A STUDY OF HETEROTIC RELATIONSHIPS IN SORGHUM

A Dissertation

by

KRISHNAMOORTHY GABRIEL

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

DOCTOR OF PHILOSOPHY

December 2005

Major Subject: Plant Breeding

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Approved by:

Chair of Committee,	William L. Rooney
Committee Members,	Darrell T. Rosenow
	Monica A. Menz
	Leonard M. Pike
	John E. Mullet
Head of Department,	C. Wayne Smith

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ABSTRACT

A Study of Heterotic Relationships in Sorghum. (December 2005)

Krishnamoorthy Gabriel, B.Sc., Acharya N.G. Ranga Agricultural University;

M.Sc., Maharana Pratap University of Agriculture and Technology

Chair of Advisory Committee: Dr. William L. Rooney

In sorghum, a predominantly self-pollinated crop, hybrid seed production relies exclusively on the cytoplasmic-genetic male sterility system. 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). These have served as heterotic groups in the absence of more information with reference to genetic diversity. Efforts to determine heterotic groups in sorghum have not been successful in clearly delineating any patterns. However, in a recent molecular marker-based study of 50 elite sorghum parental lines, groups similar to the working group system were observed, as was an absence of a consistent delineation, characteristic of heterotic groups, between the A/B- and R-lines. This study was conducted with the objective of evaluating the groups observed and assessing their potential as heterotic groups.

Two parental lines from each of the five groups, and two lines from those not conforming to any group, were chosen and crossed in a half-diallel. The twelve parents, sixty-six diallel hybrids and three commercial hybrid checks were evaluated for grain yield and other agronomic traits in five environments – College Station, TX in 2003 and 2004, Weslaco, TX in 2003, and Halfway, TX in 2003 and 2004. Within-group crosses exhibited inferior heterotic expression, for grain yield and other traits, in comparison with

across-group crosses. Furthermore, genetic similarity estimates for parental line pairs obtained from the molecular study were significantly correlated with specific combining ability and heterosis for yield of the corresponding hybrid combinations, revealing a pattern of correspondence between molecular data and heterosis.

Hybrids made among R-lines and among B-lines were significantly lower in yield compared to AxR hybrids, likely to be a result of decades of breeding efforts to develop inbreds within the mutually isolated groups, rather than a consequence of phylogenetic divergence.

An examination of the heterotic effects manifested in hybrid combinations reveals a pattern of interactions broadly in agreement with the molecular data, but differential responses between individual members of the proposed groups make it difficult to define distinct heterotic groups.

DEDICATION

To my father, S.N. Krishnamoorthy, and mother, Joyce Krishnamoorthy. I cannot count the ways in which you have made sacrifices for my sake.

Also to my brother Christopher.

I thank God for this family, and for all your love, teaching and the example that you have all set for me, in living life as a blessing to all those around you. Thank you!

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I would like to thank Dr. Bill Rooney for his patient guidance and teaching, honest and constructive criticism, and gracious hospitality over the years; I will always be grateful for his invaluable encouragement, and for the opportunity of studying at A&M.

I am also grateful to the members of my advisory committee – Dr. Darrell Rosenow, Dr. Monica Menz, Dr. Leonard Pike and Dr. John Mullet for their support in my research, and to Dr. Robert Klein for very willingly substituting on my prelims *and* defense. I would also like to express my gratitude to Dr. Javier Betran and Dr. Harry Cralle for their teaching and encouragement.

A big "thank you" to all at Sorghum Breeding – Karen Prihoda (thanks for the wake-up calls!), Delroy Collins, Cindy King; also to Stephen Labar, Mr. Bill Lyles, Nelson Reus, and Amanda Kurten - for all your help, and making these years so enjoyable. To the sorghum veterans – Rafael Mateo, Pushpak Mehta, Jorge Moran, Cleve Franks, Selahattin Aydin, and Adalberto Sanchez – thanks always for your guidance and friendhip. Lots of thanks also to the new(er) recruits – Les Kuhlman, Ryan Bading, Joaquim Mutaliano, Leo Mpofu, Hector Ramirez, Dan Packer and Satish Ambati. Many thanks also to Dan Makumbi in Corn Breeding for all the help in analyzing my data. Thanks also to the technicians at the Corpus Christi and Weslaco stations for their help.

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CHAPTER I

INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is an important food, feed and fodder crop worldwide. The world area of production for sorghum in 2004 was 43.73 million hectares with a production level of approximately 58.88 mt. The world average yield was 1.347 t ha^{-1}, much lower than the average yield in the United States (the largest sorghum producer in the world at 11.555 mt), which was 4.381 t ha^{-1} (FAO, 2005). This vast difference in yields between developing countries (most prominently India, Nigeria, Sudan, Burkina Faso and Ethiopia) and developed nations is due, in some part, to access to improved equipment, production techniques and to the widespread use of hybrid sorghums in the developed world.

