Low | 0.48 | 1.46 | -29.20 | -28.73 | -2.26 | 1.97 | 16.37 | 1.14 | 0.20 | -0.01 | 0.01 | 0.21 |
| RSC19-3 | F₂:₃ High | 0.05 | -0.58 | 1.97 | -6.87 | 6.40 | 2.34 | -16.29 | -2.65 | -0.06 | -0.29 | 0.03 | 0.02 |
| RSC19-17 | BC₁F₂:₃ High | -0.37 | 0.46 | 39.41 | 38.48 | 0.76 | 0.08 | -11.11 | -1.65 | 0.64 | -0.41 | 0.01 | 0.42 |
| RSC19-1 | F₂:₃ Low | -0.48 | 0.37 | -46.66 | -50.32 | 3.13 | 0.50 | -41.36 | -4.14 | -0.02 | -0.25 | 0.03 | 0.10 |
| RSC19-10 | BC₁F₂:₃ Low | 0.40 | 0.71 | 21.78 | 23.98 | -0.49 | -1.47 | -3.46 | -1.51 | -0.12 | 0.09 | 0.00 | -0.05 |
| **Testers†** | | | | | | | | | | | | | |
| A.301 | Tester | 0.32 | -3.93 | -33.95 | -32.96 | -0.93 | -0.09 | -15.14 | 0.40 | 0.19 | -0.05 | 0.01 | -0.13 |
| A.319 | Tester | 0.36 | 0.66 | -3.96 | -5.74 | 0.16 | 1.68 | 3.36 | -2.35 | 0.09 | -0.04 | 0.01 | 0.00 |
| A.Tx.3197 | Tester | -0.36 | -1.40 | 9.73 | 8.50 | 1.67 | -0.44 | -12.80 | 0.85 | -0.13 | 0.08 | -0.03 | 0.01 |
| A.338 | Tester | -0.32 | 4.67 | 27.75 | 29.79 | -0.90 | -1.16 | 24.38 | 1.10 | -0.14 | 0.00 | 0.00 | 0.12 |
| SE Lines | | 0.269 | 0.933 | 3.747 | 3.680 | 1.091 | 0.415 | 8.869 | 0.524 | 0.166 | 0.160 | 0.017 | 0.091 |
| SE Testers | | 0.085 | 0.295 | 1.185 | 1.164 | 0.345 | 0.131 | 2.805 | 0.166 | 0.053 | 0.051 | 0.005 | 0.029 |

†Testers were analyzed separately
‡Content in grain
δRSC represents different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.
¶Selections (S) are equal to the High and Low percentage of exotic genome recovery and the generation: High F₂:₃, BC₁F₂:₃, and the Low F₂:₃, BC₁F₂:₃.

Table 12. General Combining Ability (GCA) estimates and the combined analysis for grain yield (Mg ha$^{-1}$) for each parental line in a line x tester evaluated in six environments. Because of the absence of parental lines or hybrids, individual GCA estimates were not reported for Taylor, TX, in 2015, or Hutchinson, KS, in 2016. All six locations are included in the combined analysis.

| Parents RSC‡Lines | Selectionsδ | Vega 2015 | Hutchinson 2015 | Vega 2016 | Dumas 2016 | Combined locations | Rank |
|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | 0.019 | 1.542 | -0.616 | 0.074 | 0.276 | 15 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 1.119 | 1.764 | -0.782 | -1.019 | 0.141 | 17 |
| RSC73-1 | F$_{2:3}$ Low | -0.96 | -1.797 | -0.866 | 0.591 | -0.613 | 34 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | -1.341 | -0.28 | -0.116 | 0.396 | -0.124 | 20 |
| RSC83-1 | F$_{2:3}$ High | -0.998 | -1.58 | 0.789 | 0.082 | -0.177 | 22 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 2.074 | 0.898 | 0.348 | 1.581 | 1.130 | 2 |
| RSC83-10 | F$_{2:3}$ Low | 0.273 | -1.307 | -0.861 | 0.682 | -0.223 | 24 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 1.024 | 1.856 | 0.276 | 1.782 | 1.118 | 3 |
| RSC112-5 | F$_{2:3}$ High | 2.147 | 0.034 | 1.114 | -0.620 | 0.787 | 5 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 2.191 | 2.034 | 2.028 | 0.490 | 1.048 | 4 |
| RSC112-8 | F$_{2:3}$ Low | 0.819 | 0.156 | 0.004 | -0.370 | -0.207 | 23 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 1.970 | 0.653 | 0.756 | 0.113 | 0.557 | 7 |
| RSC76-4 | F$_{2:3}$ High | -1.447 | -1.650 | -0.184 | -0.826 | -0.978 | 39 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -2.302 | -2.442 | 0.335 | -0.157 | -0.915 | 38 |
| RSC76-13 | F$_{2:3}$ Low | -1.818 | -1.120 | -0.225 | -1.260 | -0.982 | 40 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | -1.947 | -0.438 | -0.031 | -0.861 | -0.720 | 36 |
| RSC38-5 | F$_{2:3}$ High | 0.413 | -1.385 | -0.908 | -0.586 | -0.731 | 37 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -1.870 | 0.066 | 0.225 | -1.271 | -0.478 | 30 |
| RSC38-8 | F$_{2:3}$ Low | -1.217 | -0.203 | 0.011 | -0.529 | -0.396 | 28 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | -0.602 | -0.354 | 0.085 | -1.006 | -0.598 | 33 |
| RSC37-12 | F$_{2:3}$ High | 0.271 | -0.068 | 1.014 | -1.151 | 0.272 | 16 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | -0.748 | 1.821 | -0.242 | 0.347 | 0.477 | 11 |
| RSC37-7 | F$_{2:3}$ Low | -0.951 | -0.872 | -0.476 | -0.987 | -0.500 | 32 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 0.334 | 0.582 | 0.851 | -0.219 | 0.534 | 8 |
| RSC15-13 | F$_{2:3}$ High | -0.396 | 0.069 | -1.067 | 0.611 | -0.384 | 27 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 1.550 | -1.531 | -0.483 | 0.240 | -0.131 | 21 |
| RSC15-11 | F$_{2:3}$ Low | -1.884 | -0.714 | -0.272 | 0.514 | -0.463 | 29 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | -0.736 | 0.200 | -0.877 | -0.459 | -0.369 | 26 |
| RSC124-9 | F$_{2:3}$ High | 0.996 | 2.595 | -0.045 | 0.490 | 0.703 | 6 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 0.383 | -0.781 | 0.958 | 0.533 | 0.485 | 9 |
| RSC124-3 | F$_{2:3}$ Low | -0.088 | -0.924 | -0.936 | -0.615 | -0.628 | 35 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.325 | 1.486 | -1.122 | 1.090 | 0.331 | 14 |
| RSC117-2 | F$_{2:3}$ High | 0.606 | 0.756 | 0.110 | 0.140 | 0.451 | 12 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 2.363 | 1.567 | 0.952 | 0.714 | 1.295 | 1 |
| RSC117-10 | F$_{2:3}$ Low | 0.985 | -0.831 | -0.481 | -0.231 | -0.070 | 19 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 0.455 | 0.727 | -0.019 | 1.085 | 0.481 | 10 |
| RSC19-3 | F$_{2:3}$ High | 0.752 | 0.080 | 0.569 | -0.481 | 0.054 | 18 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -0.846 | -0.904 | 0.048 | -0.019 | -0.367 | 25 |
| RSC19-1 | F$_{2:3}$ Low | 0.178 | -1.932 | -0.579 | 1.018 | -0.480 | 31 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -0.806 | 2.226 | 0.718 | 0.156 | 0.396 | 13 |
| **Testers** | | | | | | | |
| A.301 | Tester | 0.732 | 0.438 | -0.239 | 0.935 | 0.321 | 2 |
| A.319 | Tester | 0.378 | 0.255 | 0.446 | 0.271 | 0.359 | 1 |
| A.Tx.3197 | Tester | -0.635 | -0.66 | -0.344 | -0.193 | -0.359 | 4 |
| A.338 | Tester | -0.477 | -0.033 | 0.137 | -1.002 | -0.322 | 3 |
| SE Lines | | 0.376 | 0.652 | 0.417 | 0.606 | 0.269 | |
| SE Testers | | 0.119 | 0.206 | 0.132 | 0.192 | 0.085 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program and their respective families used in the study.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, and the Low F$_{2:3}$, BC$_1$F$_{2:3}$.

height, height to the flag leaf, panicle length, three-panicle weight, and 1000-kernel weight, revealing that non-additive gene action was dominant in the inheritance of grain yield and all its component traits. Rani et al. (2015) studied six lines and eight testers of grain sorghum and found similar results for grain yield and its components. Similar observations also were reported by Chaudhary et al. (2006) and Premalatha et al. (2006). Non-additive gene action for grain yield and its components in the present study was in accordance with findings by Aruna et al. (2010), Mahdy et al (2011), and Rani et al. (2015), whereas additive gene action controlling the inheritance of grain yield per plant was reported by Prabhakar et al. (2013). Line RSC117-4, a BC generation with a large percentage of exotic genome recovery ($BC_1F_{2:3}$ high) had the greatest GCA (1.295) and proved to be a good combiner for grain yield. Tester A.319 had the greatest GCA (0.359), but was followed closely by A.301 with a GCA effect of 0.321 for grain yield. This grain yield was very encouraging because plant breeders continually strive for earlier, better-yielding varieties. A.301 was generally a good combiner for the number of days to anthesis, total plant height, height to the flag leaf, and concentration of protein and fiber in grain, with GCA effects of -5.252, -33.947, -32.964, 0.189, and 0.013, respectively.

RSC76-2 $BC_1F_{2:3}$ low had the greatest GCA effect of 3.548 for the number of days to anthesis; however, if sorghum breeders are seeking earlier hybrids, line RSC37-12 $BC_1F_{2:3}$ low with a GCA effect of -3.639 would be a good combiner to shorten the duration of vegetative growth. Tester A.301 had a combined GCA effect of -5.252 and proved to be a good combiner for early maturity. For total plant height and height to the

flag leaf, RSC76-2 ranked first with GCA effects of 64.638 and 64.890, respectively; however, RSC117-10, a $F_{2:3}$ generation with small percentage of exotic genome recovery ($F_{2:3}$ low) ranked 40th and 39th with GCA effects of -47.003 and -48.605, respectively. RSC117-10 is a good general combiner to reduce plant height with the greatest panicle length GCA effect (Tables 11-16). Negative GCA effect for plant height and height to the flag leaf is useful for development of dwarf plant material (Fellahi et al., 2013). Tester A.338 had the least GCA effect for panicle length but the greatest GCA for three-panicle and 1000-kernel weight, with -1.158, 24.383, and 1.104, respectively (Tables 16, 18-19). RSC family 76 ranked 1st and 2nd for three-panicle weight, with GCA effects of 90.480 and 55.208, respectively; in addition, all four family members ranked 1-4 for 1000-kernel weight, with GCA effects of 7.360, 6.849, 6.536, and 4.720 for $BC_1$ and $F_{2:3}$ generation with large percentage of exotic genome recovery and $BC_1$ and $F_{2:3}$ generation with small percentage of exotic genome recovery, respectively. Others with large GCA effect for 1000-kernel weight were RSC117-4, RSC15-14, RSC112-5, and RSC73-5 that consisted of $BC_1F_{2:3}$ high, $BC_1F_{2:3}$ low, $F_{2:3}$ high, and $BC_1F_{2:3}$ low, respectively (Table 19). The greatest GCA effect for environmentally affected exsertion was in tester B.Tx3197 while the lines with the greatest GCA effects were RSC19-3 ($F_{2:3}$ high), RSC124-3 ($F_{2:3}$ low), RSC76-6 ($BC_1F_{2:3}$ high), RSC19-1 ($F_{2:3}$ low), and RSC15-11 ($F_{2:3}$ low) with GCA effects of 6.403, 4.666, 3.34, 3.131, and 2.825, respectively (Table 17). In sorghum, the plant height, number of days to anthesis, maturity, plant exsertion, panicle size, and kernel size in addition to grain yield are major selection criteria. A.301 had the greatest combined GCA effect (0.189) for concentration of protein in the grain that was very influenced by environment (Table 19). The greatest GCA effect (0.335)

Table 13. General Combining Ability (GCA) estimates and combined analysis for the number of days to anthesis for each parental line in a line x tester evaluated in two environments.

| Parents | | Vega | | Combined | |
|---|---|---|---|---|---|
| **RSC‡Lines** | Selectionsδ | 2015 | 2016 | locations | Rank |
| RSC73-9 | $F_{2:3}$ High | -0.468 | -2.572 | -1.827 | 33 |
| RSC73-6 | $BC_1F_{2:3}$ High | -0.343 | -3.697 | -2.389 | 36 |
| RSC73-1 | $F_{2:3}$ Low | 0.657 | -0.072 | 0.611 | 16 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 1.782 | -0.197 | 0.423 | 18 |
| RSC83-1 | $F_{2:3}$ High | 3.157 | 0.803 | 2.486 | 4 |
| RSC83-14 | $BC_1F_{2:3}$ High | 0.532 | 0.303 | 0.923 | 14 |
| RSC83-10 | $F_{2:3}$ Low | 0.532 | 1.428 | 1.173 | 10 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 0.282 | -0.447 | 0.548 | 17 |
| RSC112-5 | $F_{2:3}$ High | 1.907 | 1.428 | 1.611 | 8 |
| RSC112-19 | $BC_1F_{2:3}$ High | 1.675 | 3.178 | 2.861 | 3 |
| RSC112-8 | $F_{2:3}$ Low | 0.782 | 0.928 | 1.298 | 9 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 1.782 | 0.553 | 0.798 | 15 |
| RSC76-4 | $F_{2:3}$ High | 0.782 | 2.428 | 2.173 | 5 |
| RSC76-16 | $BC_1F_{2:3}$ High | 1.782 | 4.428 | 3.423 | 2 |
| RSC76-13 | $F_{2:3}$ Low | 0.282 | 0.428 | -0.202 | 23 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 1.782 | 4.678 | 3.548 | 1 |
| RSC38-5 | $F_{2:3}$ High | -0.343 | -1.322 | -1.014 | 29 |
| RSC38-15 | $BC_1F_{2:3}$ High | -1.218 | -0.947 | -1.827 | 34 |
| RSC38-8 | $F_{2:3}$ Low | -2.093 | -1.322 | -2.014 | 35 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -3.093 | -2.947 | -3.514 | 39 |
| RSC37-12 | $F_{2:3}$ High | -3.093 | -2.072 | -3.639 | 40 |
| RSC37-12 | $BC_1F_{2:3}$ High | -0.218 | -0.572 | -0.452 | 24 |
| RSC37-7 | $F_{2:3}$ Low | -0.843 | -1.072 | -0.764 | 27 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -0.843 | -2.322 | -1.139 | 30 |
| RSC15-13 | $F_{2:3}$ High | -1.968 | -4.197 | -3.327 | 37 |
| RSC15-15 | $BC_1F_{2:3}$ High | -0.343 | -1.697 | -1.139 | 31 |
| RSC15-11 | $F_{2:3}$ Low | -1.611 | -0.697 | -0.577 | 26 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -2.754 | -3.697 | -3.327 | 38 |
| RSC124-9 | $F_{2:3}$ High | -1.093 | 0.678 | -0.514 | 25 |
| RSC124-16 | $BC_1F_{2:3}$ High | 1.157 | 3.178 | 2.111 | 6 |
| RSC124-3 | $F_{2:3}$ Low | -0.343 | -1.072 | -0.764 | 28 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -0.468 | 2.553 | 0.986 | 13 |
| RSC117-2 | $F_{2:3}$ High | -0.843 | -0.822 | -1.139 | 32 |
| RSC117-4 | $BC_1F_{2:3}$ High | 0.907 | -1.072 | 0.111 | 21 |
| RSC117-10 | $F_{2:3}$ Low | 0.032 | 0.178 | 0.298 | 19 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 1.032 | 1.303 | 1.173 | 11 |
| RSC19-3 | $F_{2:3}$ High | -0.593 | 0.428 | -0.139 | 22 |
| RSC19-17 | $BC_1F_{2:3}$ High | 0.407 | 1.803 | 1.736 | 7 |
| RSC19-1 | $F_{2:3}$ Low | 0.282 | 0.928 | 0.298 | 20 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 0.657 | 1.178 | 1.111 | 12 |
| **Testers** | | | | | |
| A.301 | Tester | -5.557 | -5.297 | -5.252 | 4 |
| A.319 | Tester | 0.734 | 0.566 | 1.023 | 2 |
| A.Tx.3197 | Tester | -1.831 | -2.109 | -2.358 | 3 |
| A.338 | Tester | 6.762 | 6.841 | 6.586 | 1 |
| SE Lines | | 1.026 | 0.816 | 0.612 | |
| SE Testers | | 0.324 | 0.258 | 0.194 | |

†Testers were analyzed separately from the lines
‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.
δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, and the Low $F_{2:3}$, $BC_1F_{2:3}$.

Table 14. General Combining Ability (GCA) estimates and combined analysis for total plant height (cm) for each parental line in a line x tester evaluated in four environments. Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents | | | Vega | Dumas | Combined | |
|---|---|---|---|---|---|---|
| **RSC‡Lines** | Selections¶ | 2015 | 2016 | 2016 | locations | Rank |
| RSC73-9 | F$_{2:3}$ High | 6.965 | -4.23 | 4.583 | 1.747 | 19 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 3.472 | -10.686 | -9.916 | -7.076 | 26 |
| RSC73-1 | F$_{2:3}$ Low | -0.179 | 2.861 | 6.594 | 5.479 | 14 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 35.752 | 27.52 | 42.789 | 36.315 | 6 |
| RSC83-1 | F$_{2:3}$ High | 6.542 | 0.427 | -6.741 | 0.093 | 22 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -1.449 | 3.813 | -3.037 | 1.641 | 20 |
| RSC83-10 | F$_{2:3}$ Low | -40.343 | -21.375 | -44.100 | -35.863 | 35 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 3.578 | -0.843 | -1.767 | 1.006 | 21 |
| RSC112-5 | F$_{2:3}$ High | -39.178 | 2.967 | -10.445 | -22.304 | 28 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | -21.429 | -13.649 | -24.672 | -22.335 | 29 |
| RSC112-8 | F$_{2:3}$ Low | -42.248 | -27.196 | -39.443 | -38.761 | 37 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -29.601 | -12.095 | -30.977 | -26.002 | 30 |
| RSC76-4 | F$_{2:3}$ High | 58.982 | 31.436 | 73.375 | 58.766 | 3 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 66.284 | 39.585 | 75.809 | 63.818 | 2 |
| RSC76-13 | F$_{2:3}$ Low | 40.567 | 22.652 | 57.712 | 44.266 | 4 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 68.983 | 37.151 | 81.207 | 64.638 | 1 |
| RSC38-5 | F$_{2:3}$ High | -18.858 | -18.200 | -26.32 | -26.286 | 31 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 44.112 | 11.963 | 43.742 | 32.558 | 7 |
| RSC38-8 | F$_{2:3}$ Low | 17.019 | 6.353 | 20.035 | 15.413 | 11 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 12.045 | -6.452 | -0.497 | 3.255 | 16 |
| RSC37-12 | F$_{2:3}$ High | -2.348 | -5.923 | -6.106 | -4.272 | 24 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 19.877 | 12.068 | 14.532 | 15.519 | 10 |
| RSC37-7 | F$_{2:3}$ Low | 13.103 | 2.120 | 8.605 | 9.103 | 12 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 5.007 | 4.237 | 1.514 | 3.440 | 15 |
| RSC15-13 | F$_{2:3}$ High | 0.879 | -0.526 | 13.368 | -1.068 | 23 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | -26.108 | -11.638 | -37.009 | -26.974 | 32 |
| RSC15-11 | F$_{2:3}$ Low | 27.98 | 18.842 | 35.91 | 25.093 | 8 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 21.449 | -0.843 | 11.357 | 6.537 | 13 |
| RSC124-9 | F$_{2:3}$ High | -37.009 | -24.973 | -40.819 | -36.983 | 36 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | -1.661 | 15.349 | 0.985 | 3.197 | 17 |
| RSC124-3 | F$_{2:3}$ Low | -1.819 | -6.241 | -10.657 | -4.577 | 25 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -16.288 | -7.828 | -24.732 | -14.870 | 27 |
| RSC117-2 | F$_{2:3}$ High | -44.999 | -21.057 | -40.925 | -33.284 | 34 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | -42.512 | -23.703 | -48.333 | -39.819 | 38 |
| RSC117-10 | F$_{2:3}$ Low | -55.477 | -25.714 | -54.048 | -47.003 | 40 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | -43.835 | -17.565 | -37.538 | -29.195 | 33 |
| RSC19-3 | F$_{2:3}$ High | 7.071 | 7.729 | -5.259 | 1.972 | 18 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 32.841 | 29.531 | 46.282 | 39.411 | 5 |
| RSC19-1 | F$_{2:3}$ Low | -45.74 | -30.371 | -58.387 | -46.658 | 39 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 20.035 | 14.503 | 20.247 | 21.776 | 9 |
| **Testers** | | | | | | |
| A.301 | Tester | -36.046 | -25.061 | -33.033 | -33.947 | 4 |
| A.319 | Tester | -6.633 | 0.257 | -5.026 | -3.960 | 3 |
| A.Tx.3197 | Tester | 11.839 | 1.348 | 11.283 | 9.725 | 2 |
| A.338 | Tester | 31.084 | 23.456 | 26.364 | 27.752 | 1 |
| SE Lines | | 5.396 | 3.695 | 4.6997 | 3.747 | |
| SE Testers | | 1.706 | 1.169 | 1.4862 | 1.185 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, and the Low F$_{2:3}$, BC$_1$F$_{2:3}$.

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Table 15. General Combining Ability (GCA) estimates and combined analysis for height to the flag leaf (cm) for each parental line in a line x tester evaluated in four environments. Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents | | Vega | | Dumas | Combined | |
|---|---|---|---|---|---|---|
| **RSC‡Lines** | Selectionsδ | 2015 | 2016 | 2016 | locations | Rank |
| RSC73-9 | $F_{2:3}$ High | 8.761 | -5.787 | 2.863 | 2.380 | 19 |
| RSC73-6 | $BC_1F_{2:3}$ High | 5.639 | -4.835 | -6.027 | -2.486 | 23 |
| RSC73-1 | $F_{2:3}$ Low | 1.935 | 6.701 | 7.838 | 7.765 | 13 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 35.908 | 24.164 | 43.398 | 36.751 | 7 |
| RSC83-1 | $F_{2:3}$ High | 11.143 | 2.362 | -3.169 | 4.233 | 18 |
| RSC83-14 | $BC_1F_{2:3}$ High | 8.708 | 5.008 | 2.652 | 7.659 | 14 |
| RSC83-10 | $F_{2:3}$ Low | -37.117 | -22.403 | -45.608 | -36.328 | 35 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 9.396 | 0.88 | 1.911 | 4.736 | 16 |
| RSC112-5 | $F_{2:3}$ High | -39.552 | -2.295 | -14.705 | -25.40 | 29 |
| RSC112-19 | $BC_1F_{2:3}$ High | -20.139 | -11.291 | -24.940 | -20.925 | 28 |
| RSC112-8 | $F_{2:3}$ Low | -41.827 | -26.636 | -39.682 | -40.112 | 38 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -30.027 | -14.858 | -33.967 | -28.66 | 31 |
| RSC76-4 | $F_{2:3}$ High | 61.096 | 36.123 | 78.111 | 61.277 | 3 |
| RSC76-16 | $BC_1F_{2:3}$ High | 58.662 | 39.298 | 78.111 | 62.878 | 2 |
| RSC76-13 | $F_{2:3}$ Low | 45.168 | 22.364 | 58.638 | 45.626 | 4 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 62.578 | 38.557 | 82.873 | 64.89 | 1 |
| RSC38-5 | $F_{2:3}$ High | -19.761 | -18.699 | -27.617 | -27.107 | 30 |
| RSC38-15 | $BC_1F_{2:3}$ High | 49.243 | 16.332 | 50.171 | 37.359 | 6 |
| RSC38-8 | $F_{2:3}$ Low | 15.217 | 8.818 | 19.373 | 15.702 | 11 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 10.613 | -4.623 | -1.264 | 2.142 | 20 |
| RSC37-12 | $F_{2:3}$ High | -0.076 | -7.692 | -8.143 | -5.028 | 24 |
| RSC37-12 | $BC_1F_{2:3}$ High | 21.250 | 14.533 | 14.505 | 17.264 | 10 |
| RSC37-7 | $F_{2:3}$ Low | 12.889 | 3.314 | 4.768 | 8.068 | 12 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 7.756 | 3.738 | 0.535 | 4.563 | 17 |
| RSC15-13 | $F_{2:3}$ High | -1.928 | -0.496 | 14.717 | -0.971 | 22 |
| RSC15-15 | $BC_1F_{2:3}$ High | -30.662 | -14.042 | -37.036 | -30.017 | 33 |
| RSC15-11 | $F_{2:3}$ Low | 23.525 | 17.496 | 33.343 | 22.807 | 9 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 21.892 | 0.034 | 11.33 | 6.972 | 15 |
| RSC124-9 | $F_{2:3}$ High | -38.599 | -24.52 | -43.068 | -37.179 | 36 |
| RSC124-16 | $BC_1F_{2:3}$ High | -6.637 | 11.146 | 0.641 | 1.458 | 21 |
| RSC124-3 | $F_{2:3}$ Low | -5.367 | -10.656 | -18.621 | -11.880 | 26 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -12.035 | -8.962 | -25.288 | -13.994 | 27 |
| RSC117-2 | $F_{2:3}$ High | -39.869 | -20.075 | -41.057 | -32.014 | 34 |
| RSC117-4 | $BC_1F_{2:3}$ High | -42.483 | -24.414 | -44.55 | -38.846 | 37 |
| RSC117-10 | $F_{2:3}$ Low | -58.496 | -26.425 | -54.075 | -48.605 | 39 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -46.325 | -15.418 | -34.919 | -28.734 | 32 |
| RSC19-3 | $F_{2:3}$ High | -1.399 | -2.824 | -13.541 | -6.866 | 25 |
| RSC19-17 | $BC_1F_{2:3}$ High | 34.055 | 27.233 | 44.35 | 38.483 | 5 |
| RSC19-1 | $F_{2:3}$ Low | -51.299 | -30.129 | -61.907 | -50.323 | 40 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 19.821 | 18.978 | 25.935 | 23.984 | 8 |
| **Testers** | | | | | | |
| A.301 | Tester | -34.482 | -23.808 | -32.674 | -32.964 | 4 |
| A.319 | Tester | -9.527 | -0.887 | -5.794 | -5.740 | 3 |
| A.Tx.3197 | Tester | 10.341 | 1.251 | 9.669 | 8.496 | 2 |
| A.338 | Tester | 33.967 | 23.444 | 28.39 | 29.792 | 1 |
| SE Lines | | 5.110 | 3.176 | 4.554 | 3.678 | |
| SE Testers | | 1.616 | 1.004 | 1.440 | 1.164 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, and the Low $F_{2:3}$, $BC_1F_{2:3}$.

Table 16. General Combining Ability (GCA) estimates and the combined analysis for panicle length (cm) for each parental line in a line x tester evaluated in four environments. Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents RSC‡Lines | Selectionsδ | Vega 2015 | Vega 2016 | Dumas 2016 | Combined locations | Rank |
|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | -2.427 | -1.771 | -1.193 | -1.897 | 32 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | -2.531 | -2.188 | -2.901 | -2.715 | 39 |
| RSC73-1 | F$_{2:3}$ Low | -1.781 | -2.583 | -2.693 | -2.418 | 35 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | -2.136 | -2.271 | -3.235 | -2.637 | 38 |
| RSC83-1 | F$_{2:3}$ High | -0.011 | 0.062 | -2.318 | -0.934 | 23 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -2.031 | -0.021 | -1.86 | -1.485 | 28 |
| RSC83-10 | F$_{2:3}$ Low | 0.031 | 1.625 | 2.099 | 1.817 | 11 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -2.573 | -1.75 | -3.068 | -1.819 | 31 |
| RSC112-5 | F$_{2:3}$ High | -0.136 | 2.375 | 3.224 | 1.342 | 14 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | -0.088 | 0.271 | 1.504 | 0.721 | 16 |
| RSC112-8 | F$_{2:3}$ Low | 1.344 | -1.125 | 1.765 | 0.900 | 15 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 1.135 | 1.066 | 2.140 | 1.641 | 13 |
| RSC76-4 | F$_{2:3}$ High | -3.448 | -3.250 | -3.526 | -3.704 | 40 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -1.915 | -1.833 | -3.735 | -2.490 | 36 |
| RSC76-13 | F$_{2:3}$ Low | -1.823 | -2.00 | -2.693 | -2.636 | 37 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | -0.865 | -1.208 | -2.151 | -1.579 | 30 |
| RSC38-5 | F$_{2:3}$ High | 1.802 | 2.479 | 4.265 | 2.978 | 4 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -1.552 | -1.646 | -2.610 | -2.074 | 33 |
| RSC38-8 | F$_{2:3}$ Low | -1.823 | -1.083 | -2.443 | -2.189 | 34 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 1.260 | 1.729 | 3.932 | 2.375 | 7 |
| RSC37-12 | F$_{2:3}$ High | -0.823 | -1.333 | -0.776 | -1.168 | 26 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | -1.740 | -0.833 | -0.610 | -0.965 | 24 |
| RSC37-7 | F$_{2:3}$ Low | -1.156 | -1.021 | -1.651 | -1.516 | 29 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 0.989 | 0.021 | -1.526 | -0.194 | 20 |
| RSC15-13 | F$_{2:3}$ High | -1.531 | -0.938 | -0.818 | -0.996 | 25 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 3.614 | 2.271 | 2.849 | 3.462 | 2 |
| RSC15-11 | F$_{2:3}$ Low | 1.079 | -0.833 | -1.151 | -0.629 | 22 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | -0.564 | -1.271 | -0.485 | -0.585 | 21 |
| RSC124-9 | F$_{2:3}$ High | 4.427 | 2.50 | 4.015 | 3.319 | 3 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 3.802 | 2.50 | 2.307 | 2.926 | 5 |
| RSC124-3 | F$_{2:3}$ Low | 2.031 | 1.25 | 3.515 | 2.547 | 6 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -0.112 | 0.583 | 1.557 | 0.367 | 18 |
| RSC117-2 | F$_{2:3}$ High | 1.427 | 2.354 | 1.974 | 1.894 | 10 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 3.552 | 3.583 | 3.974 | 4.249 | 1 |
| RSC117-10 | F$_{2:3}$ Low | 0.698 | 1.75 | 1.265 | 1.644 | 12 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 0.906 | 1.521 | 2.224 | 1.973 | 9 |
| RSC19-3 | F$_{2:3}$ High | 3.635 | 1.646 | 2.265 | 2.343 | 8 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 0.073 | 0.708 | -1.276 | 0.077 | 19 |
| RSC19-1 | F$_{2:3}$ Low | 0.156 | -0.208 | 0.599 | 0.499 | 17 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -1.156 | -1.125 | -2.568 | -1.469 | 27 |
| **Testers** | | | | | | |
| A.301 | Tester | -0.366 | 0.204 | 0.118 | -0.093 | 3 |
| A.319 | Tester | 1.795 | 1.3 | 1.824 | 1.684 | 1 |
| A.Tx.3197 | Tester | -0.848 | 0.154 | -0.343 | -0.435 | 2 |
| A.338 | Tester | -0.578 | -1.658 | -1.597 | -1.158 | 4 |
| SE Lines | | 0.797 | 0.546 | 0.704 | 0.415 | |
| SE Testers | | 0.252 | 0.173 | 0.223 | 0.131 | |

†Testers were analyzed separately from the lines.
‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.
δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, and the Low F$_{2:3}$, BC$_1$F$_{2:3}$.