The exploitation of heterosis in sorghum began in the US in the 1950s, resulting in a quantum leap in yields. In sorghum, a predominantly self-pollinated crop, hybrid seed production relies exclusively on the cytoplasmic-genetic male sterility system (Stephens and Holland, 1954; Quinby and Martin, 1954). This male-sterility system depended on the presence of male-sterile cytoplasm and nuclear fertility-restoring genes.

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 these two groups based on whether or not it possesses fertility-restoring genes. Thus, A/B lines and the R lines have

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This thesis follows the style of Crop Science.

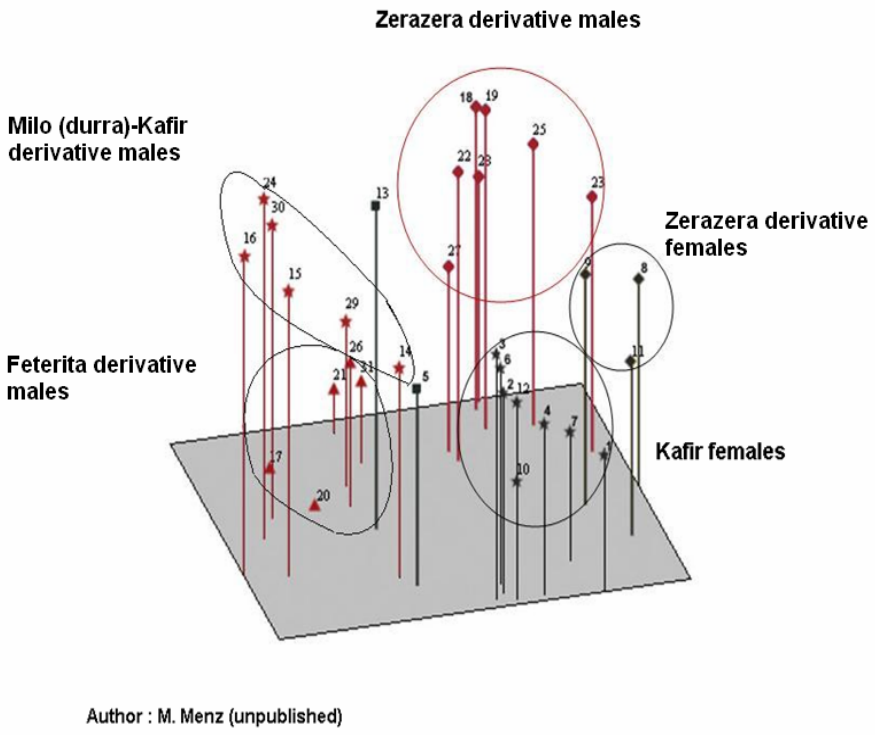

Fig 1. Principal Co-ordinate Analysis of 50 sorghum inbreds based on SSR genotypes (Menz, unpublished)

served as heterotic groups in the absence of more information with reference to genetic diversity. Efforts to determine heterotic groups in sorghum have not been successful in clearly delineating any patterns (Gilbert, 1994). However, recent molecular marker-based diversity studies that utilize more detailed analysis have indicated the existence of a more complex system of genetic relationships among elite parental lines (Menz et al., 2004). In this study, B and R lines did not show a consistent genetic dissimilarity characteristic of heterotic groups, and the groups observed through cluster analysis were somewhat in accordance with the phenotypic working group system (Murty and Govil, 1967; Harlan and deWet, 1972; Dahlberg, 2000). Five broadly-defined groups, and a sixth unrelated group, were observed (Fig. 1). The groups have been designated as: Kafir-Milo derivative males, Kafir type females, Zerazera derivative males, Zerazera derivative females and Feterita derivative males.

The goal of this study was to determine whether meaningful and useful heterotic relationships exist between these proposed groups. Information on the existence of such heterotic groups would enable breeders to maximize heterotic potential in hybrid breeding programs by a) more effective parental selection, and b) by conducting parental inbred development within mutually isolated heterotic groups, thus avoiding dilution of heterotic effects between such groups. The objectives of this study included:

1. To estimate the general combining ability (GCA) of elite parental lines chosen for the diallel.
2. To determine specific combining ability (SCA) of the diallel hybrids in the study.
3. To compare heterotic effects of the hybrids between parental lines of the various potential heterotic groups.

CHAPTER II

LITERATURE REVIEW

Origins of domestication

Sorghum originated in the continent of Africa and it remains the site of the greatest diversity of the species. The locations and times of the domestication events associated with the various races of the crop are not certain, but a number of theories based on archaeological evidence have been proposed in attempt to outline the evolutionary history of the plant (Kimber, 2000). Hypotheses claiming early domestication place the date between 6000 BC and 3000 BC (Murdock, 1959; Mann et al., 1983; Ehret, 1988; Harlan, 1989), in the region from West Africa to Sudan and Lake Chad. However, the more widely accepted theory is that of a later domestication in the same region, between 1000 BC and 1 AD (Stemler, 1980; Wigboldus, 1990). Another theory, termed the "Haaland hypothesis", proposes that all cultivated sorghums could have arisen as a result of domestication, in India, of wild races of African sorghum, and that these domesticated races were then reintroduced to the African continent (Haaland, 1995). This theory is based on the early presence of the durra race in India (estimated by some to be as early as 2000 BC), and on Harlan's theory that durras might have been domesticated in India from sorghum of African origin (Harlan, 1995).