Table 17.  General Combining Ability (GCA) estimates and the combined analysis for plant exsertion (cm) for each parental line in a line x tester evaluated in four environments.  Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents | | Vega | | Dumas | Combined | |
|---|---|---|---|---|---|---|
| **RSC‡Lines** | Selectionsδ | 2015 | 2016 | 2016 | locations | Rank |
| RSC73-9 | F$_{2:3}$ High | 0.627 | 3.200 | 2.312 | 1.198 | 13 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 0.361 | -3.749 | -0.118 | -1.83 | 30 |
| RSC73-1 | F$_{2:3}$ Low | -0.337 | -0.271 | 2.755 | 0.347 | 19 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 1.975 | 5.394 | 1.452 | 2.110 | 7 |
| RSC83-1 | F$_{2:3}$ High | -4.594 | -2.082 | 0.317 | -3.220 | 38 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -8.130 | -1.189 | -4.226 | -4.569 | 39 |
| RSC83-10 | F$_{2:3}$ Low | -3.260 | -0.832 | -1.111 | -1.428 | 29 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -3.249 | 0.089 | -1.460 | -1.927 | 31 |
| RSC112-5 | F$_{2:3}$ High | 0.505 | 2.653 | -0.306 | 1.662 | 10 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | -1.205 | -2.330 | -3.968 | -2.079 | 32 |
| RSC112-8 | F$_{2:3}$ Low | -1.768 | 0.375 | -1.092 | 0.370 | 18 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -0.713 | 1.496 | -1.590 | 0.987 | 15 |
| RSC76-4 | F$_{2:3}$ High | 1.330 | -1.330 | -0.735 | 1.185 | 14 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 9.232 | 1.885 | 0.108 | 3.340 | 3 |
| RSC76-13 | F$_{2:3}$ Low | -2.782 | 2.839 | -0.126 | 1.380 | 12 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 7.267 | 0.246 | -0.615 | 1.407 | 11 |
| RSC38-5 | F$_{2:3}$ High | -0.903 | -1.840 | -0.643 | -2.154 | 33 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -3.428 | -2.442 | -4.237 | -2.519 | 35 |
| RSC38-8 | F$_{2:3}$ Low | 3.621 | -1.616 | 3.105 | 1.807 | 9 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 0.167 | -3.669 | -0.556 | -1.321 | 28 |
| RSC37-12 | F$_{2:3}$ High | -1.453 | 2.868 | 4.44 | 1.831 | 8 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 0.365 | -1.866 | 1.757 | -0.872 | 24 |
| RSC37-7 | F$_{2:3}$ Low | 1.367 | -0.407 | 0.279 | 2.459 | 6 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -3.742 | 0.243 | 0.960 | -1.021 | 25 |
| RSC15-13 | F$_{2:3}$ High | 4.336 | 0.674 | 0.587 | 0.807 | 16 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 0.933 | 0.338 | -3.578 | -0.155 | 22 |
| RSC15-11 | F$_{2:3}$ Low | 3.374 | 1.944 | 1.767 | 2.825 | 5 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.117 | 0.161 | -0.961 | 0.058 | 20 |
| RSC124-9 | F$_{2:3}$ High | -2.840 | -2.924 | 1.450 | -3.078 | 37 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 1.171 | 1.469 | -2.148 | -1.278 | 27 |
| RSC124-3 | F$_{2:3}$ Low | 1.512 | 2.930 | 2.267 | 4.666 | 2 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -4.146 | 0.568 | 2.187 | -1.263 | 26 |
| RSC117-2 | F$_{2:3}$ High | -6.560 | -3.411 | 1.620 | -2.967 | 36 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | -3.584 | -3.057 | -3.881 | -4.964 | 40 |
| RSC117-10 | F$_{2:3}$ Low | 2.316 | -1.235 | -1.506 | -0.125 | 21 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 1.580 | -2.852 | -5.508 | -2.264 | 34 |
| RSC19-3 | F$_{2:3}$ High | 4.827 | 8.674 | 4.540 | 6.403 | 1 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -1.290 | 1.356 | 2.779 | 0.759 | 17 |
| RSC19-1 | F$_{2:3}$ Low | 5.401 | -0.047 | 4.618 | 3.131 | 4 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 1.368 | -2.250 | -1.131 | -0.492 | 23 |
| **Testers** | | | | | | |
| A.301 | Tester | -1.202 | -1.534 | -0.531 | -0.932 | 4 |
| A.319 | Tester | 1.096 | -0.088 | -0.841 | 0.156 | 2 |
| A.Tx.3197 | Tester | 2.341 | 0.009 | 1.862 | 1.665 | 1 |
| A.338 | Tester | -2.293 | 1.613 | -0.496 | -0.902 | 3 |
| SE Lines | | 2.7438 | 1.5721 | 1.8285 | 1.0909 | |
| SE Testers | | 0.8677 | 0.4972 | 0.5782 | 0.3449 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation:  High F$_{2:3}$, BC$_1$F$_{2:3}$, and the Low F$_{2:3}$, BC$_1$F$_{2:3}$.

Table 18.  General Combining Ability (GCA) estimates and combined analysis for three-panicle weight (g) for each parental line in a line x tester evaluated in four environments.  Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents RSC‡Lines | Selectionsδ | Vega 2015 | Vega 2016 | Dumas 2016 | Combined locations | Rank |
|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | -8.509 | -22.608 | -20.159 | -22.482 | 34 |
| RSC73-6 | $BC_1F_{2:3}$ High | 3.816 | -20.146 | -1.184 | -11.304 | 24 |
| RSC73-1 | $F_{2:3}$ Low | 0.554 | -11.271 | -43.134 | -18.96 | 31 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -8.459 | 16.304 | 1.754 | 3.021 | 17 |
| RSC83-1 | $F_{2:3}$ High | -5.521 | 11.229 | -6.709 | 21.405 | 8 |
| RSC83-14 | $BC_1F_{2:3}$ High | 72.466 | 24.079 | 11.454 | 36.343 | 4 |
| RSC83-10 | $F_{2:3}$ Low | -27.021 | -7.883 | -45.946 | -25.710 | 36 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 20.091 | -6.858 | 40.591 | 17.977 | 10 |
| RSC112-5 | $F_{2:3}$ High | -32.821 | 24.642 | 45.891 | 4.468 | 16 |
| RSC112-19 | $BC_1F_{2:3}$ High | -26.852 | -2.108 | 33.327 | 15.592 | 12 |
| RSC112-8 | $F_{2:3}$ Low | -26.659 | -34.583 | 10.029 | -17.542 | 29 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 8.254 | 16.029 | 18.154 | 5.702 | 15 |
| RSC76-4 | $F_{2:3}$ High | 40.341 | 24.917 | 28.116 | 22.499 | 7 |
| RSC76-16 | $BC_1F_{2:3}$ High | 50.429 | 46.729 | 74.766 | 55.208 | 2 |
| RSC76-13 | $F_{2:3}$ Low | -36.071 | 18.204 | -8.721 | -11.020 | 22 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 126.541 | 63.054 | 65.329 | 90.480 | 1 |
| RSC38-5 | $F_{2:3}$ High | -33.059 | -21.921 | 1.216 | -20.885 | 32 |
| RSC38-15 | $BC_1F_{2:3}$ High | -8.059 | -14.683 | 33.866 | 1.758 | 18 |
| RSC38-8 | $F_{2:3}$ Low | 21.604 | 6.554 | 22.854 | 18.205 | 9 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -26.284 | -12.633 | 0.041 | -13.242 | 26 |
| RSC37-12 | $F_{2:3}$ High | -7.171 | -23.758 | -7.521 | -16.007 | 27 |
| RSC37-12 | $BC_1F_{2:3}$ High | 63.416 | 29.892 | 18.666 | 38.546 | 3 |
| RSC37-7 | $F_{2:3}$ Low | 11.529 | 9.129 | -3.371 | 10.962 | 13 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 40.629 | 50.567 | -9.271 | 24.271 | 6 |
| RSC15-13 | $F_{2:3}$ High | -47.684 | -27.871 | -60.359 | -39.348 | 39 |
| RSC15-15 | $BC_1F_{2:3}$ High | 1.616 | -11.358 | -25.859 | -6.704 | 20 |
| RSC15-11 | $F_{2:3}$ Low | -45.452 | -20.296 | -29.696 | -35.541 | 37 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -35.909 | -31.171 | -28.146 | -23.826 | 35 |
| RSC124-9 | $F_{2:3}$ High | 3.791 | -24.008 | -25.384 | -18.51 | 30 |
| RSC124-16 | $BC_1F_{2:3}$ High | 10.341 | 25.817 | 63.716 | 36.184 | 5 |
| RSC124-3 | $F_{2:3}$ Low | -25.221 | -34.133 | -52.721 | -39.345 | 38 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -9.895 | -24.721 | -16.521 | -21.009 | 33 |
| RSC117-2 | $F_{2:3}$ High | -11.934 | -13.433 | -23.921 | -12.332 | 25 |
| RSC117-4 | $BC_1F_{2:3}$ High | -22.884 | 25.579 | 16.291 | 9.758 | 14 |
| RSC117-10 | $F_{2:3}$ Low | -25.768 | -1.208 | -10.434 | -8.047 | 21 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -10.371 | 15.517 | 22.629 | 16.371 | 11 |
| RSC19-3 | $F_{2:3}$ High | 2.766 | -11.033 | -26.371 | -16.285 | 28 |
| RSC19-17 | $BC_1F_{2:3}$ High | -5.621 | 3.492 | 16.654 | -11.113 | 23 |
| RSC19-1 | $F_{2:3}$ Low | -29.284 | -20.733 | -61.909 | -41.363 | 40 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 23.566 | -13.321 | -13.846 | -3.457 | 19 |
| **Testers** | | | | | | |
| A.301 | Tester | -15.729 | -11.814 | -14.29 | -15.139 | 4 |
| A.319 | Tester | -6.649 | 8.251 | 2.81 | 3.361 | 2 |
| A.Tx.3197 | Tester | -1.716 | -10.799 | -8.129 | -12.796 | 3 |
| A.338 | Tester | 24.426 | 14.363 | 19.43 | 24.383 | 1 |
| SE Lines | | 16.379 | 8.8899 | 15.6975 | 8.869 | |
| SE Testers | | 5.179 | 2.811 | 4.964 | 2.805 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BC_1F_{2:3}$, and the Low $F_{2:3}$, $BC_1F_{2:3}$.

Table 19. General Combining Ability (GCA) estimates and combined analysis for 1000-kernel weight (g) for each parental line in a line x tester evaluated in four environments. Because of the absence of 10 hybrids, individual GCA was not estimated for Perryton, TX, in 2015.

| Parents | | Vega | | Dumas | Combined | |
|---|---|---|---|---|---|---|
| RSC‡Lines | Selectionsδ | 2015 | 2016 | 2016 | locations | Rank |
| RSC73-9 | $F_{2:3}$ High | -0.575 | -2.274 | -1.665 | -1.354 | 27 |
| RSC73-6 | $BC_1F_{2:3}$ High | -0.254 | -1.308 | -1.802 | -1.617 | 30 |
| RSC73-1 | $F_{2:3}$ Low | -0.796 | 0.814 | 0.424 | 0.133 | 16 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 0.96 | 0.087 | 2.346 | 1.283 | 8 |
| RSC83-1 | $F_{2:3}$ High | 0.783 | 0.1000 | 1.362 | 0.885 | 11 |
| RSC83-14 | $BC_1F_{2:3}$ High | 1.035 | 1.032 | -0.565 | 0.412 | 14 |
| RSC83-10 | $F_{2:3}$ Low | 1.280 | -1.841 | -0.736 | -1.055 | 23 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 2.748 | 0.724 | 0.173 | 0.710 | 12 |
| RSC112-5 | $F_{2:3}$ High | 3.994 | -0.775 | -0.69 | 1.400 | 7 |
| RSC112-19 | $BC_1F_{2:3}$ High | -1.448 | 1.209 | -1.529 | -0.517 | 19 |
| RSC112-8 | $F_{2:3}$ Low | -1.102 | -0.722 | -1.097 | -1.170 | 24 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 0.603 | 1.675 | -0.401 | 0.173 | 15 |
| RSC76-4 | $F_{2:3}$ High | 6.643 | 6.150 | 7.345 | 6.849 | 2 |
| RSC76-16 | $BC_1F_{2:3}$ High | 7.453 | 7.062 | 7.481 | 7.360 | 1 |
| RSC76-13 | $F_{2:3}$ Low | 5.113 | 3.108 | 5.073 | 4.720 | 4 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 6.514 | 5.853 | 6.468 | 6.536 | 3 |
| RSC38-5 | $F_{2:3}$ High | -4.686 | -2.849 | -4.089 | -3.705 | 39 |
| RSC38-15 | $BC_1F_{2:3}$ High | -1.121 | -1.365 | 1.413 | -0.446 | 18 |
| RSC38-8 | $F_{2:3}$ Low | 0.594 | -0.585 | 0.128 | -0.043 | 17 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -1.113 | -0.893 | -1.399 | -1.186 | 25 |
| RSC37-12 | $F_{2:3}$ High | -1.223 | -1.626 | -2.96 | -2.097 | 35 |
| RSC37-12 | $BC_1F_{2:3}$ High | 0.244 | 0.566 | -2.897 | -0.733 | 21 |
| RSC37-7 | $F_{2:3}$ Low | -2.096 | -0.635 | -0.922 | -0.909 | 22 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -4.577 | -2.343 | -3.494 | -3.078 | 38 |
| RSC15-13 | $F_{2:3}$ High | 0.343 | 0.432 | 3.383 | 1.283 | 9 |
| RSC15-15 | $BC_1F_{2:3}$ High | -1.773 | -0.548 | -0.44 | -1.640 | 31 |
| RSC15-11 | $F_{2:3}$ Low | -2.097 | -2.228 | -0.056 | -1.219 | 26 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 1.630 | 0.938 | 2.432 | 1.476 | 6 |
| RSC124-9 | $F_{2:3}$ High | -4.022 | -2.03 | -1.849 | -2.623 | 36 |
| RSC124-16 | $BC_1F_{2:3}$ High | -3.289 | -1.469 | -0.927 | -1.968 | 34 |
| RSC124-3 | $F_{2:3}$ Low | 0.448 | 0.155 | -0.363 | 0.484 | 13 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -1.109 | -1.918 | -2.693 | -1.818 | 33 |
| RSC117-2 | $F_{2:3}$ High | -0.164 | -1.189 | -0.498 | -0.567 | 20 |
| RSC117-4 | $BC_1F_{2:3}$ High | 1.642 | 4.374 | 4.173 | 3.287 | 5 |
| RSC117-10 | $F_{2:3}$ Low | -2.939 | -0.537 | -0.856 | -1.441 | 28 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -0.797 | 2.141 | 1.066 | 1.144 | 10 |
| RSC19-3 | $F_{2:3}$ High | -2.450 | -2.087 | -2.106 | -2.645 | 37 |
| RSC19-17 | $BC_1F_{2:3}$ High | -0.922 | -2.157 | -1.563 | -1.647 | 32 |
| RSC19-1 | $F_{2:3}$ Low | -4.269 | -2.915 | -4.954 | -4.142 | 40 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 0.417 | -2.128 | -2.907 | -1.509 | 29 |
| **Testers** | | | | | | |
| A.301 | Tester | -0.048 | 0.668 | 0.568 | 0.398 | 3 |
| A.319 | Tester | -2.482 | -2.014 | -3.075 | -2.346 | 4 |
| A.Tx.3197 | Tester | 1.547 | 0.104 | 1.29 | 0.849 | 2 |
| A.338 | Tester | 0.976 | 1.241 | 1.224 | 1.104 | 1 |
| SE Lines | | 0.9494 | 0.8049 | 0.9795 | 0.5241 | |
| SE Testers | | 0.300 | 0.255 | 0.310 | 0.167 | |

†Testers were analyzed separately from the lines.

‡RSC represents different lines from the Reinstated Sorghum Conversion (RSC) program.

δSelections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, and the Low $F_{2:3}$, $BC_1F_{2:3}$.

for testers was from Dumas in 2016, for A.301; much variation was found across environments (Table 11).  The greatest combined GCA effect (0.746) for lines was found in RSC15-14 $BC_1F_{2:3}$ low, followed by RSC-15-13 $F_{2:3}$ high, RSC19-17 $BC_1F_{2:3}$ high, RSC15-11$F_{2:3}$ low, and RSC38-15$BC_1F_{2:3}$ high.  For concentration of protein in grain, GCA effects of 0.723, 0.641, 0.599, and 0.543, respectively, were found for the RSC15 family that dominated the GCA effect.  A.Tx3197 had the greatest GCA effect (0.081) for testers for concentration of starch in grain, while the RSC112 family ranked 1st, 2nd, and 4th best as a good combiner for starch in grain.  A.301 also had the greatest GCA effect (0.013) for concentration of fiber in grain, and RSC37-12, a $BC_1$ low line, followed by RSC117-4 ($BC_1F_{2:3}$ high), RSC19-3 ($F_{2:3}$ high), RSC19-1 ($F_{2:3}$ low), and RSC73-5 ($BC_1F_{2:3}$ low) had GCA effects of 0.043, 0.033, 0.031, 0.031, and 0.029, respectively.  Greatest tester GCA effect for concentration of fat in grain was reported for A.338 (0.118).  Greatest line GCA effect was found for RSC19-17 ($BC_1F_{2:3}$ high) with a GCA effect of 0.418, followed by RSC15-11 ($F_{2:3}$ low), RSC38-15 ($BC_1F_{2:3}$ high), and RSC15-14 ($BC_1F_{2:3}$ low) with GCA effects of 0.357, 0.315, and 0.283, respectively.  The RSC family seemed to play a greater role in the combining ability for quality grain analysis. The families RSC15, RSC19, RSC112, RSC73, and RSC117 all seemed to be good combiners for high concentrations of protein, starch, fiber, and fat in grain, depending on the quality factors a sorghum breeder is seeking.  The lines or testers with positive and significant GCA effects for plant height also showed good mean performance, indicating a strong relationship between GCA status and *per se* performance and can be considered good parents, in agreement with earlier reports by Iyanar et al. (2001), Kanawade et al. (2001), Chaudhary et al. (2006), and Kulakarni et al. (2006).  This might help in selection

of parents on the basis of *per se* performance in the absence of information on combining ability of inbreds.

**Specific Combining Ability (SCA)**

SCA effect represents the non-fixable component of genetic variation that provides information on hybrid performance. The range of combined SCA effects for grain yield varied from -1.443 (A.338*RSC76-16 $BC_1F_{2:3}$ high) to 1.334 (A.338*RSC117-4 $BC_1F_{2:3}$ high), with yields from 4.978 to 8.060 Mg ha$^{-1}$, respectively. Of the 160 crosses, A.338*RSC117-4, A.301*RSC76-2 ($BC_1F_{2:3}$ low), A.301*RSC19-17 ($BC_1F_{2:3}$ high), A.338*RSC117-2 ($F_{2:3}$ high), and A.301*RSC76-4 ($F_{2:3}$ high) had positive SCA effects greater than one and were identified as good specific combiners for grain yield (Table 20). Respectively, the crosses involved low x high, high x low, high x low, low x high, and high x low combinations in terms of GCA effects, indicating additive x dominance type of gene interaction. Thus, it can be concluded that inter- and intra-allelic interactions were involved in expression of the trait. A.301* RSC117-4 ($BC_1F_{2:3}$ high), A.Tx3197*RSC19-10 ($BC_1F_{2:3}$ high), and A.338*RSC76-16 ($BC_1F_{2:3}$ high) had the most negative SCA effects of -1.206, -1.275, and -1.443, with grain yields of 6.163, 4.515, and 3.072 Mg ha$^{-1}$, respectively. Although the two selections from RSC76 showed good SCA with A.301, the overall mean performance was less because of poor combining ability with the other three testers.

A.338*RSC117-4 $BC_1F_{2:3}$ high had significant positive MPH and large overall mean; however, the hybrid had a mean of 75.8 days to anthesis and 135.8 cm total plant height, out-yielding three of the best six commercial hybrid checks.

Table 20. Specific Combining Ability (SCA) estimates for grain yield ($Mgha^{-1}$) and overall rank for each hybrid combination in the combined analysis across six environments.

| Lines RSC† | Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | -0.164 | 101 | 0.133 | 63 | 0.456 | 31 | -0.425 | 127 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | -0.051 | 88 | 0.156 | 57 | -0.078 | 92 | -0.027 | 84 |
| RSC73-1 | F$_{2:3}$ Low | -0.300 | 114 | -0.212 | 104 | 0.320 | 41 | 0.192 | 53 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 0.331 | 39 | -0.002 | 80 | 0.109 | 66 | -0.437 | 128 |
| RSC83-1 | F$_{2:3}$ High | -0.012 | 82 | 0.234 | 45 | -0.962 | 153 | 0.74 | 16 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 0.269 | 42 | -0.031 | 86 | -0.340 | 117 | 0.102 | 67 |
| RSC83-10 | F$_{2:3}$ Low | -0.408 | 125 | -0.369 | 120 | -0.077 | 91 | 0.855 | 10 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -0.623 | 143 | 0.983 | 6 | 0.096 | 69 | -0.456 | 132 |
| RSC112-5 | F$_{2:3}$ High | -0.158 | 99 | -0.448 | 131 | 0.822 | 12 | -0.215 | 105 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 0.124 | 64 | -0.06 | 90 | 0.212 | 49 | -0.276 | 112 |
| RSC112-8 | F$_{2:3}$ Low | -0.685 | 147 | -0.219 | 106 | 0.559 | 25 | 0.344 | 37 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -0.494 | 137 | -0.575 | 142 | 0.549 | 26 | 0.519 | 28 |
| RSC76-4 | F$_{2:3}$ High | 1.009 | 5 | -0.057 | 89 | 0.163 | 55 | -1.116 | 156 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 0.872 | 9 | 0.701 | 17 | -0.130 | 96 | -1.443 | 160 |
| RSC76-13 | F$_{2:3}$ Low | 0.581 | 23 | 0.437 | 33 | -0.640 | 145 | -0.378 | 123 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 1.231 | 2 | -0.709 | 151 | 0.177 | 54 | -0.699 | 149 |
| RSC38-5 | F$_{2:3}$ High | -0.565 | 140 | 0.968 | 7 | 0.752 | 15 | -1.155 | 157 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 0.633 | 21 | 0.079 | 70 | -0.418 | 126 | -0.295 | 113 |
| RSC38-8 | F$_{2:3}$ Low | 0.231 | 46 | 0.151 | 58 | 0.269 | 43 | -0.650 | 146 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | -0.152 | 98 | 0.052 | 75 | 0.793 | 14 | -0.694 | 148 |
| RSC37-12 | F$_{2:3}$ High | -0.466 | 134 | 0.481 | 30 | -0.029 | 85 | 0.014 | 78 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 0.438 | 32 | 0.201 | 52 | -0.013 | 83 | -0.626 | 144 |
| RSC37-7 | F$_{2:3}$ Low | -0.500 | 138 | 0.568 | 24 | -0.140 | 97 | 0.072 | 72 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 0.202 | 50 | 0.226 | 47 | -0.446 | 130 | 0.018 | 77 |
| RSC15-13 | F$_{2:3}$ High | 0.428 | 34 | -0.090 | 93 | -1.003 | 154 | 0.665 | 20 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | -0.227 | 108 | -0.800 | 152 | 0.926 | 8 | 0.101 | 68 |
| RSC15-11 | F$_{2:3}$ Low | 0.070 | 73 | 0.245 | 44 | -1.008 | 155 | 0.694 | 18 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | -0.313 | 115 | -0.372 | 122 | 0.143 | 59 | 0.542 | 27 |
| RSC124-9 | F$_{2:3}$ High | -0.442 | 129 | -0.313 | 116 | 0.592 | 22 | 0.163 | 56 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 0.062 | 74 | -0.388 | 124 | 0.419 | 36 | -0.093 | 94 |
| RSC124-3 | F$_{2:3}$ Low | 0.076 | 71 | 0.329 | 40 | -0.369 | 121 | -0.036 | 87 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.002 | 79 | -0.471 | 136 | 0.335 | 38 | 0.134 | 62 |
| RSC117-2 | F$_{2:3}$ High | -0.462 | 133 | -0.344 | 119 | -0.226 | 107 | 1.032 | 4 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | -1.206 | 158 | -0.243 | 110 | 0.115 | 65 | 1.334 | 1 |
| RSC117-10 | F$_{2:3}$ Low | -0.549 | 139 | -0.006 | 81 | 0.135 | 61 | 0.420 | 35 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | -0.467 | 135 | -0.176 | 102 | -0.160 | 100 | 0.804 | 13 |
| RSC19-3 | F$_{2:3}$ High | 0.018 | 76 | -0.703 | 150 | 0.202 | 51 | 0.483 | 29 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 1.103 | 3 | -0.342 | 118 | -0.566 | 141 | -0.195 | 103 |
| RSC19-1 | F$_{2:3}$ Low | -0.102 | 95 | 0.14 | 60 | -0.263 | 111 | 0.225 | 48 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 0.668 | 19 | 0.846 | 11 | -1.275 | 159 | -0.239 | 109 |
| SE hybrid | 0.537 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

A.301*RSC76-2 $BC_1F_{2:3}$ low had large positive MPH and large overall mean *per se*

parents; however, the hybrid was earlier (71.2 days to anthesis) and taller (175.3 cm total

plant height). A.301*RSC19-17 $BC_1F_{2:3}$ high had significant positive MPH and large

overall mean grain yield while being earlier (67.5 days to anthesis) and shorter (152.9 cm

total plant height). A.338*RSC117-2 $F_{2:3}$ high had high MPH and large overall mean

grain yield, with 77.0 days to anthesis and 146.5 cm total plant height. For grain yield,

SCA variance (0.0866) was greater than that of the GCA variance (0.0054), indicating

dominance of non-additive gene action in inheritance of the trait (Table 22). Similar

trends of results were reported by Kenga et al. (2004), El-Menshawi (2005), Mahdy et al.

(2011), and Rani et al. (2015). Additive gene action for controlling the trait was reported

by Kenga et al. (2005) and Tadesse et al. (2008). Importance of both additive and non-

additive gene action in inheritance of the trait was reported by El-Mottaleb (2009) and

Makanda et al. (2010).

The range of combined SCA effects for days to anthesis varied from -5.648

(A.338*RSC37-12 $F_{2:3}$ high) to 6.164 (A.319*RSC37-12 $F_{2:3}$ high), with 79.3 to 75.5

days, respectively (Tables 3 and 21). The earliest hybrids were crosses with tester A.301

and lines RSC124-4 ($BC_1F_{2:3}$ low), RSC19-17 ($BC_1F_{2:3}$ high), RSC15-15 ($BC_1F_{2:3}$ high),

RSC37-8 ($BC_1F_{2:3}$ low), and RSC112-15 ($BC_1F_{2:3}$ low), ranging in days to anthesis of

66.3 to 67.0, with SCA effects of 0.814, -0.936, 0.939, -1.311, and -0.998, respectively.

The results of combining ability for the number of days to anthesis among lines RSC73-9

$F_{2:3}$ high, RSC73 $BC_1F_{2:3}$ high, and RSC117-2 $F_{2:3}$ high, and the family of RSC38 and

RSC15 among testers A.301 and A.Tx3197 flowered early, because they showed

Table 21. Specific Combining Ability (SCA) estimates for day to anthesis for each hybrid combination in the combined analysis across two environments with overall rank. Because of a missing entry, data for Hutchinson, KS, in 2015 were not included.

| Lines | | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|-------|-----|-------|------|-------|------|----------|------|-------|------|
| RSC† | Selections‡ | | | | | | | | |
| RSC73-9 | F$_{2:3}$ High | 0.127 | 71 | -0.398 | 88 | -1.267 | 128 | 1.539 | 26 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 0.439 | 61 | -1.086 | 119 | -0.205 | 81 | 0.852 | 43 |
| RSC73-1 | F$_{2:3}$ Low | -4.061 | 157 | 1.164 | 34 | 3.795 | 8 | -0.898 | 102 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | -1.873 | 137 | 1.352 | 30 | 0.983 | 37 | -0.461 | 93 |
| RSC83-1 | F$_{2:3}$ High | -2.436 | 153 | -0.961 | 108 | 4.420 | 5 | -1.023 | 115 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -0.873 | 99 | 0.352 | 66 | -0.017 | 75 | 0.539 | 55 |
| RSC83-10 | F$_{2:3}$ Low | -1.123 | 123 | 1.602 | 25 | 1.483 | 27 | -1.961 | 142 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -1.998 | 143 | 1.977 | 20 | 0.608 | 51 | -0.586 | 94 |
| RSC112-5 | F$_{2:3}$ High | 3.939 | 7 | 0.914 | 41 | -0.205 | 82 | -4.648 | 159 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 3.689 | 9 | -1.086 | 120 | -2.205 | 147 | -0.398 | 89 |
| RSC112-8 | F$_{2:3}$ Low | -2.248 | 150 | -1.023 | 113 | 1.608 | 24 | 1.664 | 23 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -0.998 | 109 | 0.227 | 68 | 0.108 | 72 | 0.664 | 50 |
| RSC76-4 | F$_{2:3}$ High | 0.377 | 64 | -0.648 | 95 | 3.233 | 10 | -2.961 | 155 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 3.127 | 12 | -0.898 | 100 | 0.483 | 59 | -2.711 | 154 |
| RSC76-13 | F$_{2:3}$ Low | 0.002 | 74 | -1.023 | 114 | 1.358 | 29 | -0.336 | 86 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 2.502 | 17 | -1.273 | 129 | -0.392 | 87 | -0.836 | 98 |
| RSC38-5 | F$_{2:3}$ High | -1.186 | 126 | -0.211 | 83 | 0.17 | 69 | 1.227 | 33 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -0.123 | 79 | -2.398 | 151 | -1.517 | 133 | 4.039 | 6 |
| RSC38-8 | F$_{2:3}$ Low | -0.436 | 91 | -2.211 | 148 | -2.08 | 145 | 4.727 | 3 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 0.564 | 52 | -4.211 | 158 | -1.08 | 118 | 4.727 | 4 |
| RSC37-12 | F$_{2:3}$ High | 0.439 | 62 | 6.164 | 1 | -0.955 | 107 | -5.648 | 160 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 0.502 | 57 | 1.977 | 21 | -1.142 | 124 | -1.336 | 131 |
| RSC37-7 | F$_{2:3}$ Low | -0.936 | 105 | 2.539 | 16 | -1.580 | 135 | -0.023 | 76 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -1.311 | 130 | 1.664 | 22 | -1.705 | 136 | 1.352 | 31 |
| RSC15-13 | F$_{2:3}$ High | 1.127 | 35 | -2.398 | 152 | -0.767 | 97 | 2.039 | 18 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 0.939 | 39 | -1.086 | 121 | -1.205 | 127 | 1.352 | 32 |
| RSC15-11 | F$_{2:3}$ Low | -1.873 | 138 | 3.102 | 13 | -1.017 | 111 | -0.211 | 84 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.377 | 65 | -1.898 | 140 | 0.983 | 38 | 0.539 | 56 |
| RSC124-9 | F$_{2:3}$ High | 0.564 | 53 | -2.211 | 149 | 0.17 | 70 | 1.477 | 28 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 5.689 | 2 | -3.336 | 156 | -1.455 | 132 | -0.898 | 103 |
| RSC124-3 | F$_{2:3}$ Low | 0.314 | 67 | -1.961 | 141 | 0.92 | 40 | 0.727 | 47 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.814 | 44 | 2.789 | 15 | -2.08 | 146 | -1.523 | 134 |
| RSC117-2 | F$_{2:3}$ High | -1.061 | 116 | 0.414 | 63 | -0.455 | 92 | 1.102 | 36 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | -0.311 | 85 | 0.664 | 48 | 0.545 | 54 | -0.898 | 104 |
| RSC117-10 | F$_{2:3}$ Low | 0.502 | 58 | 0.477 | 60 | -1.892 | 139 | 0.914 | 42 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | -0.123 | 80 | -0.898 | 101 | -1.017 | 112 | 2.039 | 19 |
| RSC19-3 | F$_{2:3}$ High | -1.061 | 117 | 0.664 | 49 | 0.795 | 45 | -0.398 | 90 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -0.936 | 106 | 0.039 | 73 | 2.92 | 14 | -2.023 | 144 |
| RSC19-1 | F$_{2:3}$ Low | -0.998 | 110 | 3.227 | 11 | -1.142 | 125 | -1.086 | 122 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -0.061 | 77 | -0.086 | 78 | 0.795 | 46 | -0.648 | 96 |
| SE hybrid | 1.224 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

negative GCA effects and projected their use in sorghum breeding programs for earliness (Table 13). Of the 160 crosses, A.338*RSC37-12 $F_{2:3}$ high (high x low), A.338*RSC112-5 $F_{2:3}$ high (high x high), A.319*RSC38-9 $BC_1F_{2:3}$ low (high x low), and A.301*RSC73-1 $F_{2:3}$ low (low x high) had the greatest SCA effect in the negative direction and were considered the best specific crosses for early maturity (Tables 13 and 21). A.301*RSC73-1 $F_{2:3}$ low (low x high) flowered in 68.5 days as compared to the line and testers at 71 and 65.5 days, respectively. For days to anthesis, the estimate of SCA variance (3.357) was greater than that of the GCA variance (0.296), with the ratio of variance due to GCA and SCA 0.046 indicating dominance of non-additive gene action in inheritance of the trait (Table 22). Similar results were reported by Chaudhary et al. (2006) and Premalatha et al. (2006), while opposite results were reported by Kenga et al. (2005) and Mahdy et al. (2011). The importance of both additive and non-additive gene action in inheritance of the trait was reported by Hovny et al. (2005), Mahmoud (2007), and El-Mottaleb (2009).

According to Kenga et al. (2004), a cross combination with large means, favorable SCA estimate, and involving at least one of the parents with great GCA effects probably would enhance the concentration of favorable alleles to improve targeted traits. In crosses with high x low and low x high GCA effects, selection should be delayed until further segregating generations, by which time heterozygosity would be less, while homozygosity and additive genes could be stabilized (Rani et al., 2015).

The range of combined SCA effects for total plant height varied from -35.357 (A.301*RSC37-7 $F_{2:3}$ low) to 37.428 (A.338*RSC38-5 $F_{2:3}$ high), with total heights

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Table 22. Estimates of genetic components and proportional contribution to the total variation of the line x tester analysis for the measured traits in 160 sorghum hybrids across environments.

| Genetic Component | Grain yield (Mgha⁻¹) | DTF | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight(g) | 1000-kernel weight(g) | Protein (%) | Starch (%) | Fiber (%) | Fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $\sigma^2$ GCA line | 0.2895 | 0.2962 | 847.8684 | 895.0326 | 4.0885 | 4.6573 | 633.7928 | 6.6013 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ GCA tester | 0.1456 | 13.1754 | 673.7420 | 689.4357 | 1.4352 | 1.3348 | 307.6490 | 2.4800 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ GCA | 0.0054 | 0.1529 | 18.3848 | 19.1820 | 0.0699 | 0.0765 | 11.7141 | 0.1145 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ SCA | 0.0866 | 3.3569 | 92.0435 | 94.1777 | 0.3589 | 0.0506 | 115.3883 | 0.4447 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ GCA/$\sigma^2$ SCA | 0.0624 | 0.0455 | 0.1997 | 0.2037 | 0.1947 | 1.5122 | 0.1015 | 0.2575 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ A | 0.0108 | 0.3057 | 36.7696 | 38.3639 | 0.1398 | 0.1530 | 23.4282 | 0.2290 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\sigma^2$ D | 0.0866 | 3.3569 | 92.0435 | 94.1777 | 0.3589 | 0.0506 | 115.3883 | 0.4447 | 0.00 | 0.00 | 0.00 | 0.00 |
| [$\sigma^2$D/$\sigma^2$A] ½ | 2.8318 | 3.3135 | 1.5822 | 1.5668 | 1.6024 | 0.5750 | 2.2193 | 1.3935 | N/A | N/A | N/A | N/A |
| Proportional contribution to total variation (%) | | | | | | | | | | | | |
| Lines (L) | 48.90 | 12.72 | 58.33 | 59.12 | 69.50 | 55.35 | 56.64 | 69.30 | 53.02 | 49.27 | 44.90 | 65.79 |
| Testers (T) | 15.21 | 73.77 | 34.35 | 33.82 | 17.96 | 10.57 | 18.71 | 19.22 | 9.33 | 1.56 | 19.83 | 12.01 |
| L x T | 35.89 | 13.51 | 7.33 | 7.06 | 12.54 | 34.08 | 24.64 | 11.48 | 37.65 | 49.17 | 35.28 | 22.20 |

DTF = days to flowering.

$\sigma^2$ A: additive genetic variance, $\sigma^2$ D: dominance genetic variance, $\sigma^2$ GCA: estimate of GCA variance, $\sigma^2$ SCA: estimate of SCA variance, $\sigma^2$ GCA/$\sigma^2$ SCA: average degree of dominance, [$\sigma^2$D/$\sigma^2$A] ½: degree of dominance.

*Negative component interpreted as zero.

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ranging from 101.04 to 212.80 cm, respectively. A.338*RSC38-5 $F_{2:3}$ high cross

combination had positive SCA for total plant height and 1000-kernel weight. The cross

is the best specific combiner to increase plant height and 1000-kernel weight with a high

x low combination of GCA effects and with a large SCA effect further substantiating the

operation of non-additive gene action. However, crosses such as A.301*RSC37-7 $F_{2:3}$

low and A.338*RSC112-5 $F_{2:3}$ high had negative SCA effects with GCA effects of low x

high and high x low, respectively, which would enable good combiners to reduce plant

height. For total plant height, the estimate of SCA variance (92.04) was greater than that

of the GCA variance (18.38), with a ratio of 0.199 indicating dominance of non-additive

gene action in inheritance of the trait (Table 23). Rani et al. (2015) reported similar

results for plant height. Dominance variance was more than additive variance for the

trait. The results are in agreement with earlier reports by Kulakarni et al. (2006), Yadav

and Pahuja (2007), Fellahi et al. (2013), and Rani et al. (2015), while opposite results

were reported by Tadesse et al. (2008) and Degu et al. (2009).

The range of combined SCA effects for the height to the flag leaf varied from

-34.343 (A.301*RSC37-7 $F_{2:3}$ low) to 39.778 (A.338*RSC38-5 $F_{2:3}$ high), with the height

to the flag leaf ranging from 69.1 to 179.6 cm, respectively (Table 24). This followed the

same trend as total plant height, with crosses such as A.301*RSC37-7 $F_{2:3}$ low and

A.338*RSC112-5 $F_{2:3}$ high being the best combiners to reduce plant height. The crosses

had negative SCA effects with GCA effects of low x high and high x low, respectively,

which would make good combiners to reduce plant height. For height to the flag leaf, the

estimate of SCA variance (94.18) was greater than the estimate of GCA variance (19.18),

Table 23. Specific Combining Ability (SCA) estimates for total plant height (cm) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|------|------|------|------|------|------|------|------|------|------|
| RSC73-9 | $F_{2:3}$ High | -5.142 | 117 | -1.387 | 98 | 0.203 | 79 | 6.326 | 35 |
| RSC73-6 | $BC_1F_{2:3}$ High | 1.248 | 69 | -1.136 | 97 | -4.253 | 114 | 4.142 | 49 |
| RSC73-1 | $F_{2:3}$ Low | -12.736 | 145 | 0.491 | 72 | 4.782 | 42 | 7.463 | 31 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -20.077 | 157 | 1.721 | 64 | 2.414 | 58 | 15.943 | 10 |
| RSC83-1 | $F_{2:3}$ High | -5.287 | 118 | 1.219 | 70 | -6.661 | 125 | 10.730 | 24 |
| RSC83-14 | $BC_1F_{2:3}$ High | -0.911 | 96 | 2.053 | 62 | -0.536 | 91 | -0.607 | 92 |
| RSC83-10 | $F_{2:3}$ Low | 14.317 | 15 | -0.765 | 93 | -6.212 | 123 | -7.34 | 128 |
| RSC83-1 | $BC_1F_{2:3}$ Low | -0.857 | 95 | -2.867 | 106 | 4.492 | 46 | -0.767 | 94 |
| RSC112-5 | $F_{2:3}$ High | 16.686 | 8 | 5.095 | 38 | 4.412 | 48 | -26.193 | 159 |
| RSC112-19 | $BC_1F_{2:3}$ High | 8.549 | 28 | -2.123 | 102 | 0.474 | 73 | -6.900 | 127 |
| RSC112-8 | $F_{2:3}$ Low | 14.623 | 14 | 0.333 | 75 | -2.416 | 104 | -12.54 | 144 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 2.361 | 59 | 2.815 | 56 | -0.462 | 90 | -4.714 | 115 |
| RSC76-4 | $F_{2:3}$ High | -16.438 | 149 | 1.602 | 65 | 3.670 | 52 | 11.166 | 23 |
| RSC76-16 | $BC_1F_{2:3}$ High | -19.007 | 154 | -0.433 | 89 | 9.941 | 25 | 9.499 | 26 |
| RSC76-13 | $F_{2:3}$ Low | -5.963 | 121 | 0.226 | 77 | 6.158 | 36 | -0.421 | 88 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -18.292 | 153 | 1.762 | 63 | 8.908 | 27 | 7.621 | 30 |
| RSC38-5 | $F_{2:3}$ High | -6.109 | 122 | -12.248 | 141 | -19.071 | 155 | 37.428 | 1 |
| RSC38-15 | $BC_1F_{2:3}$ High | -19.282 | 156 | -1.878 | 100 | 1.143 | 71 | 20.018 | 5 |
| RSC38-8 | $F_{2:3}$ Low | -12.407 | 143 | 3.470 | 54 | 3.843 | 50 | 5.095 | 39 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -9.454 | 133 | -3.690 | 112 | 0.073 | 83 | 13.071 | 17 |
| RSC37-12 | $F_{2:3}$ High | -5.366 | 119 | 15.692 | 12 | 4.846 | 41 | -15.172 | 147 |
| RSC37-12 | $BC_1F_{2:3}$ High | 1.407 | 67 | -10.079 | 135 | 7.387 | 32 | 1.285 | 68 |
| RSC37-7 | $F_{2:3}$ Low | -35.357 | 160 | 13.59 | 16 | 4.700 | 43 | 17.068 | 7 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -7.735 | 130 | 0.465 | 74 | 2.744 | 57 | 4.525 | 45 |
| RSC15-13 | $F_{2:3}$ High | 16.073 | 9 | -22.453 | 158 | 6.548 | 34 | -0.168 | 84 |
| RSC15-15 | $BC_1F_{2:3}$ High | 11.883 | 20 | 0.187 | 80 | -0.338 | 87 | -11.733 | 138 |
| RSC15-11 | $F_{2:3}$ Low | 28.214 | 2 | -11.741 | 139 | 0.224 | 78 | -16.696 | 150 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 4.462 | 47 | 15.31 | 13 | -3.527 | 110 | -16.245 | 148 |
| RSC124-9 | $F_{2:3}$ High | 15.734 | 11 | 3.561 | 53 | -8.714 | 132 | -10.582 | 136 |
| RSC124-16 | $BC_1F_{2:3}$ High | -4.238 | 113 | 4.667 | 44 | -7.729 | 129 | 7.299 | 33 |
| RSC124-3 | $F_{2:3}$ Low | -0.247 | 86 | -6.812 | 126 | 2.135 | 60 | 4.924 | 40 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 0.265 | 76 | -12.05 | 140 | -6.244 | 124 | 18.029 | 6 |
| RSC117-2 | $F_{2:3}$ High | 11.211 | 22 | -2.975 | 107 | 0.151 | 81 | -8.387 | 131 |
| RSC117-4 | $BC_1F_{2:3}$ High | 12.560 | 18 | 2.131 | 61 | -1.887 | 101 | -12.805 | 146 |
| RSC117-10 | $F_{2:3}$ Low | 11.383 | 21 | 3.812 | 51 | -2.853 | 105 | -12.342 | 142 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 26.595 | 3 | -4.734 | 116 | -3.618 | 111 | -18.243 | 152 |
| RSC19-3 | $F_{2:3}$ High | 6.011 | 37 | -3.04 | 108 | 0.138 | 82 | -3.109 | 109 |
| RSC19-17 | $BC_1F_{2:3}$ High | -11.214 | 137 | 11.962 | 19 | -2.268 | 103 | 1.520 | 66 |
| RSC19-1 | $F_{2:3}$ Low | 22.414 | 4 | -0.183 | 85 | -5.471 | 120 | -16.76 | 151 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -9.879 | 134 | 8.43 | 29 | 2.876 | 55 | -1.426 | 99 |
| SE hybrid | 7.493 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

Table 24. Specific Combining Ability (SCA) estimates for height to flag leaf (cm) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | -3.570 | 109 | -1.115 | 91 | 0.850 | 79 | 3.834 | 50 |
| RSC73-6 | $BC_1F_{2:3}$ High | -0.343 | 86 | -1.378 | 96 | -1.266 | 94 | 2.988 | 57 |
| RSC73-1 | $F_{2:3}$ Low | -15.677 | 150 | 1.704 | 70 | 7.162 | 30 | 6.811 | 32 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -18.731 | 155 | 2.353 | 60 | 1.512 | 74 | 14.866 | 13 |
| RSC83-1 | $F_{2:3}$ High | -2.089 | 99 | -0.056 | 83 | -7.670 | 129 | 9.814 | 25 |
| RSC83-14 | $BC_1F_{2:3}$ High | -1.283 | 95 | 3.820 | 51 | 1.658 | 72 | -4.195 | 114 |
| RSC83-10 | $F_{2:3}$ Low | 12.013 | 19 | 2.192 | 65 | -5.420 | 119 | -8.786 | 131 |
| RSC83-1 | $BC_1F_{2:3}$ Low | -3.703 | 110 | -0.135 | 84 | 5.004 | 41 | -1.166 | 93 |
| RSC112-5 | $F_{2:3}$ High | 17.545 | 9 | 6.294 | 35 | 2.597 | 59 | -26.436 | 158 |
| RSC112-19 | $BC_1F_{2:3}$ High | 7.844 | 28 | -2.326 | 102 | -0.467 | 87 | -5.051 | 117 |
| RSC112-8 | $F_{2:3}$ Low | 13.520 | 16 | 1.215 | 78 | -3.487 | 107 | -11.247 | 136 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 3.741 | 52 | 2.250 | 62 | -0.704 | 89 | -5.287 | 118 |
| RSC76-4 | $F_{2:3}$ High | -12.780 | 142 | 2.221 | 63 | -0.949 | 90 | 11.508 | 21 |
| RSC76-16 | $BC_1F_{2:3}$ High | -15.014 | 148 | -1.129 | 92 | 5.920 | 37 | 10.223 | 24 |
| RSC76-13 | $F_{2:3}$ Low | -6.812 | 124 | -0.652 | 88 | 6.976 | 31 | 0.488 | 81 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -12.580 | 141 | -2.291 | 101 | 8.934 | 26 | 5.938 | 36 |
| RSC38-5 | $F_{2:3}$ High | -7.474 | 126 | -13.059 | 146 | -19.245 | 157 | 39.778 | 1 |
| RSC38-15 | $BC_1F_{2:3}$ High | -16.905 | 152 | -1.749 | 98 | -2.272 | 100 | 20.926 | 4 |
| RSC38-8 | $F_{2:3}$ Low | -15.305 | 149 | 3.926 | 49 | 4.939 | 42 | 6.440 | 33 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -11.324 | 137 | -6.168 | 121 | 2.201 | 64 | 15.291 | 12 |
| RSC37-12 | $F_{2:3}$ High | -7.644 | 128 | 18.307 | 8 | 5.452 | 39 | -16.115 | 151 |
| RSC37-12 | $BC_1F_{2:3}$ High | 1.444 | 76 | -7.054 | 125 | 5.918 | 38 | -0.308 | 85 |
| RSC37-7 | $F_{2:3}$ Low | -34.343 | 160 | 11.825 | 20 | 3.681 | 53 | 18.837 | 6 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -10.622 | 135 | 0.779 | 80 | 1.842 | 67 | 8.002 | 27 |
| RSC15-13 | $F_{2:3}$ High | 18.769 | 7 | -26.505 | 159 | 4.511 | 46 | 3.225 | 56 |
| RSC15-15 | $BC_1F_{2:3}$ High | 13.005 | 17 | 3.502 | 54 | -3.529 | 108 | -12.978 | 145 |
| RSC15-11 | $F_{2:3}$ Low | 26.609 | 2 | -12.950 | 144 | -1.406 | 97 | -12.252 | 140 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 5.014 | 40 | 16.520 | 10 | -2.576 | 105 | -18.958 | 156 |
| RSC124-9 | $F_{2:3}$ High | 14.410 | 14 | 2.900 | 58 | -7.623 | 127 | -9.686 | 134 |
| RSC124-16 | $BC_1F_{2:3}$ High | -6.407 | 122 | 4.677 | 44 | -4.665 | 115 | 6.396 | 34 |
| RSC124-3 | $F_{2:3}$ Low | 2.118 | 66 | -6.644 | 123 | 3.259 | 55 | 1.268 | 77 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 4.139 | 48 | -14.151 | 147 | -5.534 | 120 | 15.546 | 11 |
| RSC117-2 | $F_{2:3}$ High | 10.344 | 23 | -2.435 | 103 | 1.750 | 69 | -9.658 | 133 |
| RSC117-4 | $BC_1F_{2:3}$ High | 12.257 | 18 | 4.181 | 47 | -4.774 | 116 | -11.664 | 138 |
| RSC117-10 | $F_{2:3}$ Low | 13.706 | 15 | 1.77 | 68 | -3.727 | 111 | -11.749 | 139 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 24.846 | 3 | -8.522 | 130 | 1.486 | 75 | -17.809 | 154 |
| RSC19-3 | $F_{2:3}$ High | 4.618 | 45 | -2.503 | 104 | 1.684 | 71 | -3.799 | 112 |
| RSC19-17 | $BC_1F_{2:3}$ High | -9.407 | 132 | 10.990 | 22 | -3.924 | 113 | 2.341 | 61 |
| RSC19-1 | $F_{2:3}$ Low | 18.866 | 5 | 1.636 | 73 | -2.801 | 106 | -17.702 | 153 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -12.793 | 143 | 7.763 | 29 | 4.702 | 43 | 0.328 | 82 |
| SE hybrid | 7.359 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

with a ratio of 0.2037 indicating dominance of non-additive gene action in inheritance of the trait (Table 22). Dominance variance was more than the additive variance for the trait. The results are in accordance with those obtained by Nayakar et al. (1989), Pillai et al. (1995), El-Mottaleb and Asran (2004), El-Menshawi (2005), Chaudhary et al. (2006), and Rani et al. (2015), while opposite results were reported by Tadesse et al. (2008).

The range of combined SCA effects for panicle length varied from -2.904 (A.Tx3197*RSC117-2 $F_{2:3}$ high) to 2.724 (A.319*RSC15-13 $F_{2:3}$ high). Among the hybrids, the greatest SCA effects were for A.319*RSC15-13 $F_{2:3}$ high, A.319*RSC38-9 $BC_1F_{2:3}$ low, and A.301*RSC19-10 $BC_1F_{2:3}$ low considered desirable by virtue of their positive SCA effects. The three crosses A.Tx3197*RSC117-2 $F_{2:3}$ high, A.338*RSC112-5 $F_{2:3}$ high, and A.301*RSC19-10 $BC_1F_{2:3}$ low had negative SCA effects for the trait (Table 25). Parents with high x low A.319 x RSC15-13 $F_{2:3}$ high produced crosses with positive SCA effects, indicating additive x dominance type of gene action. The findings were in agreement with Patel et al. (1993) and Naik et al. (1994). In the cross, A.301*RSC19-10 $BC_1F_{2:3}$ low, two poor combiners also resulted in large positive SCA effects that might be caused by high complementarity between the parents. This indicated that the parental combinations provided environments for full expression of genes controlling the trait, although the parents themselves would not express any superiority of the trait; accumulation of favorable genes might be the cause of parents with poor GCA effects producing hybrids with greater SCA effects. However, Premalatha et al. (2006) reported that the parental combination of low x low for GCA effects might be suitable for selection in later generations. Greater SCA variance (0.359)

Table 25. Specific Combining Ability (SCA) estimates for panicle length (cm) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | 0.760 | 30 | -0.122 | 90 | -0.218 | 100 | -0.420 | 118 |
| RSC73-6 | $BC_1F_{2:3}$ High | 0.534 | 41 | -0.762 | 136 | 0.517 | 44 | -0.288 | 105 |
| RSC73-1 | $F_{2:3}$ Low | 1.446 | 8 | -1.018 | 143 | 0.180 | 62 | -0.607 | 128 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -0.524 | 123 | -0.757 | 135 | 0.335 | 52 | 0.946 | 22 |
| RSC83-1 | $F_{2:3}$ High | -1.476 | 154 | 0.208 | 59 | 1.444 | 9 | -0.176 | 93 |
| RSC83-14 | $BC_1F_{2:3}$ High | -0.383 | 116 | -0.032 | 78 | 0.017 | 74 | 0.398 | 47 |
| RSC83-10 | $F_{2:3}$ Low | -0.061 | 80 | -0.189 | 95 | 0.800 | 28 | -0.550 | 124 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 1.556 | 6 | -1.076 | 146 | 0.206 | 60 | -0.686 | 132 |
| RSC112-5 | $F_{2:3}$ High | 1.122 | 16 | 0.534 | 42 | 0.667 | 34 | -2.324 | 159 |
| RSC112-19 | $BC_1F_{2:3}$ High | 1.371 | 11 | -1.034 | 144 | -0.589 | 126 | 0.251 | 56 |
| RSC112-8 | $F_{2:3}$ Low | -0.185 | 94 | -0.106 | 88 | -0.513 | 121 | 0.804 | 27 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -0.359 | 112 | -0.345 | 111 | 0.953 | 21 | -0.249 | 103 |
| RSC76-4 | $F_{2:3}$ High | -1.247 | 150 | -0.335 | 110 | 0.297 | 53 | 1.284 | 14 |
| RSC76-16 | $BC_1F_{2:3}$ High | -0.961 | 138 | -0.195 | 98 | 0.294 | 54 | 0.862 | 25 |
| RSC76-13 | $F_{2:3}$ Low | -0.523 | 122 | -0.424 | 119 | 0.357 | 50 | 0.590 | 37 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -1.454 | 153 | 0.123 | 67 | 0.006 | 75 | 1.325 | 12 |
| RSC38-5 | $F_{2:3}$ High | 0.402 | 46 | 1.628 | 5 | -0.006 | 76 | -2.024 | 158 |
| RSC38-15 | $BC_1F_{2:3}$ High | 0.082 | 70 | 0.035 | 73 | -0.749 | 133 | 0.633 | 35 |
| RSC38-8 | $F_{2:3}$ Low | -0.284 | 104 | -0.121 | 89 | -0.091 | 84 | 0.496 | 45 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 0.695 | 32 | 2.274 | 2 | -1.008 | 142 | -1.961 | 156 |
| RSC37-12 | $F_{2:3}$ High | 1.549 | 7 | -0.975 | 139 | -0.840 | 137 | 0.266 | 55 |
| RSC37-12 | $BC_1F_{2:3}$ High | -1.383 | 152 | 0.926 | 23 | -0.066 | 81 | 0.523 | 43 |
| RSC37-7 | $F_{2:3}$ Low | 0.128 | 65 | -0.232 | 101 | 0.195 | 61 | -0.091 | 85 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -1.008 | 141 | 1.113 | 18 | 0.038 | 72 | -0.143 | 91 |
| RSC15-13 | $F_{2:3}$ High | -1.814 | 155 | 2.724 | 1 | -0.600 | 127 | -0.311 | 107 |
| RSC15-15 | $BC_1F_{2:3}$ High | -1.186 | 149 | -0.377 | 115 | 0.133 | 64 | 1.429 | 10 |
| RSC15-11 | $F_{2:3}$ Low | -0.194 | 96 | -0.09 | 83 | 0.105 | 69 | 0.178 | 63 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -0.366 | 113 | -1.997 | 157 | 1.074 | 19 | 1.289 | 13 |
| RSC124-9 | $F_{2:3}$ High | -0.060 | 79 | 0.351 | 51 | 0.746 | 31 | -1.037 | 145 |
| RSC124-16 | $BC_1F_{2:3}$ High | 0.208 | 58 | 0.056 | 71 | -0.626 | 129 | 0.362 | 49 |
| RSC124-3 | $F_{2:3}$ Low | 0.565 | 39 | 0.811 | 26 | -0.098 | 86 | -1.278 | 151 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -0.020 | 77 | 1.114 | 17 | -0.424 | 120 | -0.669 | 131 |
| RSC117-2 | $F_{2:3}$ High | 1.756 | 4 | 0.128 | 66 | -2.904 | 160 | 1.019 | 20 |
| RSC117-4 | $BC_1F_{2:3}$ High | 0.570 | 38 | -0.371 | 114 | 0.554 | 40 | -0.753 | 134 |
| RSC117-10 | $F_{2:3}$ Low | -0.575 | 125 | -0.245 | 102 | -0.321 | 108 | 1.141 | 15 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -0.194 | 97 | -0.158 | 92 | 0.246 | 57 | 0.106 | 68 |
| RSC19-3 | $F_{2:3}$ High | -0.212 | 99 | -0.069 | 82 | -0.102 | 87 | 0.383 | 48 |
| RSC19-17 | $BC_1F_{2:3}$ High | 0.908 | 24 | -1.116 | 147 | 0.621 | 36 | -0.414 | 117 |
| RSC19-1 | $F_{2:3}$ Low | -1.158 | 148 | 0.774 | 29 | -0.300 | 106 | 0.684 | 33 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 1.976 | 3 | -0.653 | 130 | -0.331 | 109 | -0.992 | 140 |
| SE hybrid | 0.829 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

than GCA variance (0.069) indicated dominance of non-additive gene action in inheritance of the trait (Table 22). Dominance variance was more than the additive variance for the trait, with a ratio ($\sigma^2_D / \sigma^2_A$) greater than unity. The results are in accordance with those obtained by Nayakar et al. (1989), Pillai et al. (1995), El-Mottaleb and Asran (2004), El-Menshawi (2005), and Chaudhary et al. (2006), but opposite the results reported by Tadesse et al. (2008).

For plant exsertion, the range of SCA effects varied from -4.600 (A.338*RSC15-11 $F_{2:3}$ low) to 4.954 (A.338*RSC124-3 $F_{2:3}$ low). Among the hybrids, A.338*RSC124-3 $F_{2:3}$ low, A.301*RSC19-1 $F_{2:3}$ low, A.Tx3197*RSC76-4 $F_{2:3}$ high, and A.301*RSC37-8 $BC_1F_{2:3}$ had positive numbers for plant exsertion, while A.338*RSC15-11 $F_{2:3}$ low, A.Tx3197*RSC117-3 $BC_1F_{2:3}$ low, and A.301*RSC76-2 $BC_1F_{2:3}$ low had negative SCA effects (Table 26). All crosses involving low x high combination of GCA effects tended to produce the most positive SCA effects in the hybrids, indicating non-additive gene action, except for cross A.Tx3197*RSC76-4 $F_{2:3}$ high that produced a high x high combination of GCA effects. The variance of GCA was slightly larger than the estimate of SCA variance, suggesting additive gene action (Table 22). The estimate of additive variance was slightly greater than the estimate for dominant variance. It is reasonable to suggest both additive and non-additive gene action.

For three-panicle weight, the range of SCA effects varied from -47.985 (A.338* RSC112-5 $F_{2:3}$ high) to 50.282 (A.301*RSC112-5 $F_{2:3}$ high) (Table 27). This signified the importance of testers. A.338 is a high general combiner making the cross high x high GCA effects produce the worst combination, whereas low x high GCA effects produced

Table 26.  Specific Combining Ability (SCA) estimates for plant exsertion (cm) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC[†] | Lines Selections[‡] | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | -2.208 | 140 | -0.238 | 89 | -0.459 | 93 | 2.904 | 12 |
| RSC73-6 | $BC_1F_{2:3}$ High | 1.113 | 46 | 0.807 | 61 | -3.247 | 154 | 1.327 | 35 |
| RSC73-1 | $F_{2:3}$ Low | 1.244 | 39 | -0.058 | 82 | -2.156 | 139 | 0.970 | 53 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -0.780 | 105 | 0.066 | 80 | 0.564 | 67 | 0.151 | 77 |
| RSC83-1 | $F_{2:3}$ High | -1.608 | 123 | 0.930 | 54 | -0.517 | 95 | 1.195 | 43 |
| RSC83-14 | $BC_1F_{2:3}$ High | 0.922 | 55 | -1.852 | 134 | -2.227 | 142 | 3.157 | 10 |
| RSC83-10 | $F_{2:3}$ Low | 2.392 | 16 | -2.781 | 150 | -1.610 | 124 | 1.999 | 22 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 1.263 | 38 | -1.796 | 131 | -0.498 | 94 | 1.032 | 49 |
| RSC112-5 | $F_{2:3}$ High | -1.934 | 135 | -1.797 | 132 | 1.144 | 45 | 2.588 | 15 |
| RSC112-19 | $BC_1F_{2:3}$ High | -0.757 | 104 | 1.578 | 27 | 1.392 | 32 | -2.213 | 141 |
| RSC112-8 | $F_{2:3}$ Low | 1.363 | 34 | -0.848 | 109 | 1.574 | 28 | -2.089 | 138 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -1.041 | 115 | 0.820 | 60 | -0.561 | 99 | 0.783 | 62 |
| RSC76-4 | $F_{2:3}$ High | -2.456 | 146 | -0.088 | 84 | 4.233 | 3 | -1.689 | 127 |
| RSC76-16 | $BC_1F_{2:3}$ High | -2.987 | 152 | 0.824 | 58 | 3.728 | 6 | -1.565 | 122 |
| RSC76-13 | $F_{2:3}$ Low | 1.219 | 42 | 1.045 | 48 | -1.373 | 119 | -0.892 | 110 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -4.085 | 158 | 3.698 | 7 | 0.177 | 76 | 0.210 | 75 |
| RSC38-5 | $F_{2:3}$ High | 0.970 | 52 | -0.973 | 111 | 0.089 | 79 | -0.086 | 83 |
| RSC38-15 | $BC_1F_{2:3}$ High | -2.716 | 149 | -0.523 | 97 | 3.861 | 5 | -0.622 | 101 |
| RSC38-8 | $F_{2:3}$ Low | 3.227 | 9 | -0.398 | 92 | -1.007 | 112 | -1.822 | 133 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 1.184 | 44 | 0.113 | 78 | -1.153 | 118 | -0.144 | 88 |
| RSC37-12 | $F_{2:3}$ High | 0.773 | 63 | -1.699 | 128 | 0.232 | 72 | 0.694 | 65 |
| RSC37-12 | $BC_1F_{2:3}$ High | 1.390 | 33 | -4.013 | 157 | 1.534 | 29 | 1.089 | 47 |
| RSC37-7 | $F_{2:3}$ Low | -1.099 | 117 | 1.934 | 23 | 0.823 | 59 | -1.658 | 126 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 3.939 | 4 | -1.487 | 121 | 0.861 | 57 | -3.313 | 155 |
| RSC15-13 | $F_{2:3}$ High | -0.838 | 108 | 1.265 | 37 | 2.638 | 14 | -3.065 | 153 |
| RSC15-15 | $BC_1F_{2:3}$ High | 0.259 | 71 | -2.445 | 145 | 2.702 | 13 | -0.517 | 96 |
| RSC15-11 | $F_{2:3}$ Low | 1.838 | 24 | 1.239 | 40 | 1.522 | 30 | -4.600 | 160 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -0.143 | 87 | 0.722 | 64 | -2.028 | 137 | 1.449 | 31 |
| RSC124-9 | $F_{2:3}$ High | 1.295 | 36 | 0.441 | 69 | -1.963 | 136 | 0.227 | 73 |
| RSC124-16 | $BC_1F_{2:3}$ High | 2.004 | 21 | -0.126 | 86 | -2.436 | 144 | 0.558 | 68 |
| RSC124-3 | $F_{2:3}$ Low | -2.886 | 151 | -1.039 | 114 | -1.029 | 113 | 4.954 | 1 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -3.873 | 156 | 0.862 | 56 | -0.096 | 85 | 3.108 | 11 |
| RSC117-2 | $F_{2:3}$ High | -0.728 | 103 | -0.275 | 90 | 1.015 | 51 | -0.012 | 81 |
| RSC117-4 | $BC_1F_{2:3}$ High | -0.574 | 100 | -0.815 | 107 | 2.081 | 18 | -0.692 | 102 |
| RSC117-10 | $F_{2:3}$ Low | -1.716 | 129 | 2.217 | 17 | 1.223 | 41 | -1.724 | 130 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 1.725 | 25 | 3.621 | 8 | -4.565 | 159 | -0.782 | 106 |
| RSC19-3 | $F_{2:3}$ High | 1.647 | 26 | -0.529 | 98 | -1.446 | 120 | 0.328 | 70 |
| RSC19-17 | $BC_1F_{2:3}$ High | -2.675 | 148 | 2.025 | 20 | 1.031 | 50 | -0.381 | 91 |
| RSC19-1 | $F_{2:3}$ Low | 4.696 | 2 | -2.492 | 147 | -2.427 | 143 | 0.223 | 74 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 0.643 | 66 | 2.064 | 19 | -1.627 | 125 | -1.079 | 116 |
| SE hybrid | 2.182 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

Table 27.  Specific Combining Ability (SCA) estimates for three-panicle weight (g) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | -22.118 | 147 | -3.619 | 89 | -1.516 | 81 | 27.253 | 11 |
| RSC73-6 | $BC_1F_{2:3}$ High | -4.471 | 95 | -26.710 | 151 | -2.869 | 84 | 34.050 | 7 |
| RSC73-1 | $F_{2:3}$ Low | -3.190 | 87 | 14.834 | 31 | 3.975 | 65 | -15.619 | 129 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 19.592 | 24 | -17.860 | 135 | -5.769 | 101 | 4.037 | 64 |
| RSC83-1 | $F_{2:3}$ High | -19.193 | 139 | -26.169 | 150 | 8.959 | 49 | 36.403 | 4 |
| RSC83-14 | $BC_1F_{2:3}$ High | -19.455 | 140 | 7.231 | 53 | 26.759 | 12 | -14.535 | 124 |
| RSC83-10 | $F_{2:3}$ Low | 5.948 | 58 | 10.284 | 46 | -11.838 | 115 | -4.394 | 92 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 13.423 | 36 | 6.971 | 56 | -3.575 | 88 | -16.819 | 133 |
| RSC112-5 | $F_{2:3}$ High | 50.282 | 1 | -4.757 | 97 | 2.459 | 70 | -47.985 | 160 |
| RSC112-19 | $BC_1F_{2:3}$ High | -19.630 | 141 | 38.314 | 3 | -3.107 | 85 | -15.576 | 128 |
| RSC112-8 | $F_{2:3}$ Low | 23.754 | 19 | -8.297 | 109 | -6.406 | 104 | -9.050 | 111 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 2.560 | 69 | -27.629 | 152 | 7.062 | 55 | 18.006 | 25 |
| RSC76-4 | $F_{2:3}$ High | 10.826 | 44 | 11.099 | 43 | -11.959 | 116 | -9.966 | 113 |
| RSC76-16 | $BC_1F_{2:3}$ High | 16.217 | 26 | 12.078 | 40 | -7.756 | 108 | -20.538 | 143 |
| RSC76-13 | $F_{2:3}$ Low | -4.130 | 90 | 23.931 | 18 | -15.203 | 127 | -4.597 | 96 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -21.255 | 146 | 14.268 | 32 | -18.691 | 137 | 25.678 | 16 |
| RSC38-5 | $F_{2:3}$ High | -15.077 | 125 | -6.166 | 102 | 12.575 | 38 | 8.668 | 50 |
| RSC38-15 | $BC_1F_{2:3}$ High | -1.171 | 79 | 4.490 | 62 | 2.244 | 73 | -5.563 | 100 |
| RSC38-8 | $F_{2:3}$ Low | -22.393 | 148 | -6.707 | 105 | -18.253 | 136 | 47.353 | 2 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 25.779 | 14 | 13.553 | 35 | -6.294 | 103 | -33.038 | 157 |
| RSC37-12 | $F_{2:3}$ High | -4.980 | 98 | 34.093 | 6 | -12.953 | 119 | -16.16 | 132 |
| RSC37-12 | $BC_1F_{2:3}$ High | 0.392 | 76 | 25.515 | 17 | -12.594 | 117 | -13.313 | 121 |
| RSC37-7 | $F_{2:3}$ Low | -32.574 | 156 | 15.499 | 29 | 3.941 | 66 | 13.134 | 37 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -36.096 | 158 | -15.685 | 130 | 20.894 | 22 | 30.887 | 8 |
| RSC15-13 | $F_{2:3}$ High | 8.571 | 51 | 13.982 | 33 | -12.69 | 118 | -9.863 | 112 |
| RSC15-15 | $BC_1F_{2:3}$ High | -12.971 | 120 | -11.197 | 114 | -1.719 | 82 | 25.887 | 13 |
| RSC15-11 | $F_{2:3}$ Low | 7.284 | 52 | -18.717 | 138 | 9.224 | 48 | 2.209 | 74 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 10.288 | 45 | -8.351 | 110 | -27.659 | 153 | 25.722 | 15 |
| RSC124-9 | $F_{2:3}$ High | 5.900 | 59 | -21.227 | 145 | 9.923 | 47 | 5.404 | 60 |
| RSC124-16 | $BC_1F_{2:3}$ High | -6.975 | 106 | 21.978 | 20 | -15.102 | 126 | 0.100 | 78 |
| RSC124-3 | $F_{2:3}$ Low | 2.445 | 71 | -4.469 | 94 | -1.403 | 80 | 3.428 | 67 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 27.690 | 10 | -15.769 | 131 | 5.155 | 61 | -17.076 | 134 |
| RSC117-2 | $F_{2:3}$ High | 1.832 | 75 | 6.443 | 57 | -5.166 | 99 | -3.110 | 86 |
| RSC117-4 | $BC_1F_{2:3}$ High | -14.083 | 123 | -13.647 | 122 | 20.581 | 23 | 7.150 | 54 |
| RSC117-10 | $F_{2:3}$ Low | -7.753 | 107 | 4.437 | 63 | 0.212 | 77 | 3.105 | 68 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -22.758 | 149 | 28.290 | 9 | 15.644 | 27 | -21.175 | 144 |
| RSC19-3 | $F_{2:3}$ High | -4.290 | 91 | -32.516 | 155 | 15.612 | 28 | 21.193 | 21 |
| RSC19-17 | $BC_1F_{2:3}$ High | 14.851 | 30 | -30.751 | 154 | 13.616 | 34 | 2.284 | 72 |
| RSC19-1 | $F_{2:3}$ Low | 12.426 | 39 | -4.401 | 93 | 11.778 | 42 | -19.803 | 142 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 34.507 | 5 | -2.644 | 83 | 11.909 | 41 | -43.772 | 159 |
| SE hybrid | 17.739 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

the best combination. Among the hybrids, three crosses A.301*RSC112-5 $F_{2:3}$ high, A.338*RSC38-8 $BC_1F_{2:3}$ low, and A.319*RSC112-19 $BC_1F_{2:3}$ high were considered desirable by virtue of their positive SCA effects, and four crosses A.338* RSC112-5 $F_{2:3}$ high, A.338*RSC19-10 $BC_1F_{2:3}$ low, A.301*RSC37-8 $BC_1F_{2:3}$ low, and A.338*RSC38-9 $BC_1F_{2:3}$ low had negative SCA effects. Parents with a low x high (A.301*RSC112-5 $F_{2:3}$ high) GCA effect produced crosses with greatest SCA effects, indicating additive x dominance type of gene interaction. The findings were in agreement with those by Patel et al. (1993) and Naik et al. (1994). In the crosses A.338*RSC38-8 $BC_1F_{2:3}$ low, and A.319*RSC112-19 $BC_1F_{2:3}$ high, two good combiners also resulted in large positive SCA effects that might be caused by high complementarity between the parents. According to Premalatha et al. (2006), the hybrids might be desirable for biparental selection or inter-mating. Results indicated the need to exploit hybrid vigor to enhance levels of yield. For three-panicle weight, the ratio of GCA to SCA variances was less than unity, indicating the predominant role of non-additive gene action. This was in accordance with earlier reports by Badhe and Patel (1997), Siddiqui and Baig (2001), Kulakarni et al. (2006), and Aruna et al. (2010). Influence of non-additive gene action in controlling the trait also was indicated by the degree of dominance (Table 22).

For 1000-kernel weight, SCA effects ranged from -3.061 (A.338*RSC112-19 $BCF_{2:3}$ high) to 3.185 (A.Tx3197*RSC117-2 $F_{2:3}$ high). Of the 160 crosses, three crosses A.Tx3197*RSC117-2 $F_{2:3}$ high, A.319*RSC112-19 $BC_1F_{2:3}$, and A.338*RSC73-6 $BC_1F_{2:3}$ had large positive SCA effects, and four crosses A.338*RSC112-19 $BC_1F_{2:3}$ high, A.Tx3197*RSC76-13 $F_{2:3}$ low, A.338*RSC112-8 $F_{2:3}$ low, and A.301*RSC37-7

F$_{2:3}$ low had negative SCA effects (Table 28).  The hybrid A.Tx3197*RSC117-2 F$_{2:3}$ high

expressed the greatest positive SCA effect and also showed positive average heterosis.

One of the other two hybrids that had positive SCA effects was a combination of high x

low (A.338*RSC73-6 BC$_1$F$_{2:3}$) GCA effects of parents, indicating non-additive gene

action.  The other one that had positive SCA effects was a combination low x low

(A.319*RSC112-19 BC$_1$F$_{2:3}$), as previously observed; two poor combiners also resulted

in large positive SCA effects that might have been caused by great complementarity

between the parents.  According to Premalatha et al. (2006), the hybrid should be delayed

until future generations.  This indicated that the parental combinations provided an

environment for full expression of genes controlling the trait, although the parents

themselves would not express any superiority for the trait.  Accumulation of favorable

genes might be the cause of parents with poor GCA giving rise to hybrids with greater

SCA effects.  Results indicated the need to exploit hybrid vigor to enhance greater yield

potential.  For 1000-kernel weight, the estimate of SCA variance was greater than that of

the GCA variance (0.115), with a ratio of 0.258, indicating the importance of non-

additive gene action in inheritance of the trait (Table 22).  Dominance variance was

greater than the additive variance for the trait.  The results conformed to earlier reports by

Badhe and Patil (1997), El-Menshawi (2005), Chaudhary et al. (2006), and Premalatha et

al. (2006).  In opposition to results obtained in the present study, only additive gene

action as reported by Mahdy et al. (2011) and both additive and non-additive gene action

reported by Salini et al. (2008) influenced 1000-kernel weight.

Table 28. Specific Combining Ability (SCA) estimates for 1000-kernel weight (g) for each hybrid combination in the combined analysis across four environments with overall rank.

| | Lines | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC† | Selections‡ | | | | | | | | |
| RSC73-9 | $F_{2:3}$ High | -1.913 | 154 | -0.634 | 118 | 0.639 | 42 | 1.908 | 8 |
| RSC73-6 | $BC_1F_{2:3}$ High | -1.327 | 144 | -0.951 | 133 | -0.242 | 94 | 2.521 | 3 |
| RSC73-1 | $F_{2:3}$ Low | -1.031 | 136 | 0.659 | 41 | -0.167 | 89 | 0.540 | 46 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 0.788 | 37 | 0.727 | 38 | -0.372 | 102 | -1.144 | 140 |
| RSC83-1 | $F_{2:3}$ High | -1.034 | 137 | 0.144 | 67 | 0.691 | 40 | 0.199 | 62 |
| RSC83-14 | $BC_1F_{2:3}$ High | -0.020 | 78 | -0.847 | 128 | 1.159 | 25 | -0.293 | 97 |
| RSC83-10 | $F_{2:3}$ Low | 0.552 | 44 | -1.504 | 148 | 0.810 | 35 | 0.142 | 68 |
| RSC83-1 | $BC_1F_{2:3}$ Low | -0.021 | 79 | 0.104 | 71 | 1.018 | 28 | -1.100 | 139 |
| RSC112-5 | $F_{2:3}$ High | -1.815 | 153 | 1.376 | 18 | -0.969 | 135 | 1.408 | 17 |
| RSC112-19 | $BC_1F_{2:3}$ High | 0.067 | 75 | 2.626 | 2 | 0.368 | 57 | -3.061 | 160 |
| RSC112-8 | $F_{2:3}$ Low | 0.939 | 29 | 1.250 | 22 | -0.067 | 81 | -2.122 | 158 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 2.378 | 4 | 1.131 | 26 | -1.437 | 146 | -2.072 | 155 |
| RSC76-4 | $F_{2:3}$ High | 2.022 | 7 | -0.078 | 83 | -1.471 | 147 | -0.473 | 110 |
| RSC76-16 | $BC_1F_{2:3}$ High | 1.510 | 13 | 0.385 | 55 | -1.787 | 152 | -0.107 | 85 |
| RSC76-13 | $F_{2:3}$ Low | 0.374 | 56 | 2.058 | 5 | -2.301 | 159 | -0.131 | 87 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 1.842 | 9 | -0.824 | 127 | -0.203 | 92 | -0.815 | 126 |
| RSC38-5 | $F_{2:3}$ High | -0.886 | 129 | -1.358 | 145 | 0.190 | 63 | 2.054 | 6 |
| RSC38-15 | $BC_1F_{2:3}$ High | -0.586 | 112 | -0.115 | 86 | 0.542 | 45 | 0.159 | 66 |
| RSC38-8 | $F_{2:3}$ Low | -0.360 | 101 | -0.408 | 103 | 0.518 | 48 | 0.251 | 59 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -0.591 | 113 | -0.534 | 111 | 0.490 | 49 | 0.635 | 43 |
| RSC37-12 | $F_{2:3}$ High | -0.135 | 88 | 1.504 | 14 | -0.771 | 124 | -0.598 | 115 |
| RSC37-12 | $BC_1F_{2:3}$ High | 1.365 | 19 | -0.964 | 134 | 0.525 | 47 | -0.927 | 132 |
| RSC37-7 | $F_{2:3}$ Low | -2.115 | 157 | 0.186 | 64 | 1.754 | 10 | 0.175 | 65 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 0.453 | 51 | -0.438 | 104 | -0.447 | 106 | 0.432 | 53 |
| RSC15-13 | $F_{2:3}$ High | -0.718 | 121 | -0.456 | 108 | -0.303 | 99 | 1.477 | 15 |
| RSC15-15 | $BC_1F_{2:3}$ High | -0.261 | 95 | -0.613 | 117 | 0.807 | 36 | 0.067 | 76 |
| RSC15-11 | $F_{2:3}$ Low | 0.119 | 69 | -0.765 | 123 | -0.262 | 96 | 0.907 | 31 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -0.656 | 119 | 1.164 | 24 | -0.603 | 116 | 0.094 | 72 |
| RSC124-9 | $F_{2:3}$ High | 1.476 | 16 | 0.206 | 61 | -1.645 | 151 | -0.037 | 80 |
| RSC124-16 | $BC_1F_{2:3}$ High | -0.807 | 125 | 1.562 | 12 | -1.570 | 150 | 0.815 | 34 |
| RSC124-3 | $F_{2:3}$ Low | 1.619 | 11 | -0.444 | 105 | -0.469 | 109 | -0.706 | 120 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 1.164 | 23 | -2.102 | 156 | -0.314 | 100 | 1.252 | 21 |
| RSC117-2 | $F_{2:3}$ High | -0.592 | 114 | -1.321 | 143 | 3.185 | 1 | -1.272 | 142 |
| RSC117-4 | $BC_1F_{2:3}$ High | -1.257 | 141 | -0.203 | 91 | 1.350 | 20 | 0.110 | 70 |
| RSC117-10 | $F_{2:3}$ Low | 0.883 | 32 | -0.763 | 122 | 0.088 | 73 | -0.208 | 93 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 0.084 | 74 | -0.086 | 84 | -0.454 | 107 | 0.456 | 50 |
| RSC19-3 | $F_{2:3}$ High | -1.050 | 138 | -0.300 | 98 | 0.433 | 52 | 0.918 | 30 |
| RSC19-17 | $BC_1F_{2:3}$ High | 0.387 | 54 | 0.829 | 33 | 0.294 | 58 | -1.510 | 149 |
| RSC19-1 | $F_{2:3}$ Low | 0.044 | 77 | -0.908 | 131 | 1.059 | 27 | -0.195 | 90 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -0.889 | 130 | 0.708 | 39 | -0.068 | 82 | 0.249 | 60 |
| SE hybrid | 1.048 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

GCA effects of protein content in grain ranged from -0.887 (A.Tx3197*RSC37-12 $BC_1F_{2:3}$ high to 0.961 (A.319*RSC37-12 $BC_1F_{2:3}$ high) (Table 29). Of the 160 crosses, A.319*RSC37-12 $BC_1F_{2:3}$ high, A.338*RSC73-9 $F_{2:3}$ high, and A.319*RSC19-17 $BC_1F_{2:3}$ high had positive SCA effects and were identified as good specific combiners for the trait. Of the crosses, A.319 was the only good general combiner with high x high combination of GCA effects. It involved good general combiners as parents and can be used for isolating promising sorghum material in later generations for development of superior varieties (Rao, 1970). The least specific combiners were A.Tx319* RSC37-12 $BC_1F_{2:3}$ high, A.Tx3197*RSC73-9 $F_{2:3}$ high, and A.Tx319*RSC117-3 $BC_1F_{2:3}$ low, all of which had negative SCA effects. For protein content in grain, the estimate of SCA variance was less than that of the GCA variance, indicating dominance of additive gene action (Table 22). Additive variance was greater than the dominance variance for the trait. But, dominance of both additive and non-additive gene action in inheritance of the trait was reported by Govil and Murty (1973). Results of the present study with additive variance being greater than dominance were opposite those of Rani et al. (2015).

Starch content of grain ranged from -0.67 (A.301*RSC112-5 $BC_1F_{2:3}$ high) to 0.668 (A.301*RSC73-1 $F_{2:3}$ low). Of the hybrids, A.301*RSC73-1 $F_{2:3}$ low, A.301*RSC38-9 $BC_1F_{2:3}$ low, A.338*RSC124-9 $BC_1F_{2:3}$, and A.301*RSC73-9 $F_{2:3}$ high had the greatest positive SCA effects, while A.301*RSC112-5 $BC_1F_{2:3}$ high, A.301*RSC124-16 $BC_1F_{2:3}$ high, and A.338*RSC73-9 $F_{2:3}$ high had negative SCA effects (Table 30). The greatest positive SCA effects were by the cross A.301*RSC73-1 $F_{2:3}$ low, followed by A.301*RSC38-9 $BC_1F_{2:3}$ low. For starch content in grain, the

Table 29. Specific Combining Ability (SCA) estimates for concentration of protein in grain (%) for each hybrid combination in the combined analysis across four environments with overall rank.

| Lines RSC† | Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | -0.593 | 158 | 0.454 | 13 | -0.612 | 159 | 0.751 | 2 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | -0.077 | 98 | -0.036 | 86 | -0.092 | 102 | 0.206 | 35 |
| RSC73-1 | F$_{2:3}$ Low | -0.509 | 156 | 0.239 | 28 | -0.189 | 125 | 0.459 | 12 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 0.137 | 45 | -0.041 | 88 | -0.041 | 89 | -0.055 | 91 |
| RSC83-1 | F$_{2:3}$ High | 0.234 | 29 | -0.172 | 121 | 0.331 | 20 | -0.393 | 151 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -0.016 | 75 | -0.106 | 108 | 0.153 | 44 | -0.032 | 84 |
| RSC83-10 | F$_{2:3}$ Low | 0.058 | 55 | -0.015 | 73 | 0.227 | 31 | -0.269 | 138 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -0.233 | 134 | -0.144 | 113 | 0.535 | 7 | -0.158 | 116 |
| RSC112-5 | F$_{2:3}$ High | -0.039 | 87 | -0.176 | 122 | -0.006 | 67 | 0.221 | 34 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 0.325 | 21 | 0.173 | 42 | -0.311 | 143 | -0.187 | 124 |
| RSC112-8 | F$_{2:3}$ Low | 0.226 | 33 | -0.024 | 81 | 0.086 | 52 | -0.287 | 141 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 0.555 | 5 | -0.034 | 85 | -0.060 | 92 | -0.462 | 154 |
| RSC76-4 | F$_{2:3}$ High | -0.275 | 139 | -0.163 | 117 | 0.539 | 6 | -0.101 | 107 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -0.501 | 155 | -0.009 | 69 | 0.284 | 25 | 0.227 | 32 |
| RSC76-13 | F$_{2:3}$ Low | -0.374 | 149 | 0.229 | 30 | -0.127 | 110 | 0.271 | 26 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | -0.195 | 126 | -0.208 | 128 | 0.419 | 16 | -0.016 | 76 |
| RSC38-5 | F$_{2:3}$ High | -0.152 | 114 | -0.044 | 90 | 0.171 | 43 | 0.025 | 62 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 0.136 | 48 | -0.169 | 119 | 0.202 | 36 | -0.169 | 120 |
| RSC38-8 | F$_{2:3}$ Low | -0.356 | 146 | -0.265 | 137 | 0.522 | 8 | 0.099 | 51 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | -0.010 | 71 | 0.027 | 60 | -0.336 | 144 | 0.319 | 23 |
| RSC37-12 | F$_{2:3}$ High | -0.135 | 111 | 0.137 | 47 | -0.183 | 123 | 0.181 | 39 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 0.137 | 46 | 0.961 | 1 | -0.887 | 160 | -0.212 | 129 |
| RSC37-7 | F$_{2:3}$ Low | -0.075 | 97 | -0.007 | 68 | 0.065 | 53 | 0.018 | 63 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -0.093 | 103 | 0.393 | 17 | -0.227 | 133 | -0.074 | 96 |
| RSC15-13 | F$_{2:3}$ High | 0.025 | 61 | -0.224 | 131 | 0.367 | 18 | -0.168 | 118 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | -0.023 | 80 | -0.439 | 153 | -0.019 | 77 | 0.481 | 9 |
| RSC15-11 | F$_{2:3}$ Low | 0.419 | 15 | -0.225 | 132 | -0.068 | 94 | -0.125 | 109 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.062 | 54 | -0.277 | 140 | 0.180 | 40 | 0.035 | 58 |
| RSC124-9 | F$_{2:3}$ High | 0.285 | 24 | -0.243 | 136 | 0.325 | 22 | -0.366 | 147 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 0.461 | 11 | -0.233 | 135 | -0.072 | 95 | -0.157 | 115 |
| RSC124-3 | F$_{2:3}$ Low | 0.004 | 65 | 0.100 | 50 | -0.011 | 72 | -0.094 | 104 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.469 | 10 | 0.008 | 64 | -0.097 | 105 | -0.380 | 150 |
| RSC117-2 | F$_{2:3}$ High | -0.101 | 106 | -0.009 | 70 | 0.195 | 38 | -0.086 | 100 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 0.450 | 14 | -0.308 | 142 | -0.342 | 145 | 0.200 | 37 |
| RSC117-10 | F$_{2:3}$ Low | -0.065 | 93 | 0.051 | 56 | 0.030 | 59 | -0.015 | 74 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 0.586 | 4 | -0.026 | 83 | -0.562 | 157 | 0.001 | 66 |
| RSC19-3 | F$_{2:3}$ High | -0.088 | 101 | 0.178 | 41 | -0.217 | 130 | 0.127 | 49 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -0.084 | 99 | 0.620 | 3 | -0.398 | 152 | -0.138 | 112 |
| RSC19-1 | F$_{2:3}$ Low | -0.201 | 127 | -0.024 | 82 | 0.245 | 27 | -0.020 | 78 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -0.372 | 148 | 0.051 | 57 | -0.022 | 79 | 0.342 | 19 |
| SE hybrid | 0.333 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

Table 30. Specific Combining Ability (SCA) estimates for concentration for starch in grain (%) for each hybrid combination in the combined analysis across four environments with overall rank.

| | Lines | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC† | Selections‡ | | | | | | | | |
| RSC73-9 | F$_{2:3}$ High | 0.541 | 4 | -0.206 | 123 | 0.224 | 31 | -0.558 | 158 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 0.226 | 29 | -0.079 | 107 | 0.091 | 63 | -0.237 | 126 |
| RSC73-1 | F$_{2:3}$ Low | 0.668 | 1 | -0.250 | 127 | 0.098 | 60 | -0.516 | 153 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 0.125 | 51 | -0.319 | 136 | 0.402 | 15 | -0.208 | 124 |
| RSC83-1 | F$_{2:3}$ High | -0.361 | 142 | 0.253 | 23 | -0.337 | 138 | 0.445 | 11 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -0.096 | 110 | -0.047 | 96 | 0.048 | 72 | 0.096 | 61 |
| RSC83-10 | F$_{2:3}$ Low | 0.004 | 83 | 0.091 | 62 | -0.418 | 150 | 0.323 | 20 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 0.104 | 56 | -0.152 | 114 | -0.054 | 99 | 0.101 | 59 |
| RSC112-5 | F$_{2:3}$ High | -0.198 | 120 | 0.037 | 76 | 0.210 | 34 | -0.049 | 98 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | -0.489 | 151 | -0.070 | 103 | 0.535 | 5 | 0.025 | 79 |
| RSC112-8 | F$_{2:3}$ Low | -0.132 | 113 | -0.075 | 105 | 0.047 | 73 | 0.160 | 43 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -0.670 | 160 | 0.101 | 57 | 0.227 | 28 | 0.342 | 18 |
| RSC76-4 | F$_{2:3}$ High | 0.322 | 21 | -0.036 | 94 | -0.294 | 133 | 0.008 | 82 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 0.462 | 10 | -0.263 | 129 | 0.138 | 48 | -0.337 | 140 |
| RSC76-13 | F$_{2:3}$ Low | 0.441 | 12 | -0.203 | 122 | 0.060 | 69 | -0.297 | 135 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 0.115 | 55 | -0.209 | 125 | 0.203 | 37 | -0.109 | 111 |
| RSC38-5 | F$_{2:3}$ High | 0.155 | 45 | 0.195 | 40 | -0.337 | 139 | -0.013 | 87 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 0.066 | 67 | -0.010 | 86 | -0.175 | 115 | 0.120 | 54 |
| RSC38-8 | F$_{2:3}$ Low | 0.496 | 6 | 0.137 | 49 | -0.368 | 146 | -0.265 | 130 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 0.597 | 2 | -0.268 | 131 | 0.087 | 64 | -0.415 | 149 |
| RSC37-12 | F$_{2:3}$ High | -0.014 | 88 | -0.072 | 104 | 0.062 | 68 | 0.024 | 81 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | -0.365 | 143 | -0.331 | 137 | 0.209 | 35 | 0.488 | 7 |
| RSC37-7 | F$_{2:3}$ Low | -0.115 | 112 | 0.185 | 41 | -0.294 | 134 | 0.224 | 32 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -0.031 | 92 | -0.368 | 145 | 0.245 | 25 | 0.153 | 46 |
| RSC15-13 | F$_{2:3}$ High | 0.042 | 74 | 0.480 | 9 | -0.547 | 157 | 0.025 | 80 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 0.050 | 71 | 0.347 | 16 | 0.144 | 47 | -0.541 | 156 |
| RSC15-11 | F$_{2:3}$ Low | -0.367 | 144 | 0.416 | 13 | -0.077 | 106 | 0.029 | 77 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.135 | 50 | 0.177 | 42 | -0.054 | 100 | -0.258 | 128 |
| RSC124-9 | F$_{2:3}$ High | -0.513 | 152 | 0.339 | 19 | -0.400 | 147 | 0.574 | 3 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | -0.564 | 159 | 0.201 | 38 | 0.205 | 36 | 0.158 | 44 |
| RSC124-3 | F$_{2:3}$ Low | 0.002 | 84 | -0.056 | 101 | 0.002 | 85 | 0.053 | 70 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -0.198 | 121 | -0.093 | 109 | 0.041 | 75 | 0.250 | 24 |
| RSC117-2 | F$_{2:3}$ High | -0.032 | 93 | 0.232 | 27 | -0.180 | 116 | -0.019 | 90 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | -0.402 | 148 | 0.483 | 8 | 0.101 | 58 | -0.182 | 117 |
| RSC117-10 | F$_{2:3}$ Low | -0.027 | 91 | -0.079 | 108 | 0.026 | 78 | 0.079 | 65 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | -0.530 | 155 | 0.244 | 26 | 0.347 | 17 | -0.062 | 102 |
| RSC19-3 | F$_{2:3}$ High | 0.121 | 53 | -0.280 | 132 | 0.198 | 39 | -0.039 | 95 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -0.048 | 97 | -0.345 | 141 | -0.014 | 89 | 0.408 | 14 |
| RSC19-1 | F$_{2:3}$ Low | 0.226 | 30 | 0.077 | 66 | -0.520 | 154 | 0.218 | 33 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 0.254 | 22 | -0.183 | 118 | 0.123 | 52 | -0.195 | 119 |
| SE hybrid | 0.321 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

estimate of SCA variance was less than the GCA variance, indicating dominance of additive gene action (Table 22). All cross combinations involving bad general combiners tended to produce the high positive SCA effects in the hybrids, which might be caused by good complementarity between parents, except in the cross A.301*RSC38-9 $BC_1F_{2:3}$ low that had low x high combination of GCA effects. Results of the present study with additive variance being greater than dominance were opposite those of Rani et al. (2015).

Fiber content of grain ranged from -0.049 (A.Tx3197*RSC112-19 $BC_1F_{2:3}$ high) to 0.067 (A.301*RSC112-19 $BC_1F_{2:3}$ high) (Table 31). The crosses were low x high and high x high, respectively, for the combination of GCA effects. Although a very small difference, SCA variance was a smaller estimate than GCA variance, indicating dominance of additive gene action (Table 22). The action of good general combiners produced the most positive hybrid for fiber content of grain.

Fat content of grain ranged from -0.283 (A.319*RSC117-4 $BCF_{2:3}$ high) to 0.303 (A.338*RSC73-9 $F_{2:3}$ high) (Table 32). The crosses were low x high and high x low, respectively, for combination of GCA effects, indicating non-additive gene action; however, the estimate for GCA variance was slightly larger than the estimate for SCA variance, indicating dominance of additive gene action (Table 22). The predominance of both additive and non-additive gene action was evident.

**Genetic Components**

Data in Table 22 show the genetic components and contribution of the lines, testers, and their interaction for all studied traits in all environments. The line x tester analysis revealed that the contribution of the lines to the total sum of squares was greater

Table 31. Specific Combining Ability (SCA) estimates for concentration of fiber in grain (%) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|------|------|------|------|------|------|------|------|------|------|
| RSC73-9 | $F_{2:3}$ High | -0.025 | 141 | 0.027 | 17 | -0.025 | 143 | 0.024 | 22 |
| RSC73-6 | $BC_1F_{2:3}$ High | -0.023 | 138 | 0.005 | 58 | 0.013 | 45 | 0.006 | 57 |
| RSC73-1 | $F_{2:3}$ Low | -0.036 | 155 | 0.01 | 52 | 0.002 | 72 | 0.024 | 23 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -0.034 | 153 | -0.002 | 81 | 0.024 | 21 | 0.012 | 48 |
| RSC83-1 | $F_{2:3}$ High | -0.015 | 113 | 0.005 | 59 | 0.027 | 18 | -0.017 | 124 |
| RSC83-14 | $BC_1F_{2:3}$ High | 0.040 | 8 | -0.017 | 122 | 0.015 | 40 | -0.039 | 157 |
| RSC83-10 | $F_{2:3}$ Low | -0.009 | 100 | -0.019 | 129 | 0.018 | 34 | 0.010 | 54 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 0.017 | 35 | -0.001 | 79 | -0.015 | 114 | 0.000 | 78 |
| RSC112-5 | $F_{2:3}$ High | 0.002 | 68 | 0.037 | 9 | -0.02 | 134 | -0.019 | 130 |
| RSC112-19 | $BC_1F_{2:3}$ High | 0.067 | 1 | -0.004 | 87 | -0.049 | 160 | -0.014 | 112 |
| RSC112-8 | $F_{2:3}$ Low | 0.015 | 38 | -0.012 | 107 | 0.003 | 66 | -0.006 | 93 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 0.016 | 36 | -0.012 | 108 | -0.003 | 85 | -0.001 | 80 |
| RSC76-4 | $F_{2:3}$ High | -0.018 | 125 | 0.002 | 70 | 0.015 | 41 | 0.001 | 77 |
| RSC76-16 | $BC_1F_{2:3}$ High | -0.044 | 159 | 0.02 | 29 | -0.013 | 111 | 0.037 | 10 |
| RSC76-13 | $F_{2:3}$ Low | -0.024 | 140 | 0.019 | 30 | -0.015 | 115 | 0.019 | 32 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -0.029 | 146 | 0.005 | 60 | -0.004 | 89 | 0.028 | 16 |
| RSC38-5 | $F_{2:3}$ High | 0.002 | 69 | 0.001 | 75 | -0.015 | 116 | 0.012 | 49 |
| RSC38-15 | $BC_1F_{2:3}$ High | 0.026 | 19 | -0.017 | 123 | 0.003 | 67 | -0.012 | 109 |
| RSC38-8 | $F_{2:3}$ Low | -0.029 | 147 | -0.003 | 83 | 0.042 | 7 | -0.010 | 103 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -0.020 | 132 | 0.004 | 63 | 0.022 | 25 | -0.006 | 94 |
| RSC37-12 | $F_{2:3}$ High | -0.012 | 105 | -0.009 | 101 | 0.030 | 13 | -0.009 | 102 |
| RSC37-12 | $BC_1F_{2:3}$ High | -0.035 | 154 | 0.018 | 33 | 0.005 | 61 | 0.012 | 50 |
| RSC37-7 | $F_{2:3}$ Low | -0.023 | 139 | 0.019 | 31 | 0.022 | 26 | -0.019 | 131 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -0.003 | 82 | 0.001 | 76 | -0.011 | 104 | 0.013 | 46 |
| RSC15-13 | $F_{2:3}$ High | -0.012 | 106 | -0.018 | 127 | -0.016 | 120 | 0.047 | 6 |
| RSC15-15 | $BC_1F_{2:3}$ High | 0.021 | 27 | 0.002 | 71 | -0.005 | 91 | -0.018 | 128 |
| RSC15-11 | $F_{2:3}$ Low | -0.025 | 142 | 0.004 | 64 | -0.030 | 151 | 0.050 | 4 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 0.054 | 3 | -0.029 | 148 | -0.003 | 86 | -0.022 | 136 |
| RSC124-9 | $F_{2:3}$ High | 0.013 | 44 | 0.016 | 37 | -0.031 | 152 | 0.002 | 74 |
| RSC124-16 | $BC_1F_{2:3}$ High | 0.047 | 5 | -0.013 | 110 | -0.029 | 149 | -0.005 | 92 |
| RSC124-3 | $F_{2:3}$ Low | -0.017 | 121 | 0.009 | 55 | -0.015 | 117 | 0.023 | 24 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 0.036 | 11 | 0.011 | 51 | -0.026 | 144 | -0.022 | 137 |
| RSC117-2 | $F_{2:3}$ High | 0.035 | 12 | -0.008 | 96 | 0.015 | 42 | -0.042 | 158 |
| RSC117-4 | $BC_1F_{2:3}$ High | 0.026 | 20 | -0.003 | 84 | -0.015 | 118 | -0.008 | 98 |
| RSC117-10 | $F_{2:3}$ Low | 0.020 | 28 | -0.028 | 145 | 0.028 | 14 | -0.020 | 135 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 0.057 | 2 | -0.03 | 150 | 0.012 | 47 | -0.038 | 156 |
| RSC19-3 | $F_{2:3}$ High | -0.020 | 133 | 0.004 | 65 | 0.002 | 73 | 0.014 | 43 |
| RSC19-17 | $BC_1F_{2:3}$ High | -0.018 | 126 | 0.015 | 39 | 0.010 | 53 | -0.008 | 99 |
| RSC19-1 | $F_{2:3}$ Low | -0.016 | 119 | -0.008 | 97 | 0.028 | 15 | -0.004 | 90 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -0.007 | 95 | -0.004 | 88 | 0.006 | 56 | 0.005 | 62 |
| SE hybrid | 0.033 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

Table 32. Specific Combining Ability (SCA) estimates for concentration of fat in grain (%) for each hybrid combination in the combined analysis across four environments with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | -0.236 | 158 | 0.208 | 4 | -0.275 | 159 | 0.303 | 1 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 0.011 | 81 | -0.077 | 117 | 0.027 | 73 | 0.039 | 63 |
| RSC73-1 | F$_{2:3}$ Low | -0.174 | 145 | 0.109 | 31 | -0.229 | 156 | 0.294 | 2 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 0.037 | 65 | -0.043 | 102 | -0.042 | 100 | 0.048 | 56 |
| RSC83-1 | F$_{2:3}$ High | -0.052 | 107 | 0.117 | 29 | 0.036 | 67 | -0.101 | 125 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -0.088 | 120 | 0.039 | 62 | 0.082 | 40 | -0.033 | 98 |
| RSC83-10 | F$_{2:3}$ Low | -0.116 | 129 | 0.053 | 54 | 0.179 | 9 | -0.116 | 130 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 0.027 | 70 | 0.028 | 69 | 0.056 | 53 | -0.111 | 127 |
| RSC112-5 | F$_{2:3}$ High | 0.130 | 25 | 0.125 | 27 | -0.232 | 157 | -0.023 | 92 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 0.158 | 17 | -0.044 | 105 | 0.003 | 84 | -0.116 | 131 |
| RSC112-8 | F$_{2:3}$ Low | -0.019 | 91 | 0.077 | 42 | -0.145 | 140 | 0.087 | 38 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 0.197 | 6 | -0.024 | 93 | 0.025 | 75 | -0.198 | 150 |
| RSC76-4 | F$_{2:3}$ High | 0.014 | 77 | 0.042 | 58 | 0.079 | 41 | -0.135 | 138 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -0.080 | 118 | 0.027 | 72 | -0.126 | 134 | 0.179 | 10 |
| RSC76-13 | F$_{2:3}$ Low | -0.128 | 136 | 0.095 | 37 | -0.146 | 141 | 0.179 | 11 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 0.027 | 71 | -0.043 | 103 | -0.045 | 106 | 0.061 | 50 |
| RSC38-5 | F$_{2:3}$ High | 0.014 | 78 | -0.089 | 122 | 0.127 | 26 | -0.052 | 108 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 0.003 | 83 | 0.07 | 47 | 0.040 | 59 | -0.112 | 128 |
| RSC38-8 | F$_{2:3}$ Low | -0.096 | 124 | -0.014 | 89 | 0.072 | 45 | 0.038 | 64 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 0.000 | 85 | 0.036 | 66 | 0.026 | 74 | -0.061 | 111 |
| RSC37-12 | F$_{2:3}$ High | -0.009 | 86 | 0.144 | 20 | -0.075 | 115 | -0.060 | 110 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | -0.118 | 132 | 0.261 | 3 | -0.204 | 152 | 0.061 | 51 |
| RSC37-7 | F$_{2:3}$ Low | 0.169 | 15 | -0.127 | 135 | 0.157 | 18 | -0.199 | 151 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -0.106 | 126 | 0.166 | 16 | -0.036 | 99 | -0.025 | 94 |
| RSC15-13 | F$_{2:3}$ High | 0.039 | 61 | -0.129 | 137 | 0.151 | 19 | -0.061 | 112 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 0.070 | 46 | -0.176 | 146 | 0.070 | 48 | 0.036 | 68 |
| RSC15-11 | F$_{2:3}$ Low | 0.083 | 39 | -0.028 | 95 | 0.104 | 36 | -0.159 | 144 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.072 | 44 | -0.21 | 154 | 0.170 | 14 | -0.032 | 97 |
| RSC124-9 | F$_{2:3}$ High | 0.133 | 23 | -0.182 | 147 | 0.196 | 7 | -0.147 | 142 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 0.180 | 8 | -0.206 | 153 | 0.067 | 49 | -0.042 | 101 |
| RSC124-3 | F$_{2:3}$ Low | -0.076 | 116 | -0.014 | 90 | -0.081 | 119 | 0.171 | 13 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.109 | 30 | -0.125 | 133 | 0.202 | 5 | -0.186 | 148 |
| RSC117-2 | F$_{2:3}$ High | -0.075 | 114 | 0.109 | 32 | -0.140 | 139 | 0.106 | 33 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 0.105 | 34 | -0.283 | 160 | 0.040 | 60 | 0.139 | 22 |
| RSC117-10 | F$_{2:3}$ Low | 0.012 | 80 | 0.014 | 79 | -0.088 | 121 | 0.061 | 52 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 0.074 | 43 | -0.194 | 149 | 0.133 | 24 | -0.012 | 88 |
| RSC19-3 | F$_{2:3}$ High | -0.090 | 123 | 0.173 | 12 | -0.226 | 155 | 0.143 | 21 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -0.060 | 109 | 0.104 | 35 | -0.067 | 113 | 0.023 | 76 |
| RSC19-1 | F$_{2:3}$ Low | -0.149 | 143 | 0.053 | 55 | 0.125 | 28 | -0.029 | 96 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 0.009 | 82 | -0.043 | 104 | -0.010 | 87 | 0.044 | 57 |
| SE hybrid | 0.182 | | | | | | | | |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

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than that of the testers for all studied traits except the number of days to anthesis. The maximum contribution of lines (69.5%) was noted for panicle length, followed by 1000-kernel weight (69.3%), while the lowest values were for the number of days to anthesis (12.7%), followed by fiber concentration in grain (44.9%). Testers contributed a maximum for the number of days to anthesis (73.8%) and least for starch concentration in grain (1.6%). For the line x tester interaction, the maximum contribution to the total sum of squares was 49.2% for starch concentration in grain, whereas the minimum contribution was 7.1% for the height to the flag leaf. Variance due to lines was greater than that of testers for all traits except the number of days to anthesis, which is confirmed by the contributions of lines and testers. By removing NIR data because of observed negative SCA variances, the variance due to GCA ($\sigma^2_{gca}$) was less than the variance for SCA ($\sigma^2_{sca}$) for all traits except plant exsertion ($\sigma^2_{gca}/\sigma^2_{sca} = 1.5122$) and concentration of protein, starch, fiber, and fat in grain, suggesting that a preponderance of non-additive gene action controlled the characters. Dominance variance ($\sigma^2_D$) was large while additive variance ($\sigma^2_A$) was less in magnitude for all traits except plant exsertion and concentration of protein, starch, fiber, and fat in grain. The results are supported by the ratio of variance of general to specific combining ability ($\sigma^2_{gca}/\sigma^2_{sca}$) that was less than unity and by the degree of dominance ($\sigma^2_D/\sigma^2_A$) that takes values greater than unity for all traits except plant exsertion where $\sigma^2_A$ was greater than $\sigma^2_D$ with the degree of dominance being less than unity. Similar results were found by Fellahi et al. (2013) who suggested that with the preponderance of non-additive gene action, in terms of grain yield, plant height, and duration of the vegetative growth, use of sorghum varieties should be postponed until later generations. Mohammed (2009) reported that additive gene action

was important in the expression of days to flower and forage yield while non-additive gene action was important in plant height where $\sigma^2_{gca}/\sigma^2_{sca}$ was less than unity. Mahdy et al. (2011) found that both additive and non-additive gene action were important for inheritance of plant height and grain yield, and they found the additive effect controlled days to anthesis. Several researchers indicated the importance of additive and non-additive gene action in heritance of grain yield and some agronomic traits (Kenga et al., 2004; Abdel-Mottaleb, 2009; Mohammed, 2009; Mahday et al., 2011).

**Midparent Heterosis**

Exploitation of hybrid vigor is an appropriate alternative for making further breakthroughs in increasing sorghum yield. Greater yield over high-yielding check varieties and wider adaptability have been instrumental in the rapid spread of hybrid sorghum. Estimates of degree of dominance were greater than the degree of additive for grain yield and yield components except plant exsertion and protein, starch, fiber, and fat contents in grain, which indicates dominance is the primary cause of heterosis (Table 33).

The range of MPH for grain yield was -34.22 (A.338*RSC76-2 $BC_1F_{2:3}$ low) to 61.76% (A.301*RSC83-14 $BC_1F_{2:3}$ high) (Table 33). As many as 31 hybrids expressed significant positive MPH ranging from 32.45 (A.301*RSC38-9 $BC_1F_{2:3}$ low) to 61.76% (A.301*RSC83-14 $BC_1F_{2:3}$ high). Of the 160 hybrids, only two expressed significant negative MPH ranging from -34.22 (A.338*RSC76-2 $BC_1F_{2:3}$ low) to -33.62% (A.338*RSC76-16 $BC_1F_{2:3}$ high). The highest significant positive MPH larger than 50% was among hybrids A.301*RSC83-14 $BC_1F_{2:3}$ high, A.301*RSC124-9 $F_{2:3}$ high, A.319*RSC83-1 $BC_1F_{2:3}$ low, and A.301*RSC76-4 $F_{2:3}$ high. Of the 40 lines, three

Table 33. Midparent heterosis estimates for grain yield (Mgha$^{-1}$) for each hybrid combination in the combined analysis in four environments, Vega, TX (2015 and 2016), Hutchinson, KS (2015), and Dumas, TX (2016) with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | 45.09** | 9 | 18.00 | 68 | 5.91 | 107 | -12.51 | 142 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 21.78 | 58 | 22.46 | 54 | -14.36 | 148 | -15.18 | 151 |
| RSC73-1 | F$_{2:3}$ Low | 15.36 | 78 | 8.24 | 100 | -1.41 | 122 | -5.48 | 131 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 34.63* | 24 | 22.05 | 56 | -8.61 | 136 | -14.33 | 147 |
| RSC83-1 | F$_{2:3}$ High | 35.81* | 20 | 14.61 | 80 | -6.30 | 133 | 15.01 | 79 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 61.76** | 1 | 35.38* | 21 | 18.60 | 65 | 31.14 | 33 |
| RSC83-10 | F$_{2:3}$ Low | 10.78 | 93 | 8.09 | 102 | -3.53 | 128 | 13.36 | 85 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 45.25** | 8 | 53.87** | 3 | 35.92* | 19 | 22.16 | 55 |
| RSC112-5 | F$_{2:3}$ High | 29.96 | 36 | 10.84 | 92 | 22.85 | 53 | 11.79 | 90 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 39.38* | 15 | 30.44 | 34 | 42.27* | 11 | 13.80 | 82 |
| RSC112-8 | F$_{2:3}$ Low | 24.53 | 47 | 5.58 | 108 | 12.63 | 88 | 1.02 | 120 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 25.54 | 43 | 10.74 | 94 | 19.94 | 62 | 8.27 | 99 |
| RSC76-4 | F$_{2:3}$ High | 52.81** | 4 | 2.17 | 115 | 1.44 | 119 | -20.08 | 152 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 28.93 | 37 | 20.77 | 60 | 10.64 | 95 | -33.62* | 159 |
| RSC76-13 | F$_{2:3}$ Low | 21.15 | 59 | 7.41 | 104 | -14.18 | 146 | -20.51 | 153 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 35.22* | 22 | -10.54 | 137 | 14.53 | 81 | -34.22* | 160 |
| RSC38-5 | F$_{2:3}$ High | 25.73 | 42 | 33.02* | 29 | 16.79 | 70 | -12.68 | 144 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 27.69 | 38 | 15.79 | 77 | -12.60 | 143 | -24.67 | 156 |
| RSC38-8 | F$_{2:3}$ Low | 18.42 | 66 | 9.38 | 96 | -7.07 | 134 | -12.73 | 145 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 32.45* | 31 | 23.50 | 51 | 8.72 | 98 | -11.26 | 139 |
| RSC37-12 | F$_{2:3}$ High | 47.35** | 7 | 30.43 | 35 | 2.64 | 112 | -3.99 | 129 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 33.91* | 25 | 13.42 | 84 | 9.25 | 97 | -22.55 | 155 |
| RSC37-7 | F$_{2:3}$ Low | 19.48 | 64 | 18.02 | 67 | -11.86 | 140 | -3.38 | 127 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 39.55* | 14 | 11.40 | 91 | -0.52 | 121 | 2.00 | 116 |
| RSC15-13 | F$_{2:3}$ High | 24.24 | 48 | 16.78 | 71 | -25.18 | 157 | -2.25 | 124 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 33.56* | 27 | 19.82 | 63 | 23.79 | 50 | 6.63 | 105 |
| RSC15-11 | F$_{2:3}$ Low | 25.48 | 44 | 27.33 | 39 | -14.92 | 149 | -3.12 | 125 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 16.71 | 73 | -2.12 | 123 | 2.61 | 113 | 5.51 | 109 |
| RSC124-9 | F$_{2:3}$ High | 55.88** | 2 | 33.17* | 28 | 42.00* | 12 | 23.30 | 52 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 12.73 | 87 | 12.56 | 89 | 20.43 | 61 | -3.22 | 126 |
| RSC124-3 | F$_{2:3}$ Low | 26.81 | 40 | 2.95 | 111 | -12.22 | 141 | -10.84 | 138 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 38.58* | 16 | 13.58 | 83 | 16.97 | 69 | 1.94 | 117 |
| RSC117-2 | F$_{2:3}$ High | 34.75* | 23 | 24.84 | 46 | 6.30 | 106 | 31.52 | 32 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 37.38* | 18 | 32.54* | 30 | 23.91 | 49 | 49.64** | 6 |
| RSC117-10 | F$_{2:3}$ Low | 49.68** | 5 | 16.76 | 72 | 16.52 | 74 | 16.28 | 76 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 38.42* | 17 | 7.74 | 103 | 13.08 | 86 | 25.78 | 41 |
| RSC19-3 | F$_{2:3}$ High | 43.96* | 10 | 8.20 | 101 | -5.18 | 130 | 16.28 | 75 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 41.78* | 13 | 5.01 | 110 | -22.36 | 154 | -15.02 | 150 |
| RSC19-1 | F$_{2:3}$ Low | 22.05 | 57 | 2.49 | 114 | -7.54 | 135 | -5.57 | 132 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 33.75* | 26 | 25.13 | 45 | -25.94 | 158 | 1.64 | 118 |
| SE hybrid | 15.81 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

expressed significant positive MPH with three of the four testers: RSC83-1 $F_{2:3}$ high and RSC124-9 $F_{2:3}$ high with A.301, A.319, and A.Tx3197 with RSC117-4 $BC_1F_{2:3}$ high with A.301, A.319, and A.338. Significant positive heterosis for grain yield was reported by Hovny et al. (2000), Abo-Elwafa (2005), Kenga et al. (2005), Hovny and El-Dsouky (2007), Abdel-Mottaleb (2009), and Amir and Mohamed (2015). Both midparent and better parent positive heterosis were reported by Premalatha et al. (2006), Sharma and Sharma (2006), and El-Dardeer et.al. (2011).

The range of MPH for the number of days to anthesis varied from -8.97 (A.301*RSC73-5 $BC_1F_{2:3}$ low) to 9.34% (A.319*RSC37-12 $BC_1F_{2:3}$ high), with a standard error equal to 1.574 (Table 34). The MPH in the negative direction was considered to be desirable for the trait. As many as 56 hybrids expressed significant negative MPH ranging from -8.97 (A.301*RSC73-5 $BC_1F_{2:3}$ low) to -3.19% (A.319*RSC38-8 $F_{2:3}$ low). Some of the early flowering hybrids with tester A.301 consisted of lines RSC124-4 ($BC_1F_{2:3}$ low), RSC15-15 ($BC_1F_{2:3}$ high), RSC37-8 ($BC_1F_{2:3}$ low), and RSC112-15 ($BC_1F_{2:3}$ low) with the number of days to anthesis ranging from 66.3 to 67.0 and with significant negative MPH values of -4.95, -3.47, -4.08, and -4.75, respectively. The results of heterosis for earliness were in accordance with the findings of Kenga et al. (2005), Premalatha et al. (2006), Hovny and El-Dsouky (2007), Abdel-Mottaleb (2009), Essa (2009), Mahdy et al. (2011), Abou-Amer and Kewan (2014), Omar et al. (2014), and Amir and Mohamed (2015).

Almost all the hybrids were taller than their respective mid-parents. The average MPH ranged from -10.44 (A.301*RSC124-3 $F_{2:3}$ low) to 88.29% (A.338*RSC73-5

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Table 34.  Midparent heterosis estimates for days to anthesis for each hybrid combination in the combined analysis in two environments of 2015 and 2016 at Vega, TX, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | 0.12 | 58 | 3.97* | 14 | -3.07 | 101 | 4.92** | 11 |
| RSC73-6 | $BC_1F_{2:3}$ High | -1.37 | 77 | 0.73 | 47 | -4.02* | 119 | 2.29 | 25 |
| RSC73-1 | $F_{2:3}$ Low | -1.47 | 78 | 7.85** | 3 | 5.61** | 6 | 5.25** | 8 |
| RSC73-5 | $BC_1F_{2:3}$ Low | -8.97** | 160 | -0.46 | 65 | -5.12** | 134 | -2.25 | 92 |
| RSC83-1 | $F_{2:3}$ High | -2.56 | 98 | 0.83 | 44 | 2.24 | 26 | -0.76 | 69 |
| RSC83-14 | $BC_1F_{2:3}$ High | -2.07 | 90 | 1 | 42 | -4.61** | 130 | 1.56 | 37 |
| RSC83-10 | $F_{2:3}$ Low | -5.52** | 137 | 0.67 | 48 | -4.21* | 123 | -2.44 | 95 |
| RSC83-1 | $BC_1F_{2:3}$ Low | -1.62 | 80 | 4.99** | 10 | -2.18 | 91 | 2.07 | 30 |
| RSC112-5 | $F_{2:3}$ High | 1.69 | 36 | 1.31 | 41 | -5.76** | 142 | -5.71** | 140 |
| RSC112-19 | $BC_1F_{2:3}$ High | 0.85 | 43 | -0.87 | 72 | -5.65** | 139 | -3.08 | 102 |
| RSC112-8 | $F_{2:3}$ Low | -7.3** | 154 | -3.43* | 111 | -4.6** | 129 | -0.15 | 62 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -4.75** | 132 | 0.39 | 54 | -3.24* | 106 | 2.1 | 29 |
| RSC76-4 | $F_{2:3}$ High | -3.28* | 107 | 1.75 | 34 | -1.16 | 74 | -2.29 | 93 |
| RSC76-16 | $BC_1F_{2:3}$ High | 2.39 | 24 | 1.92 | 32 | -1.7 | 82 | -1.53 | 79 |
| RSC76-13 | $F_{2:3}$ Low | 0.33 | 55 | 2.42 | 23 | -0.65 | 66 | 2.84 | 19 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 0.5 | 52 | 0.76 | 46 | -3.14 | 103 | 0.14 | 56 |
| RSC38-5 | $F_{2:3}$ High | -4.31* | 126 | 2.43 | 22 | -4.03* | 120 | 1.56 | 38 |
| RSC38-15 | $BC_1F_{2:3}$ High | -5.8** | 143 | -1.86 | 86 | -7.45** | 155 | 2.01 | 31 |
| RSC38-8 | $F_{2:3}$ Low | -6.17** | 148 | -3.19* | 105 | -8.47** | 158 | 2.64 | 21 |
| RSC38-9 | $BC_1F_{2:3}$ Low | -0.33 | 63 | -0.74 | 68 | -3.92* | 116 | 7.54** | 4 |
| RSC37-12 | $F_{2:3}$ High | -3.32* | 109 | 9.34** | 1 | -5.85** | 144 | -5.41** | 135 |
| RSC37-12 | $BC_1F_{2:3}$ High | -2.51 | 96 | 2.76 | 20 | -4.68** | 131 | -0.01 | 60 |
| RSC37-7 | $F_{2:3}$ Low | -6.11** | 147 | 0.51 | 51 | -6.75** | 153 | -1.09 | 73 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -4.08* | 121 | 2.22 | 27 | -5.91** | 146 | 1.46 | 39 |
| RSC15-13 | $F_{2:3}$ High | 1.37 | 40 | 0.65 | 49 | -3.31* | 108 | 4.78** | 12 |
| RSC15-15 | $BC_1F_{2:3}$ High | -3.47* | 112 | -3.33* | 110 | -7.51** | 156 | 0.02 | 59 |
| RSC15-11 | $F_{2:3}$ Low | -0.06 | 61 | 8.15** | 2 | -1.72 | 83 | 3.87* | 15 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -2.36 | 94 | -0.82 | 71 | -3.89* | 114 | 0.77 | 45 |
| RSC124-9 | $F_{2:3}$ High | -4.31* | 125 | -5.73** | 141 | -6.66** | 152 | -1.67 | 81 |
| RSC124-16 | $BC_1F_{2:3}$ High | 2.2 | 28 | -4.39* | 127 | -6.57** | 151 | -1.94 | 87 |
| RSC124-3 | $F_{2:3}$ Low | -3.06 | 100 | -2 | 89 | -4.3* | 124 | 0.65 | 50 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -4.95** | 133 | 0.48 | 53 | -8.73** | 159 | -5.44** | 136 |
| RSC117-2 | $F_{2:3}$ High | -2.55 | 97 | 1.75 | 35 | -1.35 | 76 | 3.2* | 17 |
| RSC117-4 | $BC_1F_{2:3}$ High | -5.89** | 145 | -1.78 | 84 | -6.51** | 150 | -3.17 | 104 |
| RSC117-10 | $F_{2:3}$ Low | -3.97* | 117 | -1.16 | 75 | -7.95** | 157 | 0.13 | 57 |
| RSC117-3 | $BC_1F_{2:3}$ Low | -5.59** | 138 | -4.01* | 118 | -6.18** | 149 | -0.43 | 64 |
| RSC19-3 | $F_{2:3}$ High | -1.81 | 85 | 4.76** | 13 | -0.67 | 67 | 2.88 | 18 |
| RSC19-17 | $BC_1F_{2:3}$ High | 1.77 | 33 | 5.44** | 7 | 4.99** | 9 | 3.38* | 16 |
| RSC19-1 | $F_{2:3}$ Low | -3.66* | 113 | 6.29** | 5 | -4.19* | 122 | -0.81 | 70 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -4.44* | 128 | -1.99 | 88 | -3.9* | 115 | -2.67 | 99 |
| SE hybrid | 1.57 | | | | | | | | |

SE:  Standard error, * and **:  significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

$BC_1F_{2:3}$ low) (Table 35). One hundred twenty-five hybrids had significant positive MPH, with a maximum plant height (255.6 cm) set by the cross A.338*RSC76-16 $BC_1F_{2:3}$ high with all four selections of RSC76 ranking the best of the four tallest hybrids. The minimum plant height (92.6 cm) for all the crosses was set by A.301*RSC117-10 $F_{2:3}$ low with a MPH value of -1.96%. The testers from shortest to tallest were A.301, A.319, A.Tx3197, and A.338, with average total plant heights of 92.0, 104.3, 112.3, and 128.6 cm, respectively, while the lines ranged from 80.4 (RSC83-1 $BC_1F_{2:3}$ low) to 204.9 cm (RSC76-16 $BC_1F_{2:3}$ high). The findings were in agreement with those obtained by Hovny and El-Dsouky (2007), Abdel-Mottaleb (2009), Essa (2009), Mahdy et al. (2011), and Amir and Mohamed (2015).

The average MPH for height to flag leaf varied from -14.09 (A.301*RSC124-3 $F_{2:3}$ low) to 116.34% (A.338*RSC38-5 $F_{2:3}$ high) (Table 36). One-hundred eleven hybrids had significant positive MPH, with the maximum height to the flag leaf (221.1 cm) by the cross A.338*RSC76-4 $F_{2:3}$ high with all four selections of RSC76 being in the top five for height to the flag leaf. The minimum height to the flag leaf (59.7 cm) for all crosses was by A.301*RSC117-10 $F_{2:3}$ low, followed by A.301*RSC38-5 $F_{2:3}$ high (61.4 cm) with MPH values of -2.87 and -2.05%, respectively. With most of the hybrids being taller than their parents, the height to the flag leaf followed a similar pattern, and the findings are in agreement with those of Hovny and El-Dsouky (2007), Abdel-Mottaleb (2009), Essa (2009), Mahdy et al. (2011), and Amir and Mohamed (2015).

Longer panicle, greater panicle weight, and 1000-kernel weight were generally associated with greater yields and were some of the attributes for greater grain yield by

Table 35. Midparent heterosis estimates for total plant height (cm) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | 34.22** | 78 | 58.97** | 30 | 63.06** | 22 | 71.63** | 10 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 45.56** | 56 | 60.51** | 28 | 61.01** | 26 | 73.26** | 7 |
| RSC73-1 | F$_{2:3}$ Low | 12.73 | 127 | 43.29** | 60 | 48.84** | 46 | 59.29** | 29 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 38.46** | 70 | 68.45** | 12 | 77.82** | 5 | 88.29** | 1 |
| RSC83-1 | F$_{2:3}$ High | 20.17** | 100 | 45.49** | 57 | 46.07** | 55 | 60.57** | 27 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 43.21** | 61 | 68.44** | 13 | 67.09** | 16 | 72.58** | 8 |
| RSC83-10 | F$_{2:3}$ Low | 0.85 | 152 | 9.12 | 142 | 11.58 | 133 | 17.97* | 106 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 47.48** | 50 | 65.27** | 20 | 81.17** | 3 | 77.05** | 6 |
| RSC112-5 | F$_{2:3}$ High | 8.81 | 143 | 12.57 | 129 | 20.74** | 99 | -1.19 | 156 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 6.71 | 147 | 14.75* | 121 | 22.95** | 92 | 24.09** | 87 |
| RSC112-8 | F$_{2:3}$ Low | 1.15 | 151 | 11.39 | 135 | 15.57* | 118 | 15.03* | 120 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -6.42 | 158 | 14.71* | 123 | 19.45* | 103 | 23.89** | 88 |
| RSC76-4 | F$_{2:3}$ High | 27.9** | 82 | 55.01** | 33 | 61.82** | 24 | 69.24** | 11 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 17* | 110 | 38.5** | 69 | 50.99** | 41 | 53.34** | 38 |
| RSC76-13 | F$_{2:3}$ Low | 33.5** | 79 | 48.36** | 49 | 53.42** | 37 | 51.24** | 40 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 30.15** | 81 | 57.11** | 32 | 66.8** | 17 | 66.51** | 18 |
| RSC38-5 | F$_{2:3}$ High | 0.12 | 153 | 19.43* | 104 | 19.66* | 101 | 85.58** | 2 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 17.01* | 109 | 47.39** | 51 | 50.52** | 43 | 71.76** | 9 |
| RSC38-8 | F$_{2:3}$ Low | 8.36 | 144 | 37.72** | 72 | 40.35** | 67 | 54.34** | 34 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 10.68 | 139 | 35.47** | 74 | 37.82** | 71 | 54.29** | 35 |
| RSC37-12 | F$_{2:3}$ High | 32.82** | 80 | 79.59** | 4 | 68.12** | 15 | 54.18** | 36 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 43.08** | 62 | 43.68** | 59 | 65.22** | 21 | 65.36** | 19 |
| RSC37-7 | F$_{2:3}$ Low | -8.14 | 159 | 52.66** | 39 | 49.12** | 44 | 62.62** | 23 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 27.12** | 83 | 57.6** | 31 | 61.42** | 25 | 68.22** | 14 |
| RSC15-13 | F$_{2:3}$ High | 26.82** | 84 | 11.88 | 132 | 48.78** | 47 | 47.07** | 53 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 7.61 | 145 | 15.66* | 116 | 21.42** | 96 | 25.87** | 86 |
| RSC15-11 | F$_{2:3}$ Low | 23.64** | 89 | 15.85* | 115 | 23.61** | 90 | 23.33** | 91 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 22.89** | 93 | 47.36** | 52 | 41.76** | 65 | 47.01** | 54 |
| RSC124-9 | F$_{2:3}$ High | 2.49 | 150 | 12.66 | 128 | 10.35 | 141 | 10.97 | 137 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | -0.9 | 155 | 19.6* | 102 | 20.85** | 98 | 34.38** | 77 |
| RSC124-3 | F$_{2:3}$ Low | -10.44 | 160 | -0.47 | 154 | 10.48 | 140 | 16.47* | 112 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 3.8 | 149 | 12.82 | 126 | 15.22* | 119 | 48.59** | 48 |
| RSC117-2 | F$_{2:3}$ High | 7.3 | 146 | 11.39 | 136 | 21.64** | 95 | 26.8** | 85 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 4.58 | 148 | 16.03* | 114 | 17.95* | 107 | 16.46* | 113 |
| RSC117-10 | F$_{2:3}$ Low | -1.96 | 157 | 15.62* | 117 | 14.72* | 122 | 16.91* | 111 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 34.49** | 76 | 12.39 | 130 | 22.17** | 94 | 21.13** | 97 |
| RSC19-3 | F$_{2:3}$ High | 18.65* | 105 | 35.2** | 75 | 35.59** | 73 | 38.6** | 68 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 17.52* | 108 | 50.84** | 42 | 45.12** | 58 | 49.06** | 45 |
| RSC19-1 | F$_{2:3}$ Low | 11.56 | 134 | 13.89* | 125 | 12.32 | 131 | 14.16* | 124 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 10.95 | 138 | 43.07** | 63 | 40.83** | 66 | 42.13** | 64 |
| SE hybrid | 6.88 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

Table 36. Midparent heterosis estimates for height to flag leaf (cm) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | 40.29** | 75 | 68.81** | 25 | 65.65** | 33 | 80.33** | 15 |
| RSC73-6 | $BC_1F_{2:3}$ High | 50.61** | 64 | 71.29** | 24 | 67.37** | 28 | 84.56** | 9 |
| RSC73-1 | $F_{2:3}$ Low | 12.68 | 130 | 59.43** | 46 | 60.64** | 44 | 73.28** | 22 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 43.41** | 70 | 80.66** | 14 | 83.19** | 10 | 101.79** | 3 |
| RSC83-1 | $F_{2:3}$ High | 32.52* | 85 | 58.48** | 49 | 52.57** | 62 | 77.42** | 19 |
| RSC83-14 | $BC_1F_{2:3}$ High | 57.61** | 52 | 93.27** | 4 | 82.01** | 13 | 85.34** | 8 |
| RSC83-10 | $F_{2:3}$ Low | 0.21 | 151 | 15.82 | 122 | 11.24 | 135 | 22.74** | 102 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 55.46** | 56 | 78.63** | 18 | 87.8** | 6 | 87.67** | 7 |
| RSC112-5 | $F_{2:3}$ High | 6.46 | 146 | 11.32 | 134 | 14.67 | 125 | -6.63 | 157 |
| RSC112-19 | $BC_1F_{2:3}$ High | 7.47 | 142 | 19.52** | 109 | 24.1** | 100 | 34.0* | 84 |
| RSC112-8 | $F_{2:3}$ Low | 1.01 | 149 | 17.14 | 113 | 13.14 | 126 | 19.9** | 107 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -6.75 | 158 | 18.64** | 111 | 18.89** | 110 | 29.18* | 91 |
| RSC76-4 | $F_{2:3}$ High | 35.2** | 83 | 63.75** | 37 | 65.79** | 32 | 79** | 17 |
| RSC76-16 | $BC_1F_{2:3}$ High | 24.2** | 99 | 48.22** | 66 | 55.37** | 57 | 65.54** | 35 |
| RSC76-13 | $F_{2:3}$ Low | 35.24** | 82 | 53.72** | 59 | 58.04** | 50 | 58.52** | 48 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 38.72** | 76 | 62.2** | 40 | 72.69** | 23 | 74.78** | 21 |
| RSC38-5 | $F_{2:3}$ High | -2.05 | 153 | 21.16** | 104 | 16.24 | 120 | 116.34** | 1 |
| RSC38-15 | $BC_1F_{2:3}$ High | 25.35** | 95 | 58.64** | 47 | 57.65** | 51 | 92.93** | 5 |
| RSC38-8 | $F_{2:3}$ Low | 6.38 | 147 | 47.67** | 68 | 43.91** | 69 | 66.93** | 30 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 7.26 | 144 | 36.28** | 79 | 42.59** | 71 | 66.96** | 29 |
| RSC37-12 | $F_{2:3}$ High | 38.31** | 77 | 107.92** | 2 | 80.28** | 16 | 62.75** | 39 |
| RSC37-12 | $BC_1F_{2:3}$ High | 53.18** | 60 | 54.31** | 58 | 68.02** | 27 | 76.35** | 20 |
| RSC37-7 | $F_{2:3}$ Low | -9.41 | 159 | 68.16** | 26 | 56.66** | 54 | 82.51** | 12 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 24.48** | 98 | 65.55** | 34 | 63.01** | 38 | 82.94** | 11 |
| RSC15-13 | $F_{2:3}$ High | 38.16** | 78 | 6.79 | 145 | 53.14** | 61 | 61.2** | 43 |
| RSC15-15 | $BC_1F_{2:3}$ High | 10.08 | 138 | 22.77** | 101 | 16.24 | 119 | 31.05* | 88 |
| RSC15-11 | $F_{2:3}$ Low | 29.91* | 89 | 16.72 | 114 | 24.71** | 97 | 31.77* | 86 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 29.67* | 90 | 62.1** | 41 | 47.77** | 67 | 59.52** | 45 |
| RSC124-9 | $F_{2:3}$ High | 0.26 | 150 | 12.99 | 129 | 7.29 | 143 | 17.39 | 112 |
| RSC124-16 | $BC_1F_{2:3}$ High | -6.48 | 156 | 20.57** | 106 | 21.24** | 103 | 40.86** | 73 |
| RSC124-3 | $F_{2:3}$ Low | -14.09 | 160 | -3.39 | 155 | 10.29 | 137 | 16.72 | 115 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 13.09 | 127 | 16.55 | 116 | 20.88** | 105 | 66.7** | 31 |
| RSC117-2 | $F_{2:3}$ High | 10.71 | 136 | 14.74 | 124 | 24.85** | 96 | 35.28** | 81 |
| RSC117-4 | $BC_1F_{2:3}$ High | -0.69 | 152 | 16.17 | 121 | 8.03 | 140 | 16.38 | 118 |
| RSC117-10 | $F_{2:3}$ Low | -2.87 | 154 | 11.33 | 133 | 11.52 | 132 | 19.54** | 108 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 42.27** | 72 | 3.59 | 148 | 26.86* | 92 | 25.76* | 93 |
| RSC19-3 | $F_{2:3}$ High | 15.11 | 123 | 35.9** | 80 | 31.33* | 87 | 40.43** | 74 |
| RSC19-17 | $BC_1F_{2:3}$ High | 25.75* | 94 | 64.66** | 36 | 50.03** | 65 | 61.92** | 42 |
| RSC19-1 | $F_{2:3}$ Low | 7.95 | 141 | 16.52 | 117 | 9.68 | 139 | 12.42 | 131 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 13.09 | 128 | 56.97** | 53 | 52.51** | 63 | 55.78** | 55 |
| SE hybrid | 8.92 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

the sorghum in the study. A large panicle in a hybrid is imitated earlier and develops faster than parents (Blum and Pnuel, 1990). For panicle length, MPH varied from -10.43 (A.338*RSC73-1 $F_{2:3}$ low) to 22.48% (A.301*RSC112-5 $F_{2:3}$ high) (Table 37). Fifty-four hybrids expressed significant positive MPH for panicle length while only one hybrid expressed significant negative MPH. Two hybrids expressed significant positive MPH for all four testers RSC83-14 $BC_1F_{2:3}$ high and RSC19-3 $F_{2-3}$ high, while four other hybrids expressed significant positive MPH for three of the four testers. RSC112-5 $F_{2:3}$ high and RSC124-9 $F_{2:3}$ high expressed significant positive MPH with A.301, A.319, and A.Tx3197, while RSC112-19 $BCF_{2:3}$ high and RSC117-2 $F_{2:3}$ high expressed significant positive MPH with A.301, A.319, and A.338. Midparent significant positive heterosis was reported by Sharma and Sharma (2006) and Kanbar et al. (2011) for panicle length. This also was in agreement with the findings of Hovny and El-Dsouky (2007), Abdel-Mottaleb (2009), Essa (2009), Mahdy et al. (2011), and Amir and Mohamed (2015), while Premalatha et al. (2006) reported negative heterosis for the trait.

MPH estimates for plant exsertion ranged from -62.6 (A.301*RSC38-15 $BC_1F_{2:3}$ high) to 557.8% (A.319*RSC73-9 $F_{2:3}$ high) (Table 38). Thirty hybrids expressed significant positive MPH ranging from 207.4 (A.338*RSC38-9 $BC_1F_{2:3}$ low) to 557.8% (A.319*RSC73-9 $F_{2:3}$ high), while 30 hybrids expressed non-significant negative MPH ranging from -62.6 (A.301*RSC38-15 $BC_1F_{2:3}$ high) to -4.52% (A.319*RSC19-1 $F_{2:3}$ low). One line (RSC37-12 $BC_1F_{2:3}$ high) expressed significant positive MPH for all four testers, while RSC37-8 $BC_1F_{2:3}$ low expressed significant positive estimates for A.301, A.319, A.Tx3197, and RSC73-9 $F_{2:3}$ high, and RSC83-1 $F_{2:3}$ high expressed significant

Table 37. Midparent heterosis estimates for panicle length (cm) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | 1.15 | 121 | 2.25 | 111 | -4.14 | 150 | -3.85 | 149 |
| RSC73-6 | $BC_1F_{2:3}$ High | 5.11 | 80 | 2.09 | 114 | 3.26 | 102 | -0.78 | 135 |
| RSC73-1 | $F_{2:3}$ Low | 0.45 | 129 | -5.01 | 154 | -4.94 | 153 | -10.43* | 160 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 5.86 | 77 | 7.78 | 60 | 3.99 | 92 | 8.93* | 49 |
| RSC83-1 | $F_{2:3}$ High | -1.59 | 139 | 9.88* | 39 | 8.49* | 52 | 2 | 115 |
| RSC83-14 | $BC_1F_{2:3}$ High | 12.77** | 20 | 15.69** | 12 | 10* | 38 | 12.58** | 22 |
| RSC83-10 | $F_{2:3}$ Low | 4.68 | 88 | 7.73 | 61 | 5.62 | 79 | 1.88 | 116 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 4.17 | 91 | 3.36 | 101 | 7.03 | 67 | 2.76 | 107 |
| RSC112-5 | $F_{2:3}$ High | 22.48** | 1 | 16.56** | 10 | 19.25** | 2 | 3.6 | 99 |
| RSC112-19 | $BC_1F_{2:3}$ High | 17.98** | 5 | 4.71 | 87 | 8.48* | 53 | 9.44* | 42 |
| RSC112-8 | $F_{2:3}$ Low | 9.75* | 40 | 6.95 | 69 | 2.14 | 113 | 7.4 | 64 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 2.92 | 105 | 4.79 | 84 | 7.62 | 63 | 3.75 | 95 |
| RSC76-4 | $F_{2:3}$ High | -5.1 | 155 | -0.08 | 131 | 0.09 | 130 | 2.6 | 108 |
| RSC76-16 | $BC_1F_{2:3}$ High | 3.69 | 96 | 8.99* | 47 | 7.28 | 65 | 9.33* | 43 |
| RSC76-13 | $F_{2:3}$ Low | 4.77 | 85 | 6.58 | 72 | 8.35* | 54 | 7.91 | 57 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 2.94 | 104 | 8.96* | 48 | 5.66 | 78 | 11.33* | 27 |
| RSC38-5 | $F_{2:3}$ High | 10.62* | 32 | 16.64** | 9 | 4.87 | 83 | 1.46 | 117 |
| RSC38-15 | $BC_1F_{2:3}$ High | -0.3 | 133 | 0.68 | 125 | -8.11 | 159 | -0.39 | 134 |
| RSC38-8 | $F_{2:3}$ Low | -2.11 | 142 | 2.15 | 112 | 1.37 | 118 | 2.55 | 109 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 10.66* | 31 | 16.45** | 11 | 3.62 | 97 | 0.54 | 127 |
| RSC37-12 | $F_{2:3}$ High | 8.07 | 55 | -1.89 | 141 | -5.71 | 156 | 4.77 | 86 |
| RSC37-12 | $BC_1F_{2:3}$ High | -4.84 | 152 | 3.83 | 94 | -2.25 | 143 | 0.53 | 128 |
| RSC37-7 | $F_{2:3}$ Low | 0.99 | 123 | 2.53 | 110 | -1.31 | 136 | -3.79 | 148 |
| RSC37-8 | $BC_1F_{2:3}$ Low | -4.37 | 151 | 9.54* | 41 | -1.32 | 137 | -2.52 | 145 |
| RSC15-13 | $F_{2:3}$ High | -3.54 | 147 | 13.06** | 18 | -1.72 | 140 | 1.13 | 122 |
| RSC15-15 | $BC_1F_{2:3}$ High | 3.15 | 103 | 7.87 | 58 | 6.77 | 71 | 10.01* | 37 |
| RSC15-11 | $F_{2:3}$ Low | 9.15* | 45 | 11.52* | 25 | 9.32* | 44 | 8.05 | 56 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 10.22* | 35 | 3.49 | 100 | 17.24** | 6 | 5.88 | 75 |
| RSC124-9 | $F_{2:3}$ High | 11.91** | 24 | 14.62** | 15 | 12.39** | 23 | 3.6 | 98 |
| RSC124-16 | $BC_1F_{2:3}$ High | 10.34* | 33 | 7.62 | 62 | 5.01 | 82 | 9.12* | 46 |
| RSC124-3 | $F_{2:3}$ Low | 11.29* | 28 | 14.14** | 16 | 1.28 | 119 | 3.92 | 93 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 2.85 | 106 | 8.92* | 50 | -1.4 | 138 | -2.44 | 144 |
| RSC117-2 | $F_{2:3}$ High | 18.27** | 4 | 11.47* | 26 | -6.07 | 158 | 13.29** | 17 |
| RSC117-4 | $BC_1F_{2:3}$ High | 12.91** | 19 | 10.09* | 36 | 12.62** | 21 | 6.77 | 70 |
| RSC117-10 | $F_{2:3}$ Low | 6.97 | 68 | 10.67* | 30 | 7.05 | 66 | 10.32* | 34 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 5.87 | 76 | 7.79 | 59 | 5.02 | 81 | 4.5 | 89 |
| RSC19-3 | $F_{2:3}$ High | 15.57** | 13 | 19.04** | 3 | 16.86** | 8 | 16.86** | 7 |
| RSC19-17 | $BC_1F_{2:3}$ High | 6.41 | 73 | 1.24 | 120 | -0.18 | 132 | 0.7 | 124 |
| RSC19-1 | $F_{2:3}$ Low | 4.25 | 90 | 15.03** | 14 | 6.28 | 74 | 8.9* | 51 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 10.72* | 29 | 0.56 | 126 | -3.34 | 146 | -6.04 | 157 |
| SE hybrid | 4.08 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

Table 38. Midparent heterosis estimates for plant exsertion (cm) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|------|------|------|------|------|------|------|------|------|------|
| RSC73-9 | $F_{2:3}$ High | 179.16 | 35 | 557.79** | 1 | 526.67** | 2 | 210.79* | 29 |
| RSC73-6 | $BC_1F_{2:3}$ High | 153.69 | 41 | 379.31** | 8 | 182.48 | 33 | 212.94* | 25 |
| RSC73-1 | $F_{2:3}$ Low | 80.4 | 65 | 314.06** | 13 | 185.96 | 32 | 94.06 | 54 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 93.43 | 55 | 230.31* | 22 | 300.37** | 14 | 182.12 | 34 |
| RSC83-1 | $F_{2:3}$ High | 77.62 | 67 | 241.44* | 19 | 147.82 | 43 | 23.1 | 104 |
| RSC83-14 | $BC_1F_{2:3}$ High | 59.24 | 75 | 75.41 | 68 | 53.85 | 80 | 84.39 | 63 |
| RSC83-10 | $F_{2:3}$ Low | -5.5 | 133 | -48.16 | 156 | 23.89 | 102 | 16.87 | 111 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 154.44 | 39 | 318.17** | 11 | 342.97** | 10 | 220.83* | 24 |
| RSC112-5 | $F_{2:3}$ High | -10.38 | 139 | 36.84 | 91 | 92.11 | 58 | 61.82 | 74 |
| RSC112-19 | $BC_1F_{2:3}$ High | -15.48 | 145 | 1.62 | 128 | 43.03 | 87 | -40.33 | 155 |
| RSC112-8 | $F_{2:3}$ Low | -25.74 | 152 | -10.89 | 140 | 72.12 | 70 | -6.56 | 135 |
| RSC112-15 | $BC_1F_{2:3}$ Low | -19.42 | 148 | 22.56 | 106 | 54.24 | 79 | 25.91 | 101 |
| RSC76-4 | $F_{2:3}$ High | 91.19 | 59 | 211.31* | 28 | 270.06* | 17 | 92.57 | 56 |
| RSC76-16 | $BC_1F_{2:3}$ High | -12.03 | 142 | 6.09 | 121 | 57.77 | 77 | 0.25 | 129 |
| RSC76-13 | $F_{2:3}$ Low | 120.78 | 47 | 403.06** | 6 | 153.98 | 40 | 33.74 | 95 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 63.9 | 73 | 400.39** | 7 | 162.96 | 37 | 90.19 | 60 |
| RSC38-5 | $F_{2:3}$ High | -24.94 | 151 | 94.16 | 53 | 199.48 | 31 | 21.11 | 107 |
| RSC38-15 | $BC_1F_{2:3}$ High | -50.64 | 157 | 283.65* | 15 | 246.91* | 18 | -53.53 | 158 |
| RSC38-8 | $F_{2:3}$ Low | 79.67 | 66 | 30.61 | 97 | 105.28 | 50 | 31.93 | 96 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 115.02 | 49 | 236.68* | 20 | 167.42 | 36 | 207.4* | 30 |
| RSC37-12 | $F_{2:3}$ High | 149.89 | 42 | 376.27** | 9 | 314.16** | 12 | 144.74 | 44 |
| RSC37-12 | $BC_1F_{2:3}$ High | 222.45* | 23 | 211.67* | 27 | 487.86** | 3 | 212.91* | 26 |
| RSC37-7 | $F_{2:3}$ Low | -22.01 | 150 | 84.5 | 62 | 87.35 | 61 | 23.36 | 103 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 279.3* | 16 | 448.05** | 5 | 486.86** | 4 | 49.52 | 83 |
| RSC15-13 | $F_{2:3}$ High | 7.1 | 119 | 55.53 | 78 | 155.16 | 38 | 13.43 | 115 |
| RSC15-15 | $BC_1F_{2:3}$ High | 0.13 | 130 | -15.07 | 144 | 141.9 | 45 | 14.54 | 114 |
| RSC15-11 | $F_{2:3}$ Low | 2.76 | 125 | 38.59 | 89 | 17.36 | 110 | -35.31 | 154 |
| RSC15-14 | $BC_1F_{2:3}$ Low | -4.94 | 132 | 26.01 | 100 | 16.56 | 112 | 1.79 | 127 |
| RSC124-9 | $F_{2:3}$ High | 1.83 | 126 | 3.35 | 124 | 34.46 | 92 | -6.44 | 134 |
| RSC124-16 | $BC_1F_{2:3}$ High | 22.64 | 105 | 41.91 | 88 | 66.96 | 71 | 18.92 | 108 |
| RSC124-3 | $F_{2:3}$ Low | -19.08 | 147 | 14.67 | 113 | 57.98 | 76 | 47.05 | 85 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -55.45 | 159 | -10.38 | 138 | -11.07 | 141 | 12.2 | 116 |
| RSC117-2 | $F_{2:3}$ High | -62.59 | 160 | 30.1 | 98 | 100.37 | 52 | -17.59 | 146 |
| RSC117-4 | $BC_1F_{2:3}$ High | 6.27 | 120 | 34.15 | 93 | 235.33* | 21 | 33.91 | 94 |
| RSC117-10 | $F_{2:3}$ Low | -20.94 | 149 | 26.62 | 99 | 44.97 | 86 | 8.8 | 118 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 49.96 | 82 | 131.48 | 46 | 5.37 | 123 | 18.34 | 109 |
| RSC19-3 | $F_{2:3}$ High | 65.99 | 72 | 101.38 | 51 | 118.18 | 48 | 75.36 | 69 |
| RSC19-17 | $BC_1F_{2:3}$ High | -31.64 | 153 | 48.52 | 84 | 92.4 | 57 | 5.54 | 122 |
| RSC19-1 | $F_{2:3}$ Low | 82.94 | 64 | -4.52 | 131 | 53.31 | 81 | 37.23 | 90 |
| RSC19-10 | $BC_1F_{2:3}$ Low | -9.56 | 137 | 9.68 | 117 | -13.6 | 143 | -7.53 | 136 |
| SE hybrid | 99.05 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

positive estimates for A.319, A.Tx3197, and A.338. Many lines had a zero value for plant exsertion, causing the magnitude of variation expressed by plant exsertion MPH.

For all the hybrids, MPH estimates of three-panicle weight were positive values, suggesting greater panicle weights for hybrids over their parents. MPH for three-panicle weight ranged from 3.22 (A.301*RSC112-19 $BC_1F_{2:3}$ high) to 126.75% (A.319*RSC37-12 $F_{2:3}$ high). Of the 160 hybrids, 74 expressed significant positive MPH ranging from 48.42 (A.301*RSC15-15 $BC_1F_{2:3}$ high) to 126.75% (A.319*RSC37-12 $F_{2:3}$ high) (Table 39). Both RSC112-5 $F_{2:3}$ high and RSC83-14 $BCF_{2:3}$ high each appeared twice in the top six significant positive MPH estimates, with A.319, then A.301 and A.Tx3197, respectively. MPH for significant positive heterosis for panicle weight was reported by Sharma and Sharma (2006).

For 1000-kernel weight, MPH estimates ranged from -7.22 (A.Tx3197*RSC124-16 $BC_1F_{2:3}$ high) to 46.6% (A.338*RSC112-5 $F_{2:3}$ high), with RSC112-5 $F_{2:3}$ high reporting the top two most significant positive MPH (Table 40). Of the 160 hybrids, 68 had significantly positive MPH estimates ranging from 12.63 (A.338*RSC83-1 $F_{2:3}$ high) to 46.6% (A.338*RSC112-5 $F_{2:3}$ high). Significance for 100-kernel weight heterosis was reported by Premalatha et al. (2006), and significant 1000-kernel weight MPH was reported by Mahdy et al. (2011).

MPH estimates for protein concentration in grain ranged from -12.03 (A.319*RSC112-19 $BC_1F_{2:3}$ high) to 17.7% (A.Tx3197*RSC15-13 $F_{2:3}$ high) (Table 41). Of the 160 hybrids, 20 had significant positive MPH estimates while six had significant

Table 39. Midparent heterosis estimates for three-panicle weight (g) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|------|-------------------|-------|------|-------|------|----------|------|-------|------|
| RSC73-9 | F$_{2:3}$ High | 6.52 | 158 | 65.85* | 37 | 35.42 | 111 | 71.41** | 28 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 89.2** | 10 | 70.82** | 30 | 67.79* | 34 | 92.05** | 7 |
| RSC73-1 | F$_{2:3}$ Low | 26.63 | 129 | 72.2** | 26 | 46.85 | 75 | 30.22 | 124 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 63.15* | 43 | 46.46 | 76 | 40.64 | 95 | 55.7* | 51 |
| RSC83-1 | F$_{2:3}$ High | 21.23 | 136 | 32.46 | 116 | 39.75 | 97 | 63.07* | 44 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 44.69 | 86 | 110.29** | 2 | 96.06** | 5 | 74.95** | 24 |
| RSC83-10 | F$_{2:3}$ Low | 18.02 | 141 | 52.55* | 61 | 14.04 | 145 | 19.38 | 139 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 48.49* | 73 | 84.51** | 17 | 84.68** | 16 | 72.93** | 25 |
| RSC112-5 | F$_{2:3}$ High | 107.47** | 4 | 93.86** | 6 | 71.1** | 29 | 18.55 | 140 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 3.22 | 160 | 37.79 | 103 | 51.78* | 63 | 23.64 | 130 |
| RSC112-8 | F$_{2:3}$ Low | 45.59 | 83 | 29.59 | 125 | 17.08 | 142 | 19.91 | 137 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 53.74* | 55 | 36.59 | 107 | 50.4* | 70 | 69.95** | 32 |
| RSC76-4 | F$_{2:3}$ High | 44.6 | 87 | 77.58** | 23 | 49.89* | 71 | 50.95* | 67 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | 51.28* | 66 | 84.17** | 19 | 65.24* | 39 | 45.05 | 85 |
| RSC76-13 | F$_{2:3}$ Low | 35.6 | 110 | 67.2* | 35 | 46.25 | 78 | 46.42 | 77 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 37.01 | 106 | 89.04** | 11 | 81.23** | 21 | 89.98** | 8 |
| RSC38-5 | F$_{2:3}$ High | 23.42 | 131 | 53.46* | 56 | 46.2 | 80 | 55.84* | 50 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | 53.45* | 57 | 59.78* | 46 | 32.05 | 119 | 39.61 | 98 |
| RSC38-8 | F$_{2:3}$ Low | 11.14 | 151 | 51.7* | 64 | 13.32 | 146 | 85.22** | 15 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 37.08 | 105 | 50.93* | 68 | 32.23 | 117 | 19.69 | 138 |
| RSC37-12 | F$_{2:3}$ High | 43.89 | 91 | 126.75** | 1 | 26.87 | 128 | 35.22 | 113 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 58.59* | 47 | 83.71** | 20 | 66.65* | 36 | 65.43* | 38 |
| RSC37-7 | F$_{2:3}$ Low | 10.45 | 152 | 80.38** | 22 | 32.06 | 118 | 64.32* | 42 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 16.4 | 143 | 87.03** | 13 | 86.04** | 14 | 84.3** | 18 |
| RSC15-13 | F$_{2:3}$ High | 8.63 | 154 | 30.56 | 122 | 7.25 | 157 | 39.52 | 100 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 48.42* | 74 | 87.47** | 12 | 62.37* | 45 | 64.85* | 40 |
| RSC15-11 | F$_{2:3}$ Low | 28.91 | 126 | 44.54 | 88 | 37.71 | 104 | 51.83* | 62 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 39.58 | 99 | 28.86 | 127 | 15.73 | 144 | 53.32* | 58 |
| RSC124-9 | F$_{2:3}$ High | 50.6* | 69 | 52.69* | 60 | 55.44* | 52 | 44.13 | 89 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 31.51 | 120 | 45.18 | 84 | 22.09 | 134 | 36.47 | 108 |
| RSC124-3 | F$_{2:3}$ Low | 31.4 | 121 | 34.41 | 115 | 12.64 | 148 | 42.01 | 93 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 41.33 | 94 | 22.77 | 133 | 23.02 | 132 | 11.56 | 150 |
| RSC117-2 | F$_{2:3}$ High | 49.09* | 72 | 70.65** | 31 | 21.37 | 135 | 51.35* | 65 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 40.4 | 96 | 44.1 | 90 | 57.39* | 49 | 45.9 | 82 |
| RSC117-10 | F$_{2:3}$ Low | 38.11 | 102 | 46.1 | 81 | 36.28 | 109 | 43.36 | 92 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 54.01* | 54 | 108.95** | 3 | 89.82** | 9 | 35.3 | 112 |
| RSC19-3 | F$_{2:3}$ High | 30.47 | 123 | 9.14 | 153 | 38.86 | 101 | 58.31* | 48 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 54.77* | 53 | 35.04 | 114 | 46.21 | 79 | 52.81* | 59 |
| RSC19-1 | F$_{2:3}$ Low | 11.91 | 149 | 7.5 | 155 | 7.28 | 156 | 6.3 | 159 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | 72.11** | 27 | 64.75* | 41 | 67.87* | 33 | 12.66 | 147 |
| SE hybrid | 23.92 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.

‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

Table 40. Midparent heterosis estimates for 1000-kernel weight (g) for each hybrid combination in the combined analysis in three environments, Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016, with overall rank.

| Lines RSC† | Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | $F_{2:3}$ High | 10.99 | 81 | 24.82** | 15 | 25.3** | 14 | 38.66** | 3 |
| RSC73-6 | $BC_1F_{2:3}$ High | 9.11 | 94 | 11.91 | 78 | 12.92* | 65 | 32.47** | 4 |
| RSC73-1 | $F_{2:3}$ Low | 3.46 | 129 | 15.34* | 47 | 9.46 | 92 | 20.16** | 29 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 20.94** | 26 | 23.33** | 18 | 15.67* | 45 | 17.08* | 41 |
| RSC83-1 | $F_{2:3}$ High | -1.22 | 151 | 6.99 | 113 | 7.35 | 111 | 9.7 | 90 |
| RSC83-14 | $BC_1F_{2:3}$ High | 12.04 | 73 | 13.44* | 60 | 15.22* | 48 | 20.37** | 28 |
| RSC83-10 | $F_{2:3}$ Low | 22.95** | 21 | 8.56 | 102 | 25.38** | 12 | 25.3** | 13 |
| RSC83-1 | $BC_1F_{2:3}$ Low | 14.29* | 54 | 11.91 | 77 | 15.89* | 44 | 12.63* | 68 |
| RSC112-5 | $F_{2:3}$ High | 19.93** | 30 | 42.79** | 2 | 25.82** | 10 | 46.6** | 1 |
| RSC112-19 | $BC_1F_{2:3}$ High | 0.52 | 146 | 8.26 | 105 | 1.43 | 141 | -6.98 | 159 |
| RSC112-8 | $F_{2:3}$ Low | 5.64 | 118 | 10.5 | 83 | 8.21 | 107 | 1.97 | 139 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 10.36 | 85 | 10.84 | 82 | 1.67 | 140 | 1.22 | 144 |
| RSC76-4 | $F_{2:3}$ High | 24.3** | 17 | 21.96** | 24 | 14.84* | 51 | 25.43** | 11 |
| RSC76-16 | $BC_1F_{2:3}$ High | 22.77** | 23 | 21.72** | 25 | 14.15* | 55 | 26.33** | 8 |
| RSC76-13 | $F_{2:3}$ Low | 14.44* | 52 | 26.12** | 9 | 8.97 | 95 | 23.13** | 20 |
| RSC76-2 | $BC_1F_{2:3}$ Low | 19.82** | 31 | 10.39 | 84 | 11.93 | 75 | 18.23** | 36 |
| RSC38-5 | $F_{2:3}$ High | 3.84 | 127 | 3.39 | 130 | 8.81 | 98 | 19.13** | 32 |
| RSC38-15 | $BC_1F_{2:3}$ High | 13.9* | 57 | 18.07** | 38 | 15.49* | 46 | 20.79** | 27 |
| RSC38-8 | $F_{2:3}$ Low | 12.2 | 71 | 16.75* | 42 | 16.44* | 43 | 23.19** | 19 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 5.34 | 119 | 3.85 | 126 | 7.17 | 112 | 12.5 | 69 |
| RSC37-12 | $F_{2:3}$ High | 7.49 | 110 | 17.87** | 39 | 1.41 | 142 | 8.31 | 104 |
| RSC37-12 | $BC_1F_{2:3}$ High | 13.26* | 61 | 6.79 | 114 | 8.64 | 100 | 11.93 | 76 |
| RSC37-7 | $F_{2:3}$ Low | -4.51 | 158 | 9.96 | 89 | 13.58* | 59 | 13.98* | 56 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 2.28 | 137 | -2.18 | 154 | -0.42 | 150 | 1.97 | 138 |
| RSC15-13 | $F_{2:3}$ High | 6.48 | 115 | 11.83 | 79 | 8.45 | 103 | 22.77** | 22 |
| RSC15-15 | $BC_1F_{2:3}$ High | 1.37 | 143 | -0.03 | 148 | 3.52 | 128 | 8.25 | 106 |
| RSC15-11 | $F_{2:3}$ Low | 12.70* | 67 | 9.64 | 91 | 10.23 | 87 | 24.43** | 16 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 10.08 | 88 | 18.8** | 33 | 7.96 | 108 | 26.61** | 7 |
| RSC124-9 | $F_{2:3}$ High | 8.73 | 99 | 6.24 | 116 | -3.49 | 155 | 8.92 | 97 |
| RSC124-16 | $BC_1F_{2:3}$ High | -3.97 | 156 | 6.14 | 117 | -7.22 | 160 | 8.92 | 96 |
| RSC124-3 | $F_{2:3}$ Low | 17.21* | 40 | 7.69 | 109 | 9.35 | 93 | 12.02 | 74 |
| RSC124-4 | $BC_1F_{2:3}$ Low | 12.25 | 70 | 0.72 | 145 | 4.95 | 122 | 18.1** | 37 |
| RSC117-2 | $F_{2:3}$ High | 3.00 | 132 | 0.25 | 147 | 15.16* | 49 | 4.97 | 121 |
| RSC117-4 | $BC_1F_{2:3}$ High | -3.99 | 157 | 4.75 | 123 | 8.59 | 101 | 10.29 | 86 |
| RSC117-10 | $F_{2:3}$ Low | 12.04 | 72 | 5.16 | 120 | 13.73* | 58 | 12.81* | 66 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 2.74 | 135 | -0.12 | 149 | 2.9 | 133 | 12.95* | 64 |
| RSC19-3 | $F_{2:3}$ High | -1.97 | 152 | 2.55 | 136 | 3.26 | 131 | 13.22* | 62 |
| RSC19-17 | $BC_1F_{2:3}$ High | 12.97* | 63 | 18.51** | 34 | 15.16* | 50 | 11.32 | 80 |
| RSC19-1 | $F_{2:3}$ Low | 2.77 | 134 | -2.07 | 153 | 4.47 | 125 | 4.64 | 124 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 14.32* | 53 | 28.36** | 6 | 18.27** | 35 | 28.68** | 5 |
| SE hybrid | 6.21 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

Table 41. Midparent heterosis estimates for protein concentration in grain (%) for each hybrid combination in the combined analysis in two environments, Vega, TX, in 2015, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | 1.49 | 73 | 6.87 | 24 | 3.09 | 54 | 4.46 | 45 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | -1.96 | 110 | 3.60 | 49 | -3.52 | 131 | -2.30 | 114 |
| RSC73-1 | F$_{2:3}$ Low | -3.73 | 133 | 2.57 | 60 | 1.32 | 78 | -0.12 | 97 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | -4.23 | 134 | 0.13 | 94 | 5.09 | 38 | -3.40 | 126 |
| RSC83-1 | F$_{2:3}$ High | -7.63* | 155 | 0.33 | 91 | 2.00 | 64 | 0.48 | 88 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -3.20 | 123 | 4.80 | 40 | 3.44 | 51 | 1.67 | 67 |
| RSC83-10 | F$_{2:3}$ Low | 4.48 | 43 | 11.34** | 4 | 9.60* | 11 | 8.68* | 13 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | -4.52 | 138 | 3.66 | 46 | 3.38 | 52 | -5.40 | 146 |
| RSC112-5 | F$_{2:3}$ High | -6.32 | 151 | -5.12 | 143 | 1.11 | 81 | -3.43 | 128 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | -0.05 | 96 | -12.03** | 160 | -11.98** | 159 | -5.92 | 149 |
| RSC112-8 | F$_{2:3}$ Low | -1.04 | 102 | -4.66 | 139 | -4.68 | 140 | -0.31 | 98 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -1.95 | 109 | -3.06 | 120 | -2.78 | 117 | 0.29 | 92 |
| RSC76-4 | F$_{2:3}$ High | -6.08 | 150 | 1.45 | 74 | 9.71* | 10 | -1.71 | 107 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -7.35 | 154 | 4.57 | 41 | 2.92 | 56 | -1.60 | 106 |
| RSC76-13 | F$_{2:3}$ Low | 0.02 | 95 | 3.14 | 53 | 7.48 | 21 | 8.43* | 15 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | -9.74* | 158 | -3.46 | 129 | 6.59 | 25 | -3.47 | 130 |
| RSC38-5 | F$_{2:3}$ High | 7.97* | 18 | 8.33* | 16 | 5.66 | 34 | 11.03** | 6 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -1.38 | 103 | 2.33 | 61 | 8.48* | 14 | 1.55 | 72 |
| RSC38-8 | F$_{2:3}$ Low | -2.87 | 118 | -4.25 | 136 | 7.98* | 17 | 1.64 | 68 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 0.47 | 90 | 6.41 | 28 | 3.65 | 47 | 2.07 | 63 |
| RSC37-12 | F$_{2:3}$ High | 1.10 | 83 | 6.43 | 27 | -5.31 | 145 | -1.88 | 108 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 7.09 | 23 | 11.19** | 5 | -0.93 | 101 | 2.69 | 58 |
| RSC37-7 | F$_{2:3}$ Low | 2.96 | 55 | 2.61 | 59 | 1.16 | 80 | 0.69 | 86 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 5.68 | 33 | 10.15* | 8 | -4.38 | 137 | 4.53 | 42 |
| RSC15-13 | F$_{2:3}$ High | 2.26 | 62 | 1.11 | 82 | 17.70** | 1 | 9.72* | 9 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 1.62 | 69 | -7.88* | 156 | 2.70 | 57 | -3.36 | 125 |
| RSC15-11 | F$_{2:3}$ Low | 5.12 | 37 | -7.31 | 153 | 5.34 | 35 | 6.26 | 29 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 1.10 | 84 | 3.51 | 50 | 7.69* | 19 | 9.01* | 12 |
| RSC124-9 | F$_{2:3}$ High | 1.37 | 77 | -1.54 | 105 | 4.47 | 44 | 1.57 | 70 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | -9.64* | 157 | -6.38 | 152 | 1.00 | 85 | -5.30 | 144 |
| RSC124-3 | F$_{2:3}$ Low | -4.78 | 141 | -2.66 | 116 | 1.56 | 71 | -5.71 | 147 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -0.6 | 100 | -5.79 | 148 | -2.63 | 115 | 3.65 | 48 |
| RSC117-2 | F$_{2:3}$ High | 1.92 | 65 | 1.89 | 66 | 5.75 | 32 | -1.98 | 111 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 0.48 | 89 | -2.14 | 113 | 0.55 | 87 | -1.47 | 104 |
| RSC117-10 | F$_{2:3}$ Low | -3.26 | 124 | 5.25 | 36 | -4.24 | 135 | -3.11 | 122 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 5.86 | 31 | -2.96 | 119 | 1.26 | 79 | -5.07 | 142 |
| RSC19-3 | F$_{2:3}$ High | 0.24 | 93 | 7.47 | 22 | -3.10 | 121 | 1.40 | 76 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 6.55 | 26 | 14.88** | 2 | 5.90 | 30 | 13.23** | 3 |
| RSC19-1 | F$_{2:3}$ Low | -3.73 | 132 | 1.45 | 75 | -2.05 | 112 | -0.51 | 99 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -3.43 | 127 | 10.6* | 7 | 4.92 | 39 | 7.64* | 20 |
| SE hybrid | 3.72 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

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negative MPH estimates. MPH estimates for starch concentration in grain ranged from -2.22 (A.Tx3197*RSC38-15 $BC_1F_{2:3}$ high) to 1.62% (A.Tx3197*RSC112-19 $BC_1F_{2:3}$ high) (Table 42). Of the 160 hybrids, four had significant positive MPH estimates while 36 had significant negative MPH estimates.

MPH estimates for fiber concentration in grain ranged from -8.496 (A.319*RSC38-15 $BC_1F_{2:3}$ high) to 7.604% (A.301*RSC112-19 $BC_1F_{2:3}$ high) (Table 43). Of the 160 hybrids, nine had significant positive MPH estimates, while 17 had significant negative MPH estimates. MPH estimates for fat concentration in the grain ranged from -20.136 (A.338*RSC76-4 $F_{2:3}$ high) to 30.74% (A.Tx3197*RSC83-14 $BC_1F_{2:3}$ high) (Table 44). Of the 160 hybrids, 25 had significant positive MPH estimates, while two had significant negative MPH estimates.

The degree of MPH varied considerably for all measured traits except starch concentration in grain. The high percentage of average MPH was observed for plant exsertion, because some parents had a zero value, followed by the height to the flag leaf, three-panicle weight, total height, grain yield, 1000-kernel weight, fat concentration in grain, panicle length, protein concentration in grain, number of days to anthesis, and fiber concentration in grain. Negative MPH was observed for the number of days to anthesis, total plant height, and height to the flag leaf for early maturing hybrids with dwarfing genes. MPH estimates for three-panicle weight was reported without any negative heterosis.

Table 42. Midparent heterosis estimates for starch concentration in grain (%) for each hybrid combination in the combined analysis in two environments, Vega, TX, in 2015, and Dumas, TX, in 2016, with overall rank.

| RSC† | Lines Selections‡ | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC73-9 | F$_{2:3}$ High | -0.886 | 106 | -0.995 | 113 | -1.463* | 145 | -0.871 | 104 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | -1.228* | 129 | -1.519* | 146 | -1.658** | 155 | -0.842 | 100 |
| RSC73-1 | F$_{2:3}$ Low | -0.357 | 67 | -0.952 | 112 | -1.105 | 122 | -0.936 | 111 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | -0.383 | 69 | -0.637 | 88 | -0.641 | 90 | -0.621 | 84 |
| RSC83-1 | F$_{2:3}$ High | 0.533 | 19 | -0.621 | 83 | -1.147* | 125 | -0.788 | 97 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | -0.809 | 98 | -1.291* | 135 | -1.543* | 150 | -1.108 | 123 |
| RSC83-10 | F$_{2:3}$ Low | -0.568 | 80 | -1.457* | 143 | -0.671 | 92 | -1.401* | 140 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 0.126 | 36 | -1.268* | 133 | -1.531* | 148 | -0.091 | 48 |
| RSC112-5 | F$_{2:3}$ High | 0.042 | 40 | 0.002 | 43 | -0.463 | 76 | -0.626 | 85 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 0.147 | 35 | 1.52* | 2 | 1.619** | 1 | 0.202 | 31 |
| RSC112-8 | F$_{2:3}$ Low | 0.843 | 9 | 0.882 | 8 | 0.704 | 12 | -0.428 | 71 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | -0.178 | 55 | 0.677 | 13 | 0.383 | 25 | -1.024 | 116 |
| RSC76-4 | F$_{2:3}$ High | -0.188 | 56 | -1.339* | 138 | -1.318* | 137 | -0.764 | 95 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -0.013 | 44 | -1.43* | 141 | -0.379 | 68 | -1.046 | 118 |
| RSC76-13 | F$_{2:3}$ Low | 0.27 | 30 | -0.143 | 53 | -0.779 | 96 | -1.26* | 132 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | -0.086 | 47 | -1.008 | 114 | -0.923 | 109 | -0.812 | 99 |
| RSC38-5 | F$_{2:3}$ High | -0.85 | 101 | -1.207* | 128 | -1.763** | 158 | -1.678** | 156 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -1.10 | 121 | -1.021 | 115 | -2.216** | 160 | -1.535* | 149 |
| RSC38-8 | F$_{2:3}$ Low | 0.005 | 42 | 0.009 | 41 | -1.07 | 119 | -0.64 | 89 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | -0.432 | 72 | -1.304* | 136 | -1.718** | 157 | -1.12 | 124 |
| RSC37-12 | F$_{2:3}$ High | -0.858 | 102 | -0.936 | 110 | -0.177 | 54 | -0.14 | 52 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | -1.455* | 142 | -1.372* | 139 | -1.196* | 127 | -0.565 | 79 |
| RSC37-7 | F$_{2:3}$ Low | -0.491 | 77 | -0.663 | 91 | -0.552 | 78 | -0.328 | 66 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | -1.237* | 130 | -1.527* | 147 | -0.635 | 87 | -1.073 | 120 |
| RSC15-13 | F$_{2:3}$ High | -0.213 | 58 | 0.45 | 22 | -1.648** | 154 | -1.156* | 126 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | 0.981 | 5 | 1.472* | 3 | 0.185 | 32 | 0.812 | 11 |
| RSC15-11 | F$_{2:3}$ Low | 0.098 | 37 | 1.362* | 4 | -0.462 | 75 | -0.894 | 108 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | 0.917 | 7 | 0.579 | 16 | -0.859 | 103 | -0.889 | 107 |
| RSC124-9 | F$_{2:3}$ High | -0.101 | 49 | 0.362 | 27 | -0.016 | 45 | -0.441 | 73 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 0.54 | 18 | 0.347 | 28 | -0.27 | 62 | -0.189 | 57 |
| RSC124-3 | F$_{2:3}$ Low | 0.53 | 20 | 0.375 | 26 | -0.572 | 81 | 0.152 | 34 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | -0.056 | 46 | 0.59 | 15 | 0.042 | 39 | -0.424 | 70 |
| RSC117-2 | F$_{2:3}$ High | 0.082 | 38 | -0.279 | 63 | -0.718 | 94 | -0.235 | 59 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 0.178 | 33 | 0.415 | 23 | -0.325 | 65 | -0.268 | 61 |
| RSC117-10 | F$_{2:3}$ Low | 0.963 | 6 | -0.267 | 60 | 0.826 | 10 | 0.272 | 29 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | -0.311 | 64 | 0.566 | 17 | -0.7 | 93 | 0.494 | 21 |
| RSC19-3 | F$_{2:3}$ High | -0.611 | 82 | -1.29* | 134 | -0.878 | 105 | -1.027 | 117 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | -1.807** | 159 | -1.251* | 131 | -1.461* | 144 | -1.553* | 151 |
| RSC19-1 | F$_{2:3}$ Low | 0.397 | 24 | -0.127 | 50 | 0.611 | 14 | -0.14 | 51 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -0.451 | 74 | -1.615* | 152 | -0.63 | 86 | -1.647** | 153 |
| SE hybrid | 0.561 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

Table 43. Midparent heterosis estimates for fiber concentration in grain (%) for each hybrid combination in the combined analysis in two environments, Vega, TX, in 2015, and Dumas, TX, in 2016, with overall rank.

| | Lines | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC† | Selections‡ | | | | | | | | |
| RSC73-9 | F$_{2:3}$ High | -0.252 | 77 | -3.562 | 141 | 2.29 | 28 | -3.454 | 136 |
| RSC73-6 | BC$_1$F$_{2:3}$ High | 2.776 | 20 | -2.059 | 111 | 3.091 | 16 | 1.555 | 37 |
| RSC73-1 | F$_{2:3}$ Low | -0.433 | 82 | -1.018 | 96 | 1.704 | 35 | 0.846 | 49 |
| RSC73-5 | BC$_1$F$_{2:3}$ Low | 0.457 | 63 | -2.109 | 115 | 3.798 | 10 | -0.587 | 86 |
| RSC83-1 | F$_{2:3}$ High | -0.055 | 73 | -4.203* | 150 | -0.302 | 79 | -2.873 | 126 |
| RSC83-14 | BC$_1$F$_{2:3}$ High | 1.844 | 34 | -0.222 | 76 | 2.727 | 21 | -1.32 | 99 |
| RSC83-10 | F$_{2:3}$ Low | -0.397 | 80 | -3.459 | 137 | -2.458 | 119 | -2.101 | 114 |
| RSC83-1 | BC$_1$F$_{2:3}$ Low | 2.938 | 19 | -0.006 | 71 | 5.644** | 5 | 1.116 | 45 |
| RSC112-5 | F$_{2:3}$ High | -0.679 | 89 | -5.35* | 156 | -4.465* | 152 | 0.545 | 56 |
| RSC112-19 | BC$_1$F$_{2:3}$ High | 7.604** | 1 | 0.409 | 64 | -1.872 | 106 | -0.968 | 94 |
| RSC112-8 | F$_{2:3}$ Low | 3.561 | 11 | -3.036 | 130 | -4.169* | 148 | 0.289 | 66 |
| RSC112-15 | BC$_1$F$_{2:3}$ Low | 1.139 | 42 | -1.994 | 109 | -8.288** | 159 | -4.136* | 147 |
| RSC76-4 | F$_{2:3}$ High | -1.609 | 102 | -3.378 | 134 | 3.472 | 12 | -0.133 | 75 |
| RSC76-16 | BC$_1$F$_{2:3}$ High | -1.422 | 101 | -1.885 | 107 | 0.072 | 68 | -2.355 | 117 |
| RSC76-13 | F$_{2:3}$ Low | 1.138 | 43 | -5.155* | 154 | 1.118 | 44 | 1.22 | 40 |
| RSC76-2 | BC$_1$F$_{2:3}$ Low | 1.006 | 47 | -3.769 | 143 | 0.521 | 60 | -1.678 | 103 |
| RSC38-5 | F$_{2:3}$ High | 2.322 | 27 | -3.315 | 133 | 0.609 | 55 | 0.521 | 59 |
| RSC38-15 | BC$_1$F$_{2:3}$ High | -0.646 | 87 | -8.496** | 160 | -0.828 | 91 | -5.204* | 155 |
| RSC38-8 | F$_{2:3}$ Low | -0.504 | 83 | -2.657 | 122 | 1.664 | 36 | -0.421 | 81 |
| RSC38-9 | BC$_1$F$_{2:3}$ Low | 3.041 | 17 | 1.365 | 39 | 5.831** | 4 | 2.697 | 22 |
| RSC37-12 | F$_{2:3}$ High | 3.174 | 14 | -4.189* | 149 | 6.336** | 3 | 6.868** | 2 |
| RSC37-12 | BC$_1$F$_{2:3}$ High | 2.975 | 18 | 0.462 | 62 | 0.000 | 70 | -2.747 | 123 |
| RSC37-7 | F$_{2:3}$ Low | 1.181 | 41 | -1.959 | 108 | 3.834* | 9 | -0.797 | 90 |
| RSC37-8 | BC$_1$F$_{2:3}$ Low | 4.743* | 6 | 0.088 | 67 | 2.194 | 29 | 3.157 | 15 |
| RSC15-13 | F$_{2:3}$ High | -0.076 | 74 | -3.236 | 132 | -3.385 | 135 | 0.616 | 54 |
| RSC15-15 | BC$_1$F$_{2:3}$ High | -3.713 | 142 | -3.922* | 145 | -5.013* | 153 | -2.605 | 121 |
| RSC15-11 | F$_{2:3}$ Low | 2.013 | 33 | -1.168 | 98 | 0.693 | 53 | 4.558* | 7 |
| RSC15-14 | BC$_1$F$_{2:3}$ Low | -0.549 | 85 | -3.535 | 140 | -2.787 | 125 | 0.529 | 58 |
| RSC124-9 | F$_{2:3}$ High | 2.191 | 30 | -2.038 | 110 | 0.532 | 57 | -2.77 | 124 |
| RSC124-16 | BC$_1$F$_{2:3}$ High | 2.673 | 23 | -2.993 | 129 | -6.809** | 158 | -2.516 | 120 |
| RSC124-3 | F$_{2:3}$ Low | -2.976 | 128 | -3.959* | 146 | -0.666 | 88 | -0.034 | 72 |
| RSC124-4 | BC$_1$F$_{2:3}$ Low | 0.961 | 48 | 0.841 | 51 | -0.921 | 93 | 1.064 | 46 |
| RSC117-2 | F$_{2:3}$ High | 2.181 | 31 | -2.077 | 112 | -1.145 | 97 | -0.296 | 78 |
| RSC117-4 | BC$_1$F$_{2:3}$ High | 3.232 | 13 | -4.375* | 151 | -3.535 | 139 | 0.783 | 52 |
| RSC117-10 | F$_{2:3}$ Low | 2.497 | 25 | -1.795 | 105 | -0.869 | 92 | 0.844 | 50 |
| RSC117-3 | BC$_1$F$_{2:3}$ Low | 2.014 | 32 | -6.173** | 157 | -3.51 | 138 | -3.1 | 131 |
| RSC19-3 | F$_{2:3}$ High | 1.511 | 38 | -0.978 | 95 | 0.021 | 69 | -1.706 | 104 |
| RSC19-17 | BC$_1$F$_{2:3}$ High | 2.603 | 24 | -3.892* | 144 | 4.046* | 8 | -1.385 | 100 |
| RSC19-1 | F$_{2:3}$ Low | 0.389 | 65 | -2.885 | 127 | -2.398 | 118 | -2.34 | 116 |
| RSC19-10 | BC$_1$F$_{2:3}$ Low | -0.526 | 84 | -2.099 | 113 | 0.516 | 61 | 2.462 | 26 |
| SE hybrid | 1.892 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High F$_{2:3}$, BC$_1$F$_{2:3}$, Low F$_{2:3}$, and BC$_1$F$_{2:3}$.

Table 44. Midparent heterosis estimates for fat concentration in grain (%) for each hybrid combination in the combined analysis in two environments, Vega, TX, in 2015, and Dumas, TX, in 2016, with overall rank.

| | Lines | A.301 | Rank | A.319 | Rank | A.Tx3197 | Rank | A.338 | Rank |
|---|---|---|---|---|---|---|---|---|---|
| RSC† | Selections‡ | | | | | | | | |
| RSC73-9 | $F_{2:3}$ High | 6.424 | 78 | 18.845* | 15 | 11.085 | 54 | -1.579 | 122 |
| RSC73-6 | $BC_1F_{2:3}$ High | 14.866 | 33 | 21.655* | 8 | 27.764** | 3 | 8.367 | 67 |
| RSC73-1 | $F_{2:3}$ Low | 12.891 | 42 | 15.792 | 30 | 11.498 | 50 | 15.288 | 31 |
| RSC73-5 | $BC_1F_{2:3}$ Low | 3.908 | 97 | 13.303 | 39 | -11.098 | 152 | -0.624 | 114 |
| RSC83-1 | $F_{2:3}$ High | -5.107 | 135 | -0.789 | 117 | 19.73* | 12 | 2.874 | 101 |
| RSC83-14 | $BC_1F_{2:3}$ High | 13.191 | 41 | 24.78** | 6 | 30.744** | 1 | 18.466* | 17 |
| RSC83-10 | $F_{2:3}$ Low | -0.893 | 118 | 20.848* | 11 | -2.66 | 129 | 13.348 | 38 |
| RSC83-1 | $BC_1F_{2:3}$ Low | -3.916 | 131 | 20.982* | 10 | 22.158* | 7 | 0.611 | 108 |
| RSC112-5 | $F_{2:3}$ High | 2.551 | 104 | 4.564 | 92 | 5.244 | 85 | 2.581 | 103 |
| RSC112-19 | $BC_1F_{2:3}$ High | 4.645 | 90 | 17.522* | 23 | 4.714 | 89 | 10.513 | 59 |
| RSC112-8 | $F_{2:3}$ Low | 3.972 | 96 | -9.552 | 150 | -18.515* | 159 | 4.609 | 91 |
| RSC112-15 | $BC_1F_{2:3}$ Low | 12.551 | 43 | 11.333 | 52 | 4.891 | 87 | 18.29* | 19 |
| RSC76-4 | $F_{2:3}$ High | -11.905 | 154 | -1.491 | 121 | -9.961 | 151 | -20.136* | 160 |
| RSC76-16 | $BC_1F_{2:3}$ High | -8.988 | 147 | 4.829 | 88 | -16.325 | 158 | -2.638 | 128 |
| RSC76-13 | $F_{2:3}$ Low | -12.421 | 156 | -6.745 | 143 | 3.331 | 100 | -0.391 | 113 |
| RSC76-2 | $BC_1F_{2:3}$ Low | -5.639 | 139 | -7.33 | 145 | -4.077 | 133 | -9.491 | 149 |
| RSC38-5 | $F_{2:3}$ High | -0.751 | 115 | 16.97* | 25 | 17.406* | 24 | 12.14 | 44 |
| RSC38-15 | $BC_1F_{2:3}$ High | 10.478 | 61 | 17.79* | 21 | 9.297 | 64 | 11.773 | 48 |
| RSC38-8 | $F_{2:3}$ Low | -9.027 | 148 | 2.674 | 102 | 3.758 | 98 | -2.333 | 126 |
| RSC38-9 | $BC_1F_{2:3}$ Low | 5.187 | 86 | 18.071* | 20 | 8.193 | 70 | 8.806 | 66 |
| RSC37-12 | $F_{2:3}$ High | 10.601 | 58 | 19.492* | 14 | 11.063 | 56 | 4.274 | 95 |
| RSC37-12 | $BC_1F_{2:3}$ High | 11.635 | 49 | 14.129 | 35 | 16.815 | 26 | 5.574 | 82 |
| RSC37-7 | $F_{2:3}$ Low | -4.952 | 134 | 4.373 | 94 | 3.602 | 99 | -2.562 | 127 |
| RSC37-8 | $BC_1F_{2:3}$ Low | 8.205 | 69 | 11.356 | 51 | 21.391* | 9 | 6.772 | 76 |
| RSC15-13 | $F_{2:3}$ High | 19.564* | 13 | 13.51 | 36 | 25.818** | 4 | 11.835 | 47 |
| RSC15-15 | $BC_1F_{2:3}$ High | 0.733 | 107 | 5.578 | 81 | 15.079 | 32 | 1.6 | 106 |
| RSC15-11 | $F_{2:3}$ Low | 10.876 | 57 | 7.416 | 74 | 17.606* | 22 | 13.428 | 37 |
| RSC15-14 | $BC_1F_{2:3}$ Low | 11.937 | 45 | 18.796* | 16 | 18.386* | 18 | 6.221 | 80 |
| RSC124-9 | $F_{2:3}$ High | -7.307 | 144 | -2.041 | 125 | -1.896 | 124 | 0.452 | 109 |
| RSC124-16 | $BC_1F_{2:3}$ High | 6.824 | 75 | 2.316 | 105 | -1.08 | 120 | -1.015 | 119 |
| RSC124-3 | $F_{2:3}$ Low | -11.429 | 153 | -1.764 | 123 | -6.106 | 141 | -5.302 | 136 |
| RSC124-4 | $BC_1F_{2:3}$ Low | -7.803 | 146 | -6.24 | 142 | -5.585 | 137 | -0.153 | 111 |
| RSC117-2 | $F_{2:3}$ High | -0.759 | 116 | 9.654 | 63 | 15.92 | 28 | 6.446 | 77 |
| RSC117-4 | $BC_1F_{2:3}$ High | -0.252 | 112 | 8.251 | 68 | 6.225 | 79 | -0.128 | 110 |
| RSC117-10 | $F_{2:3}$ Low | -12.076 | 155 | 10.506 | 60 | -3.527 | 130 | -5.952 | 140 |
| RSC117-3 | $BC_1F_{2:3}$ Low | 8.174 | 71 | 11.886 | 46 | 15.9 | 29 | -3.992 | 132 |
| RSC19-3 | $F_{2:3}$ High | 8.011 | 72 | 29.132** | 2 | 13.294 | 40 | 10.177 | 62 |
| RSC19-17 | $BC_1F_{2:3}$ High | 8.815 | 65 | 11.084 | 55 | 16.476 | 27 | 25.739** | 5 |
| RSC19-1 | $F_{2:3}$ Low | -5.618 | 138 | 11.176 | 53 | -12.95 | 157 | 4.478 | 93 |
| RSC19-10 | $BC_1F_{2:3}$ Low | 5.301 | 84 | 14.698 | 34 | 7.682 | 73 | 5.457 | 83 |
| SE hybrid | 8.346 | | | | | | | | |

SE: Standard error, * and **: significant at the 0.05 and 0.01 probability levels.
†RSC represents the different Reinstated Sorghum Conversion (RSC) lines.
‡Selections are equal to the High and Low percentage of exotic genome recovery and the generation: High $F_{2:3}$, $BC_1F_{2:3}$, Low $F_{2:3}$, and $BC_1F_{2:3}$.

**Correlation Estimates**

The objective of any plant breeder is to select for one or more superior characters in a natural or artificially developed population. Because grain yield in sorghum is quantitative, selection only on the basis of the grain yield character is usually not very effective. However, selection based on its component characters could be more efficient and reliable. Knowledge of association between yield and its component traits and among the component parameters themselves can improve efficiency of selection in plant breeding. Correlation coefficient measures the mutual association between a pair of variables independent of other variables to be considered.

In the present investigation, character associations were studied and presented in Tables 45-51 to assess relationships among yield and its components for enhancing the usefulness of selection. Correlations were estimated separately for parents, including lines and testers, hybrids, checks, and for all genotypes combined at three parental locations: Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016. Correlation coefficient estimates for SCA and heterosis for yield and agronomic traits of the 160 sorghum hybrids across environments and in the combined analysis were significant for all variables analyzed (Table 52).

Grain yield was significantly positively correlated with panicle length (0.219), three-panicle weight (0.205), and concentration of fiber and fat (0.235 and 0.163), respectively, in grain in the combined analysis across environments (Table 45). Significant negative correlations were found with the number of days to anthesis (-0.312), total plant height (-0.137), and height to the flag leaf (-0.158). Grain yield

Table 45.  Pearson correlation coefficients among grain yield and agronomic traits based on six environments – Taylor and Vega, TX, and Hutchinson, KS, in 2015, and Dumas and Vega, TX, and Hutchinson, KS, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain Protein (%) | Grain Starch (%) | Grain Fiber (%) | Grain Fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | -0.312** | -0.137** | -0.158*** | 0.219** | -0.032 | 0.205** | -0.007 | 0.022 | 0.050 | 0.235** | 0.163** |
| Days to anthesis | | 1.000 | 0.151** | 0.227** | -0.223*** | -0.169*** | 0.015 | 0.101** | -0.017 | -0.036 | -0.030 | 0.202** |
| Total height | | | 1.000 | 0.979*** | -0.080*** | 0.354*** | 0.476*** | 0.358*** | -0.133*** | 0.024 | -0.209* | -0.067* |
| Height to flag leaf | | | | 1.000 | -0.197*** | 0.174*** | 0.436*** | 0.379*** | -0.122*** | 0.019 | -0.198* | -0.056* |
| Panicle length | | | | | 1.000 | 0.118*** | 0.361*** | -0.262*** | 0.000 | -0.015 | 0.072* | 0.108*** |
| Plant exsertion | | | | | | 1.000 | 0.125*** | 0.088*** | -0.081*** | 0.041 | -0.130*** | -0.125*** |
| 3-panicle weight | | | | | | | 1.000 | 0.250*** | -0.220*** | 0.051 | 0.003 | 0.038 |
| 1000-seed weight | | | | | | | | 1.000 | -0.068* | 0.113*** | -0.096*** | -0.203*** |
| Grain protein | | | | | | | | | 1.000 | -0.661*** | 0.208*** | 0.540*** |
| Grain starch | | | | | | | | | | 1.000 | -0.149*** | -0.525*** |
| Grain fiber | | | | | | | | | | | 1.000 | 0.385*** |

* and ** significant at the 0.05 and 0.01 probability levels, N is variable.

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Table 46. Pearson correlation coefficients among grain yield and agronomic traits for all genotypes (hybrids, parents, and checks) based on data from three all-parent locations of Vega, TX, in *2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | DTF | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-kernel weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | -0.007 | -0.254** | -0.283** | 0.188** | -0.042 | 0.057 | -0.021 | -0.078 | 0.058 | 0.241** | 0.184** |
| DTF | | 1.000 | 0.149** | 0.215** | -0.152** | -0.173** | 0.068 | 0.105* | -0.017 | -0.035 | -0.031 | 0.204** |
| Total height | | | 1.000 | 0.973** | 0.095* | 0.449** | 0.531** | 0.340** | -0.154** | -0.011 | -0.185** | -0.124** |
| Height to flag leaf | | | | 1.000 | -0.030 | 0.246** | 0.480** | 0.356** | -0.136** | -0.019 | -0.185** | -0.099* |
| Panicle length | | | | | 1.000 | 0.168** | 0.390** | -0.229** | -0.037 | -0.083 | -0.001 | -0.013 |
| Plant exsertion | | | | | | 1.000 | 0.256** | 0.154** | -0.120** | 0.066 | -0.070 | -0.153** |
| 3-panicle weight | | | | | | | 1.000 | 0.297** | -0.280** | 0.039 | -0.082* | -0.157** |
| 1000-seed weight | | | | | | | | 1.000 | -0.179** | 0.293** | -0.002 | -0.236** |
| Grain protein | | | | | | | | | 1.000 | -0.646** | 0.270** | 0.577** |
| Grain starch | | | | | | | | | | 1.000 | -0.167** | -0.582** |
| Grain fiber | | | | | | | | | | | 1.000 | 0.422** |

* and **: significant at the 0.05 and 0.01 probability levels, N = 626.

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Table 47. Pearson correlation coefficients among grain yield and agronomic traits for hybrids based on data from three all-parent locations at Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | -0.002 | -0.486** | -0.491** | 0.080 | -0.165** | -0.133** | -0.179** | 0.0162 | -0.000 | 0.181** | 0.172** |
| Days to anthesis | | 1.000 | 0.230** | 0.301** | -0.176** | -0.181** | 0.112* | 0.103* | -0.036 | -0.015 | -0.031 | 0.254** |
| Total height | | | 1.000 | 0.973** | 0.055 | 0.412** | 0.500** | 0.317** | -0.154** | -0.063 | -0.301** | -0.199** |
| Height to flag leaf | | | | 1.000 | -0.070 | 0.207** | 0.451** | 0.338** | -0.138** | -0.072 | -0.283** | -0.152** |
| Panicle length | | | | | 1.000 | 0.174** | 0.343** | -0.328** | -0.033 | -0.040 | -0.108* | -0.154** |
| Plant exsertion | | | | | | 1.000 | 0.237** | 0.140** | -0.105* | 0.039 | -0.134** | -0.215** |
| 3-panicle weight | | | | | | | 1.000 | 0.223** | -0.277** | 0.026 | -0.179** | -0.268** |
| 1000-seed weight | | | | | | | | 1.000 | -0.206** | 0.317** | -0.117* | -0.331** |
| Grain protein | | | | | | | | | 1.000 | -0.631** | 0.316** | 0.610** |
| Grain starch | | | | | | | | | | 1.000 | -0.204** | -0.550** |
| Grain fiber | | | | | | | | | | | 1.000 | 0.386** |

* and **: significant at the 0.05 and 0.01 probability levels, N = 473.

Table 48. Pearson correlation coefficients among grain yield and agronomic traits for parents based on data from three all-parent locations at Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | 0.157 | 0.081 | 0.035 | 0.092 | 0.151 | 0.127 | 0.123 | -0.154 | 0.215* | 0.210* | 0.006 |
| Days to anthesis | | 1.000 | 0.007 | 0.020 | -0.002 | -0.040 | 0.121 | 0.246* | -0.039 | -0.014 | 0.011 | 0.085 |
| Total height | | | 1.000 | 0.960** | 0.017 | 0.540** | 0.342** | 0.180* | -0.094 | 0.282** | -0.225* | -0.241* |
| Height to flag leaf | | | | 1.000 | -0.101 | 0.303** | 0.308** | 0.209* | -0.095 | 0.323** | -0.246** | -0.281** |
| Panicle length | | | | | 1.000 | 0.008 | 0.298** | -0.250* | 0.130 | -0.347** | 0.035 | 0.263** |
| Plant exsertion | | | | | | 1.000 | 0.136 | 0.075 | -0.087 | 0.115 | -0.039 | -0.071 |
| 3-panicle weight | | | | | | | 1.000 | 0.296** | -0.244* | 0.151 | -0.282** | -0.293** |
| 1000-seed weight | | | | | | | | 1.000 | -0.131 | 0.366** | 0.014 | -0.331** |
| Grain protein | | | | | | | | | 1.000 | -0.730** | 0.289** | 0.630** |
| Grain starch | | | | | | | | | | 1.000 | -0.141 | -0.730** |
| Grain fiber | | | | | | | | | | | 1.000 | 0.392** |

* and **: significant at the 0.05 and 0.01 probability levels, N = 132.

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Table 49. Pearson correlation coefficients among grain yield and agronomic traits for lines based on data from three all-parent locations at Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | 0.160 | 0.076 | 0.034 | 0.034 | 0.157 | 0.093 | 0.170 | -0.076 | 0.182 | 0.166 | -0.003 |
| Days to anthesis | | 1.000 | -0.034 | -0.045 | 0.040 | 0.005 | 0.130 | 0.269** | -0.091 | 0.028 | 0.055 | 0.032 |
| Total height | | | 1.000 | 0.962** | 0.011 | 0.568** | 0.337** | 0.176 | -0.117 | 0.320** | -0.188* | -0.246* |
| Height to flag leaf | | | | 1.000 | -0.101 | 0.342** | 0.308** | 0.120* | -0.131 | 0.375** | -0.195* | -0.298** |
| Panicle length | | | | | 1.000 | -0.015 | 0.289** | -0.239* | 0.182 | -0.385** | 0.020 | 0.305*** |
| Plant exsertion | | | | | | 1.000 | 0.135 | 0.094 | -0.078 | 0.110 | -0.068 | -0.056 |
| 3-panicle weight | | | | | | | 1.000 | 0.318** | -0.239* | 0.155 | -0.302** | -0.304** |
| 1000-seed weight | | | | | | | | 1.000 | -0.158 | 0.396** | 0.061 | -0.340** |
| Grain protein | | | | | | | | | 1.000 | -0.714** | 0.405** | 0.659** |
| Grain starch | | | | | | | | | | 1.000 | -0.230* | -0.761** |
| Grain fiber | | | | | | | | | | | 1.000 | 0.413*** |

* and **: significant at the 0.05 and 0.01 probability levels, N = 120.

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Table 50. Pearson correlation coefficients among grain yield and agronomic traits for testers based on data from three all-parent locations at Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | 0.356 | 0.793** | 0.648* | 0.548 | 0.051 | 0.393 | -0.143 | -0.431 | -0.045 | -0.194 | -0.045 |
| Days to anthesis | | 1.000 | 0.468 | 0.667* | -0.329 | -0.520 | 0.099 | -0.065 | 0.353 | -0.401 | -0.133 | 0.836** |
| Total height | | | 1.000 | 0.910** | 0.327 | -0.041 | 0.664* | 0.035 | -0.378 | -0.025 | -0.639* | 0.002 |
| Height to flag leaf | | | | 1.000 | 0.027 | -0.429 | 0.524 | 0.227 | -0.197 | -0.065 | -0.700* | 0.257 |
| Panicle length | | | | | 1.000 | 0.378 | 0.397 | -0.457 | -0.558 | -0.007 | -0.042 | -0.601* |
| Plant exsertion | | | | | | 1.000 | 0.130 | -0.367 | -0.221 | 0.131 | 0.306 | -0.485 |
| 3-panicle weight | | | | | | | 1.000 | -0.055 | -0.264 | -0.118 | -0.514 | -0.141 |
| 1000-seed weight | | | | | | | | 1.000 | -0.127 | 0.293 | -0.462 | 0.043 |
| Grain protein | | | | | | | | | 1.000 | -0.760** | 0.214 | 0.706* |
| Grain starch | | | | | | | | | | 1.000 | -0.014 | -0.575 |
| Grain fiber | | | | | | | | | | | 1.000 | 0.106 |

* and **: significant at the 0.05 and 0.01 probability levels, N = 12.

Table 51. Pearson correlation coefficients among grain yield and agronomic traits for commercial hybrid checks based on data from three all-parent locations at Vega, TX, in 2015 and 2016, and Dumas, TX, in 2016.

| Variable | Grain yield (Mgha-1) | Days to anthesis | Total height (cm) | Height to flag leaf (cm) | Panicle length (cm) | Plant exsertion (cm) | 3-panicle weight (g) | 1000-seed weight (g) | Grain protein (%) | Grain starch (%) | Grain fiber (%) | Grain fat (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield | 1.000 | 0.506* | 0.481* | 0.482* | 0.395 | -0.012 | 0.368 | -0.046 | -0.523* | -0.135 | -0.075 | 0.001 |
| Days to anthesis | | 1.000 | 0.267 | 0.493* | 0.110 | -0.402 | 0.271 | 0.199 | 0.035 | -0.444* | 0.423 | 0.565** |
| Total height | | | 1.000 | 0.868** | 0.380 | 0.535* | 0.521* | 0.399 | -0.231 | -0.073 | -0.111 | -0.098 |
| Height to flag leaf | | | | 1.000 | 0.070 | 0.121 | 0.328 | 0.499* | 0.025 | -0.411 | 0.076 | 0.172 |
| Panicle length | | | | | 1.000 | 0.194 | 0.740** | -0.270 | -0.416* | 0.464* | -0.065 | -0.161 |
| Plant exsertion | | | | | | 1.000 | 0.191 | 0.168 | -0.377 | 0.363 | -0.399 | -0.504* |
| 3-panicle weight | | | | | | | 1.000 | -0.026 | -0.217 | 0.246 | 0.056 | 0.085 |
| 1000-seed weight | | | | | | | | 1.000 | 0.544* | -0.124 | 0.255 | 0.303 |
| Grain protein | | | | | | | | | 1.000 | -0.196 | 0.372 | 0.591** |
| Grain starch | | | | | | | | | | 1.000 | -0.085 | -0.375 |
| Grain fiber | | | | | | | | | | | 1.000 | 0.733** |

* and **: significant at the 0.05 and 0.01 probability levels, N = 12.

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Table 52. Pearson correlation coefficients between Specific Combining Ability (SCA) and the corresponding Midparent Heterosis (MPH) for yield and agronomic traits for 160 sorghum hybrids in three environments and combined analysis.

| Variable | Vega 2015 | Vega 2016 | Dumas 2016 | Combined locations |
|---|---|---|---|---|
| Grain yield (Mg ha$^{-1}$) | 0.519*** | 0.566*** | 0.706*** | 0.539*** |
| DTF | 0.592*** | 0.602*** | . | 0.595*** |
| Total height (cm) | 0.410*** | 0.451*** | 0.396*** | 0.409*** |
| Height to flag leaf (cm) | 0.421*** | 0.482*** | 0.425*** | 0.430*** |
| Panicle length (cm) | 0.679*** | 0.673*** | 0.618*** | 0.647*** |
| Plant exsertion (cm) | 0.406*** | 0.424*** | 0.304*** | 0.346*** |
| 3-panicle weight (g) | 0.682*** | 0.643*** | 0.662*** | 0.580*** |
| 1000-kernel weight (g) | 0.530*** | 0.631*** | 0.608*** | 0.557*** |
| Protein content in grain (g) | 0.726*** | . | 0.655*** | 0.665*** |
| Starch content in grain (%) | 0.600*** | . | 0.537*** | 0.547*** |
| Fiber content in grain (%) | 0.615*** | . | 0.690*** | 0.621*** |
| Fat content in grain (%) | 0.593*** | . | 0.555*** | 0.550*** |

***Probability of correlation different from zero is <0.001.

had the same pattern except for the number of days to anthesis and three-panicle weight when analyzed for the three-parent environments (Table 46). In the analysis for hybrids, significant positive correlations were found for grain yield and the concentrations of fiber and fat (0.181 and 0.172), respectively, in grain, while significant negative correlations were reported for total plant height (-0.486), height to the flag leaf (-0.491), plant exsertion (-0.165), three-panicle weight (-0.133), and 1000-kernel weight (-0.179) (Table 47). In the analysis of parents, concentration of starch and fiber in grain were the only

traits significantly positively correlated with grain yield (Table 48). In the analysis for

testers, grain yield was significantly and positively correlated with total plant height

(0.793) and height to the flag leaf (0.648) (Table 49). In the analysis for checks, grain

yield was significantly and positively correlated with the number of days to anthesis

(0.506), total plant height (0.482), and height to the flag leaf (0.482), while significant

negative correlations were found for concentration of protein in grain (Table 50).

Almeida Filho et al. (2014) reported a positive association between plant height and grain

yield and a negative correlation with the number of days to anthesis. Omar et al. (2014)

found that plant height was significantly positively correlated with grain yield, while

1000-kernel weight had significant negative correlation. The negative correlation for

grain yield and the number of days to anthesis also was reported by Exeaku and

Mohammed (2006). This might have been caused by poor adaptation of very late-

flowering materials included in the experiment in variable environments.

The number of days to anthesis was significantly positively correlated with total

plant height (0.151), height to the flag leaf (0.227), 1000-kernel weight (0.101), and

concentration of fat in grain (0.163), while significant negative correlations were found

for panicle length (-0.223), plant exsertion (-0.169), and concentration of fat in grain

(0.1629) for genotypes in seven environments (Table 45). The number of days to

anthesis exhibited the same pattern when analyzed in the three-parent environments

(Table 46). In the analysis for hybrids, the number of days to anthesis had the same

pattern except was positively significant for three-panicle weight (0.112) (Table 47). In

the analysis for parents, the only significant positive correlation with the number of days

to anthesis was 1000-kernel weight (0.246) (Table 48). In the analysis of lines and testers, lines had a positive correlation for the number of days to anthesis with 1000-kernel weight (0.269), while testers had significant positive correlations with height to the flag leaf (0.667) and fat concentration in the grain (0.836) (Tables 49 and 50). Bohra et al. (1985), Jeyaprakash et al. (1997), and Iyanar et al. (2001) reported similar association between grain yield and the number of days to 50% flowering.

Total plant height was significantly positively associated with all traits evaluated except starch concentration in the grain for genotypes in seven environments and across parent environments only (Tables 45 and 46). In the analysis of hybrids and parents, panicle length was not significant (Tables 47 and 48). In the analysis of lines, 1000-kernel weight was not significantly correlated with total plant height (Table 49). In the analysis of testers, the only positive significant correlations with total plant height were height to the flag leaf (0.910) and three-panicle weight (0.664) (Table 50). Plant height had a high positive correlation coefficient with panicle length, three-panicle weight, and grain yield, indicating the possibility of obtaining taller plants with longer and heavier panicles that yielded more grain. This is in agreement with the findings of Gupta and Sidhu (1972). Similar results for the association of sorghum grain yield with plant height were reported by Mallinath et al. (2004), Ezeaku and Mohammed (2006), Mahajan et al. (2011), and El-Naim et al. (2012).

Three-panicle weight was significantly correlated with all traits except the number of days to anthesis and starch concentration in the grain for genotypes in seven environments (Table 45). Plants in environments with only sorghum parents exhibited

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the same behavior except for grain yield which could be attributed to the few kernels produced at Vega, TX, in 2016.  Replications were combined for the NIR analysis because three-panicle kernel weight was very small.

In the hybrid analysis, significant correlations were found for all traits except starch concentration in the grain, with negative correlations for grain yield (-0.133) and protein, starch, and fat concentration in the grain (-0.277, -0.179, and -0.268, respectively) (Table 47).  Results on panicle weight correlated with grain yield conformed with results of Jeyaprakash et al. (1997), Ezeaku and Mohammed (2006), and Deepalakshmi and Ganesamurthy (2007).  Panicle weight was significantly positively correlated with plant height, as was reported also by El-Naim et al. (2012).

Thousand-kernel weight was positively correlated with all traits except grain yield for all genotypes in the seven environments and except for fiber concentration in the grain in sorghum in the environment with only parents (Tables 45 and 46).  In the hybrid analysis, 1000-kernel weight was significantly correlated with all traits, but with only a 0.05 probably for the number of days to anthesis and fiber concentration in the grain (Table 47).  1000-kernal weight revealed significant negative correlations were with grain yield (-0.179), panicle length (-0.327), and protein, fiber, and fat concentration in grain (-0.206, -0.117, and -0.331), respectively) (Table 47).  In analysis of hybrids, significant negative correlations were between 1000-kernel weight and grain yield, and 1000-kernel weight and panicle length.  Ezeaku and Mohanned (2006) found nonsignificant correlation between 1000-kernel weight and panicle length (0.005), while 1000-kernel weight and grain yield were significantly correlated (0.522).  Omar et al. (2014) found

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that plant height was significantly positively correlated with grain yield, while 1000-kernel weight was significantly negatively correlated.

Concentration of protein in grain was significantly negatively correlated with concentration of starch in grain across all analyses except commercial hybrid checks, while commercial hybrid checks had significant correlation with 1000-kernel weight (0.544) (Tables 45-51). No significant correlation was found for grain yield and protein across all analyses except commercial hybrid checks which was significantly negative (-0.553) (Table 51). This confirmed earlier reports by El-Hifney et al. (1972), Crook and Casady (1974), El-Gasim (1975), Ross et al. (1981), and Bohra et al. (1985). Rani et al. (2015) reported no correlation between protein and starch concentration in grain.

## Means Separation

Yield, with a standard error of 0.4068, was significantly different ($P < 0.0001$) for all the 160 hybrids in the six environments. Yield varied from 3.072 (A.338*RSC76-16 $BC_1F_{2:3}$ high) to 8.21 Mg ha$^{-1}$ (A.319*RSC83-1 $BC_1F_{2:3}$ low). Lines were significantly different ($P < 0.0001$), with a standard error of 0.2034, with yields ranging from 4.771 (RSC76-13 $F_{2:3}$ low) to 7.048 Mg ha$^{-1}$ (RSC117-4 $BC_1F_{2:3}$ high). Testers were significantly different ($P < 0.0001$), with a standard error of 0.0646, with yields ranging from 5.429 (A.338) to 6.073 Mg ha$^{-1}$ (A.301). Line x tester interaction was significant ($P < 0.0001$), with a standard error of 0.4068. Yields were high among testers, with A.319 ranging from 4.68 (RSC76-2 $BC_1F_{2:3}$ low) to 8.21 Mg ha$^{-1}$ (RSC83-1 $BC_1F_{2:3}$ low), followed by A.338 ranging from 3.072 (RSC76-16 $BC_1F_{2:3}$ high) to 8.06 Mg ha$^{-1}$ (RSC117-4 $BC_1F_{2:3}$ high), A.301 ranging from 4.78 (RSC38-5 $F_{2:3}$ high ) to 7.47 Mg ha$^{-1}$

(RSC83-14 $BC_1F_{2:3}$ high), and A.Tx3197 ranging from 3.77 (RSC76-13 $F_{2:3}$ low) to 7.003 Mg ha$^{-1}$ (RSC112-5 $F_{2:3}$ high). Line x environment interaction was significantly different to at least $P < 0.002$, with a standard error of 0.4982, indicating little variability in the standard error among environments. Yield was least at Taylor, TX, in 2015, varying from 1.557 (RSC15-14 $BC_1F_{2:3}$ low) to 3.82 Mg ha$^{-1}$ (RSC112-5 $F_{2:3}$), followed by Vega, TX, in 2015, varying from 3.215 (RSC76-16 $BC_1F_{2:3}$ high) to 7.88 Mg ha$^{-1}$ (RSC117-4 $BC_1F_{2:3}$ high), Vega in 2016, ranging from 4.73 (RSC124-4 $BC_1F_{2:3}$ low) to 7.882 Mg ha$^{-1}$ (RSC112-19 $BC_1F_{2:3}$ high), Hutchinson, KS, in 2016, ranging from 4.052 (RSC38-5 $BC_1F_{2:3}$ high) to 7.962 Mg ha$^{-1}$ (RSC124-16 $BCF_{2:3}$ high), Dumas, TX, in 2016, ranging from 5.30 (RSC38-15 $F_{2:3}$ high) to 8.353 Mg ha$^{-1}$ (RSC83-1 $BC_1F_{2:3}$ low), and the greatest yield at Hutchinson in 2015, ranging from 5.72 (RSC76-16 $BCF_{2:3}$ high) to 10.757 Mg ha$^{-1}$ (RSC124-9 $F_{2:3}$ high). Tester x environment interaction was significantly different ($P < 0.0001$), with a standard error of 0.1595 without variation among the environments. High grain yields were produced at Hutchinson in 2015, ranging from 7.50, 8.13, 8.42, and 8.60 Mg ha$^{-1}$ for A.Tx3197 A.338, A.319, and A.301, respectively. A.301 yielded most at Vega in 2015, followed by A.319, A.338, and A.Tx3197, with yields of 6.28, 5.88, 5.03, and 4.91 Mg ha$^{-1}$, respectively. At Hutchinson in 2016 and Vega in 2016, A.319 yielded most, while at Dumas in 2016, A.301 yielded the most, followed by A.319. At Taylor in 2015, record low yields were obtained from all testers A.338, A.Tx3197, A.301, and A.319, with 2.23, 2.34, 2.64, and 2.79 Mg ha$^{-1}$, respectively. The lowest yields were produced at Taylor, which could be attributed to low nitrogen in the soil, as reported by local farmers and fellow researchers. Late

planting at Hutchinson in 2015 might have contributed to the low yield of A.338 hybrids (Table 2).

Ten RSC families (RSC15, 19, 37, 38, 73, 76, 83, 112, 117, and 124) from different counties of origin, races, working groups, and their respective selections with percentage of exotic genome recovered in the research are presented in Table 1. Hybrids with RSC15 significantly differed with a greater mean (5.43 Mg ha$^{-1}$) than that of RSC76 (4.85 Mg ha$^{-1}$), and significant differences with a lesser mean with RSC37, 83, 112, 117, and 124, with grain yield means of 5.95, 6.22, 6.29, 6.29, and 5.98 Mg ha$^{-1}$, respectively (Table 53). RSC19 (5.65 Mg ha$^{-1}$) significantly differed from RSC76, 83, 112, and 117, while RSC37 differed significantly from RSC38 and 76. RSC38 differed significantly from RSC83, 112, 117, and 124, while RSC73 was significantly different from RSC76, 83, 112, and 117. RSC76 differed significantly from RSC83, 112, 117, and 124. The significant differences confirmed the variability already mentioned in the research. Hybrids of RSC83, 112, and 117 yielded most; however, not significantly more than each other (6.21, 6.29, and 6.29 Mg ha$^{-1}$, respectively). The low grain yield was observed for hybrids of RSC76 (4.85 Mg ha$^{-1}$). Grain yield was significantly different for all 10 RSC families for the RSC * environment interaction ($P < 0.0001$), with a standard error from 0.2762 to 0.2858 based on environment. RSC112 hybrids had the high grain yield at Hutchinson in 2015 and Vega in 2015 and 2016, with 8.88, 7.27, and 6.83 Mg ha$^{-1}$, respectively. RSC37 hybrids yielded most at Hutchinson in 2016 and Taylor in 2015, with yields of 6.68 and 3.03 Mg ha$^{-1}$, respectively, while RSC83 hybrids ranked the highest at Dumas in 2016, with a yield of 7.60 Mg ha$^{-1}$. RSC76 hybrids at Vega in 2015

Table 53.  Mean and  *P*-values from pairwise *t*-test comparing differences in the RSC families (15, 19, 37, 38, 73, 76, 83, 112, 117, and 124) represented in this research for 160 hybrids across six locations - Taylor and Vega, TX, and Hutchinson, KS, in 2015, and Dumas and Vega, TX, and Hutchinson, KS, in 2016 for grain yield Mgha$^{-1}$.

| RSC† | 15 | 19 | 37 | 38 | 73 | 76 | 83 | 112 | 117 | 124 |
|---|---|---|---|---|---|---|---|---|---|---|
| 15 | | 0.1605 | 0.0012 | 0.1565 | 0.128 | 0.0003 | <.0001 | <.0001 | <.0001 | 0.0006 |
| 19 | 0.1605 | | 0.0645 | 0.0047 | 0.9052 | <.0001 | 0.0004 | <.0001 | <.0001 | 0.0418 |
| 37 | 0.0012 | 0.0645 | | <.0001 | 0.0836 | <.0001 | 0.0952 | 0.0318 | 0.031 | 0.8496 |
| 38 | 0.1565 | 0.0047 | <.0001 | | 0.0032 | 0.0291 | <.0001 | <.0001 | <.0001 | <.0001 |
| 73 | 0.128 | 0.9052 | 0.0836 | 0.0032 | | <.0001 | 0.0007 | 0.0001 | 0.0001 | 0.0553 |
| 76 | 0.0003 | <.0001 | <.0001 | 0.0291 | <.0001 | | <.0001 | <.0001 | <.0001 | <.0001 |
| 83 | <.0001 | 0.0004 | 0.0952 | <.0001 | 0.0007 | <.0001 | | 0.6269 | 0.6228 | 0.1398 |
| 112 | <.0001 | <.0001 | 0.0318 | <.0001 | 0.0001 | <.0001 | 0.6269 | | 0.9965 | 0.0506 |
| 117 | <.0001 | <.0001 | 0.031 | <.0001 | 0.0001 | <.0001 | 0.6228 | 0.9965 | | 0.0494 |
| 124 | 0.0006 | 0.0418 | 0.8496 | <.0001 | 0.0553 | <.0001 | 0.1398 | 0.0506 | 0.0494 | |

| RSC† | Grain Yield Mgha$^{-1}$ |
|---|---|
| 112 | 6.29 |
| 117 | 6.29 |
| 83 | 6.21 |
| 124 | 5.98 |
| 37 | 5.95 |
| 73 | 5.67 |
| 19 | 5.65 |
| 15 | 5.43 |
| 38 | 5.20 |
| 76 | 4.85 |

†RSC represents the different Reinstated Sorghum Conversion (RSC) lines and their respective families used in the study.

and at Hutchinson in 2016 and 2015 yielded least, with 3.64, 5.06, and 6.75 Mg ha$^{-1}$, respectively.  RSC38 hybrids yielded least at Dumas in 2016, while RSC15 hybrids were least at Taylor in 2015 and Vega in 2016, with yields of 5.72, and 1.90, and 5.18 Mg ha$^{-1}$, respectively.  Grain yield was significantly different for the RSC * tester interaction (*P* < 0.0001), and standard error ranged from 0.2255 to 0.2282 depending on the environment. The small grain yield for RSC76 with A.338, A.Tx3197, and A.301 was 3.62, 4.39, and

5.31 Mg ha$^{-1}$, respectively.  Small grain yield in A.301 was observed with RSC38 (5.56

Mg ha$^{-1}$).  High grain yield varied by tester and RSC family; A.338 yielded most with

RSC117 (6.87 Mg ha$^{-1}$), followed by A.319 with RSC83 (6.78 Mg ha$^{-1}$), A.Tx3197 with

RSC112 (6.48 Mg ha$^{-1}$), and A.301 with RSC19 (6.40 Mg ha$^{-1}$).  *P*-values for combined

percentage of exotic genome recovery for RSC families are presented in Table 54.

The sorghum selections in this research consisted of the high and low percentage

of exotic genome recovery and the generation:  $BC_1F_{2:3}$ high, $BC_1F_{2:3}$ low, $F_{2:3}$ high, and

$F_{2:3}$ low.  The $BC_1F_{2:3}$ high differed significantly from the $F_{2:3}$ low with a $P < 0.0001$,

while the significant difference with $F_{2:3}$ high was $P < 0.03601$ (Table 55).  The $BC_1F_{2:3}$

low and $F_{2:3}$ high generation differed significantly from the $F_{2:3}$ low ($P < 0.0001$), while

the $F_{2:3}$ low significantly differed ($P < 0.0001$) from all three other generation selections.

The advantage of the additional backcross with the high percentage of exotic genome

Table 54.  *P*-values and means of the percentage of exotic genome recovered value (%) for 160 sorghum hybrids classified by RSC family based on combined analysis across six environments, Vega, TX, in 2015 and 2016, Hutchinson, KS, in 2015 and 2016, Taylor, TX, in 2015, and Dumas, TX, in 2016.

| RSC† | Value of exotic RSC† genome recovered | RSC† | 15 | 19 | 37 | 38 | 73 | 76 | 83 | 112 | 117 | 124 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 15 | 0.39875 | 15 | | <.0001 | 0.4284 | 0.0001 | 0.0071 | <.0001 | 0.0521 | 0.0727 | 0.2862 | 0.7675 |
| 19 | 0.286 | 19 | <.0001 | | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 | 0.0002 | <.0001 |
| 37 | 0.4175 | 37 | 0.4284 | <.0001 | | 0.002 | 0.0574 | <.0001 | 0.2498 | 0.3158 | 0.0632 | 0.2768 |
| 38 | 0.49075 | 38 | 0.0001 | <.0001 | 0.002 | | 0.2328 | 0.1311 | 0.0521 | 0.0366 | <.0001 | <.0001 |
| 73 | 0.4625 | 73 | 0.0071 | <.0001 | 0.0574 | 0.2328 | | 0.0069 | 0.4534 | 0.3694 | 0.0002 | 0.0028 |
| 76 | 0.5265 | 76 | <.0001 | <.0001 | <.0001 | 0.1311 | 0.0069 | | 0.0006 | 0.0003 | <.0001 | <.0001 |
| 83 | 0.44475 | 83 | 0.0521 | <.0001 | 0.2498 | 0.0521 | 0.4534 | 0.0006 | | 0.8825 | 0.0026 | 0.0253 |
| 112 | 0.44125 | 112 | 0.0727 | <.0001 | 0.3158 | 0.0366 | 0.3694 | 0.0003 | 0.8825 | | 0.0043 | 0.0366 |
| 117 | 0.3735 | 117 | 0.2862 | 0.0002 | 0.0632 | <.0001 | 0.0002 | <.0001 | 0.0026 | 0.0043 | | 0.4408 |
| 124 | 0.39175 | 124 | 0.7675 | <.0001 | 0.2768 | <.0001 | 0.0028 | <.0001 | 0.0253 | 0.0366 | 0.4408 | |

† RSC represents the different Reinstated Sorghum Conversion (RSC) lines and their respective families used in the study.

Table 55. *P*-values and mean grain yield Mgha$^{-1}$ for 160 sorghum hybrids classified by generation and the percentage of recovered exotic genome:  High BC$_1$F$_{2:3}$ or F$_{2:3}$ and Low BC$_1$F$_{2:3}$ or F$_{2:3}$ based on combined analysis across six environments, Vega, TX, in 2015 and 2016, Hutchinson, KS, in 2015 and 2016, Taylor, TX, in 2015, and Dumas, TX, in 2016.  *P*-values are presented as BCF$_{2:3}$ High and Low percentage of exotic genome recovered and F$_{2:3}$ High and Low percentage of exotic genome recovered.

| Selections† | BC$_1$F$_{2:3}$ High | BC$_1$F$_{2:3}$ Low | F$_{2:3}$ High | F$_{2:3}$ Low |
|---|---|---|---|---|
| BC$_1$F$_{2:3}$ High | | 0.3076 | 0.0301 | <.0001 |
| BC$_1$F$_{2:3}$ Low | 0.3076 | | 0.2519 | <.0001 |
| F$_{2:3}$ High | 0.0301 | 0.2519 | | <.0001 |
| F$_{2:3}$ Low | <.0001 | <.0001 | <.0001 | |

| Selections† | Grain yield (Mgha$^{-1}$) |
|---|---|
| BC$_1$F$_{2:3}$ High | 6.02 |
| BC$_1$F$_{2:3}$ Low | 5.91 |
| F$_{2:3}$ High | 5.78 |
| F$_{2:3}$ Low | 5.30 |

†Selections are equal to the high and low percentage of exotic genome recovery and the generation:  High F$_{2:3}$, BCF$_{2:3}$, Low F$_{2:3}$, and BCF$_{2:3}$.

recovery contributed to the significant increase in grain yield over that of the F$_{2:3}$ generation.  There was no difference in the high and low percentage of exotic genome recovery in the backcross generation, thus confirming that the additional backcross generation was beneficial to the sorghum breeder.  However, for early testing, a combination of resources, including genomic recovery, would benefit a sorghum breeder.  The interaction for selection x environment was significant at *P* < 0.001, with a standard error from 0.1893 to 0.1906 based on environment.  The BC$_1$F$_{2:3}$ high yielded most grain, while F$_{2:3}$ low yielded least grain in the environments of Hutchinson in 2015 and 2016, Vega and Dumas in 2016, and Taylor in 2015.  Vega in 2015 had the high grain yield BC$_1$F$_{2:3}$ low, with the low grain yield F$_{2:3}$ high.  Vega in 2015 was planted later than

usual because of additional rainfall in May (Table 2).  With the later planting date,

hybrids required fewer days before anthesis as compared to other environments.  The

environment plays an integral component when selecting hybrids.  *P*-values for combined

percentage of exotic genome recovery for selections are presented in Table 56.


Table 56.  *P*-values and means of the percentage of exotic genome recovered value (%) for 160 sorghum hybrids classified by RSC selections based on combined analysis across six environments, Vega, TX, in 2015 and 2016, Hutchinson, KS, in 2015 and 2016, Taylor, TX, in 2015, and Dumas, TX, in 2016.  *P*-values presented.

| Selections† | Value of exotic genome recovered | Selections | $BC_1F_{2:3}$ High | $BC_1F_{2:3}$ Low | $F_{2:3}$ High | $F_{2:3}$ Low |
|---|---|---|---|---|---|---|
| $BC_1F_{2:3}$ High | 0.7 | $BCF_{2:3}$ High | | <.0001 | <.0001 | <.0001 |
| $BC_1F_{2:3}$ Low | 0.509 | $BCF_{2:3}$ Low | <.0001 | | <.0001 | <.0001 |
| $F_{2:3}$ High | 0.3597 | $F_{2:3}$ High | <.0001 | <.0001 | | <.0001 |
| $F_{2:3}$ Low | 0.1246 | $F_{2:3}$ Low | <.0001 | <.0001 | <.0001 | |

†Selections are equal to the high and low percentage of exotic genome recovery and the generation:  High $F_{2:3}$, $BCF_{2:3}$, Low $F_{2:3}$, and $BCF_{2:3}$.

# Chapter V

# Conclusions

In summary, A.301*RSC83-14 $BC_1F_{2:3}$ high had the third-highest mean of overall grain yield for hybrids, yielding slightly more than the commercial check 301/41, with 67.3 days to anthesis and 127.5 cm total plant height.  The hybrid had significant MPH with a positive SCA effect and GCA combining effect combination of high x high.  The hybrid would have a good combination for earliness, dwarfing genes, and high yield. A.319*RSC83-1 $F_{2:3}$ high had the largest overall mean for grain yield, out-yielding four of the best six commercial check hybrids with a positive MPH and SCA effect.  The hybrid flowered in 72.2 days, with a total plant height of 153.0 cm and a high x low GCA effects combination.  Further observations included line RSC112-19 $BC_1F_{2:3}$ high, with large overall mean grain yield among all four testers A.301 (7.22), A.319 (7.10), A.Tx3197 (6.67), and A.338 (6.20 Mg ha$^{-1}$); SCA effects of 0.124, -0.06, 0.212, and -0.276, with GCA combination effects of (high x high), (high x high), (low x high), and (low x high), respectively, with all exhibiting positive MPH, and corresponding number of days to anthesis and plant height of 71.2, 72.2, 70.8, and 75.5 days and 116.1, 131.9, 146.8, and 157.8 cm.

Selection of sorghum parental lines with larger percentage of exotic genome recovery in the $F_{2:3}$ produced greater yielding $F_1$ hybrids over those with smaller percentage of exotic genome recovery.  It is possible to improve grain yield and

important agronomic traits using the high percentage of exotic genome recovery in the $F_2$ population. This research aimed to develop earlier hybrids through evaluation of $F_1$ hybrids produced from exotic germplasm within the generation of $F_{2:3}$'s or $BC_1F_{2:3}$'s and to understand the nature of gene action involved in control of grain yield and its components. The significant differences confirmed the variability already mentioned in the research. Hybrids of RSC83, 112, and 117 yielded most, but not significantly different from each other (6.21, 6.29, and 6.29 Mg ha$^{-1}$, respectively). The low grain yield was by hybrids of RSC76 (4.85 Mg ha$^{-1}$). Grain yield was significantly different for all 10 RSC families for the RSC * environment interaction ($P < 0.0001$), with a standard error from 0.2762 to 0.2858 based on environment.

After removing the NIR data, combining ability estimates of SCA variance were greater than GCA variance, i.e., the ratio of GCA to SCA variances was less than unity for all traits except plant exsertion, which showed that non-additive gene action was dominant in the inheritance of all traits studied except panicle length. The results were supported by the ratio of variance of general to specific combining ability ($\sigma^2_{gca}/\sigma^2_{sca}$) which was smaller than unity and by the degree of dominance ($\sigma^2_D/\sigma^2_A$) that requires values greater than unity for all traits except plant exsertion. Therefore, superior hybrids can be developed through exploitation of heterosis.

Analysis of GCA revealed that among the parents, lines RSC117-4 $BC_1F_{2:3}$ high, RSC83-1 $BC_1F_{2:3}$ low, RSC83-14 $BC_1F_{2:3}$ high, and RSC112-19 $BC_1F_{2:3}$ high, and the testers A.301 and A.319 were promising general combiners for grain yield and most of the traits. Therefore, the parents can be used in sorghum breeding programs to develop

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high-yielding hybrids. The family of RSC15 was a good general combiner for concentration of protein in grain, RSC112 for concentration of starch in grain, and RSC117-4 $BC_1F_{2:3}$ high for fiber concentration in grain.

Based on MPH, specific agronomic traits of interest, and SCA effects of the hybrids, five hybrids were identified as good combinations for grain yield: A.319*RSC83-1 $BC_1F_{2:3}$ low (high x high), A.338*RSC117-4 $BC_1F_{2:3}$ high (low x high), A.301*RSC83-14 $BC_1F_{2:3}$ high (high x high), A.301*RSC112-19 $BC_1F_{2:3}$ high (high x high), and A.319* RSC112-19 $BC_1F_{2:3}$ high, while considering the combination effect of GCA. The hybrid A.301*RSC83-14 $BC_1F_{2:3}$ high had significant positive MPH for grain yield, total plant height, height to the flag leaf, panicle length, three-panicle weight, and 1000-kernel weight. The hybrids A.319*RSC83-1 $BC_1F_{2:3}$ low, A.338*RSC117-4 $BC_1F_{2:3}$ high, A.301*RSC83-14 $BC_1F_{2:3}$ high, A.319*RSC19-10 $BC_1F_{2:3}$ low, and A.301*RSC112-19 $BC_1F_{2:3}$ high were taller and yielded more than the parents, with significantly greater MPH *per se* parents. Line RSC19-17 $BC_1F_{2:3}$ high when crossed to A.319 and A.338 had significantly positive MPH for protein in the grain but significantly negative MPH for starch in the grain. Crosses with high x low or low x high GCA effects of parents indicated the presence of additive x dominance type of gene interaction. Therefore, the crosses might produce desirable transgressive segregates because of an additive genetic system in one general combiner of the parent and complimentary epistatic effects in the other. Tester A.301 was observed to promote earliness and dwarfing genes while A.319 produced greater three-panicle weight and 1000-kernel weight.

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In addition, understanding the nature of association among grain yield, yield components, and agronomic traits was emphasized. Significant positive correlation coefficients were found for grain yield with panicle length, three-panicle weight, and concentration of fiber and fat in grain, while significant negative correlations were observed for the number of days to anthesis, total plant height, and height to the flag leaf. Correlation association between SCA and MPH for yield and agronomic traits of the 160 sorghum hybrids were significant for all variables analyzed.

For early testing, the percentage of exotic genome recovery would be a beneficial option for selecting in the $F_{2:3}$ generation over the $BC_1F_{2:3}$ generation. Selection in the $F_{2:3}$, revealed the family of RSC112, 117, and 73 on the basis of GCA effects within the $F_{2:3}$ generation with ranks of 2, 3, and 4, respectively; however, RSC83 could have been missed based solely on the $F_{2:3}$ generation, while RSC124 could have been selected. RSC83 benefited from the additional backcross generation while RSC124 did not. A plant breeder relies on a combination of resources to aid in selection for early testing. The high-yielding RSC families were 117, 112, and 83. Significant differences were found in selection generation, the $F_{2:3}$ low significantly differed from the other three ($BC_1F_{2:3}$ high, low, and $F_{2:3}$ high), while the value of exotic genome recovery would provide insight into the early selection process because grain yield of the highest $F_{2:3}$ significantly differed from that of the lowest $F_{2:3}$. The backcross generation significantly improved grain yield; however, stricter selection in the $F_{2:3,}$ with available resources, could potentially reduce the workload in the future backcross generation. Relying on the GCA effects in the combination of hybrids provides insight as previously discussed;

however, the low x low combination might be suitable for selection in later generations while the high x high combination would provide complimentary gene interaction.  The magnitude of the research provides insight into early testing that would provide an opportunity for a sorghum breeder to select the high percentage of genome recovery in the $F_{2:3}$ generation, thus potentially reducing the number of hybrids to be evaluated and also the cost associated with phenotyping a large number of hybrids in the field.  From the study, it can be concluded that selection in the $F_{2:3}$ generation, with the aid of selecting the most genome recovery materials over the low genome recovery, would provide insight for greater yielding hybrids with early maturity and dwarfing genes before the backcross generation.  Although hybrid-breeding technology has been a great success in increasing yields in many cereal crops including sorghum, the process of developing and evaluating the performance of hybrids is the most expensive and time-consuming activity.  Developing sorghum parental inbred lines and evaluating their potential hybrid performance are very expensive and time-consuming.

Future research should include an understanding of the RSC families that were 2 or 3-dwarf and separate the hybrids into these categories for forage or grain harvest, respectively, and harvest accordingly.  The amount of total dry matter would provide insight into limitation by mechanical harvesting of grain, thus allowing calculation for harvest index.  Population and tiller counts could aid in explaining negative correlations found in lines and hybrids.  The Reinstated Sorghum Conversion Program strives to substitute recessive $Ma_1$ and $Dw_2$ and $Dw_3$, with additional knowledge of $Ma_5$ and $Ma_6$. Additional substitution of these height and maturity genes might provide insight into

earlier populations with variable height.  More research into the sorghums in the

Reinstated Sorghum Conversion Program is needed to facilitate more diversity by

crossing Caudatum and Durra varieties.  The understanding of RSC76 being tall, late, and

having large kernels gives insight into its race being a Caudatum-Durra type.  RSC73 and

83 are Caudatum while RSC112 and 117 are Durra, and with a potential to cross these

races might give rise to additional diversity within the R- and B-lines for sorghum

breeding programs.  Further investigation of the fertility of these exotic lines would

provide sorghum breeders with more diversity in elite inbreds.  The magnitude of this

research would need to be simplified to a smaller scale for constraints in resources.

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