Classification

Harlan et al. (1976) identified four wild and five cultivated races of *Sorghum bicolor*. The four wild races - arundinaceum, virgatum, aethiopicum and verticilliflorum – now placed in *S. bicolor* ssp. *verticilliflorum* (formerly subsp. *arundinaceum*) - are

associated with specific eco-geographical regions of sub-Saharan Africa. The five cultivated races are *S. bicolor* ssp. bicolor, guinea, caudatum, kafir and durra. The race bicolor, considered to be the most primitive grain sorghum, is widely distributed in Africa and also in Asia (de Wet and Price, 1976). The guinea race is well adapted to habitats in the wet and humid environments of equatorial West Africa and the high altitude regions of east Africa (Dahlberg, 2000). The race caudatum is associated with the Chari-Nile linguistic group (Stemler et al., 1975) and kafir sorghums with Bantu speakers from east Africa to southern Africa (Harlan and Stemler, 1976). Durras, thought to have been reintroduced from India (where they have an early history) to Africa as early as 2000 BC, are grown predominantly by Muslim farmers of Ethiopia, Egypt, and Sudan, and also in the Indian subcontinent (Kimber, 2000).

Murty and Govil (1967) proposed a system of working groups to classify cultivated races of sorghum. Harlan and DeWet (1972) proposed a system of classification of cultivated sorghum in which these 5 races, and intermediates between these races were described. These two approaches were revised to develop a modified numeric classification system by Dahlberg (2000), in which each working group is designated by a two- or three-digit number, the first digit indicating the race (Bicolor-1, Guinea-2, Caudatum-3, Kafir-4, Durra-5). Various combinations of the above races have numbers from 6 to 18, and 19, 20 and 21 are unclassified types. The last digit of a working group's number indicated the actual subtype of the working group. A last digit '0' indicates the working group that is closest to the essential characteristics of the race. Zerazera is a working group designated by the number 37, being a part of the race caudatum.

Introduction of sorghum to the US

Many sorghum varieties were introduced to the United States in the second half of the 19th century. Most of these introductions were from the kafir and durra races (milos). The early decades of the 20th century saw the development of many sorghum varieties, such as Redlan, Martin and Wheatland, most of which were derived from the kafir and milo races. Martin covered 80% of the sorghum acreage in the US from the early 1940s to 1955 (Duncan et al., 1991).

History of hybrid sorghum

Until the early 1950s, hybrids for research purposes were made by hand emasculation, or mechanical sterilization methods like hot water emasculation. These experimental hybrids documented the heterotic potential of sorghum but they also confirmed that an economically viable hybrid seed production was needed (Karper and Quinby, 1937).

Stephens and Holland (1954) identified and characterized a method for creating sorghum hybrids based on a cytoplasmic male sterility system. This system was based on a sterility-inducing cytoplasm from 'Day' milo. Backcrossing kafir with milo (using the milo as the female parent) and with the kafir as the recurrent parent, would result in kafir nuclear genes in milo male-sterile cytoplasm. This, in effect, produces a male sterile version of the kafir line. This male-sterile kafir line could then be crossed with a durra male, or any of a large number of milo/kafir derivative lines, and the F_1 plant will have restored male fertility. This system made large-scale hybrid seed production possible

(Quinby and Martin, 1954), and these kafir female x milo/kafir derivative male hybrids occupied most of the sorghum area in the US within a few years (Duncan et al., 1991).

Sorghum Conversion Program

Soon after hybrid sorghums were developed, breeding programs realized that the genetic base of sorghums in the US was limited due in large part to the difficulty in utilizing tropical tall, photoperiod-sensitive sorghums in the temperate US. This concern led to the development of the TAES-USDA Sorghum Conversion Program which was initiated in 1963. The purpose of the Conversion Program was to convert exotic tropical photoperiod-sensitive sorghum lines into temperate-adapted photoperiod-insensitive lines suitable for breeding programs in the US, which has enabled the 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 sorghum hybrids grown today that do not have sorghum conversion germplasm in their pedigree.

Another reason for the narrow genetic base was that a large majority of hybrid sorghum production was based (and is still based) on the same cytoplasm system (known as A1 sterile cytoplasm). Different male-sterility inducing systems, such as the A2 and A3 cytoplasm, have been discovered in the last few decades, and these hold promise for widening the genetic variability of elite sorghums. 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 as A3 cytoplasm, whose limited sources of fertility-restorer genes have precluded a widespread utilization (Rooney, 2000). Other cytoplasmic male-

sterile systems have been reported as well (Schertz and Pring, 1982). Apart from different cytoplasmic sterility sources, the conversion program has made available agronomically desirable lines with resistance to economically significant diseases like anthracnose and downy mildew. Sources of resistance to insect pests like greenbug and sorghum midge, and to pre- and post-flowering stress, have been found in converted materials (Rosenow and Dahlberg, 2000).

Heterosis

The characteristically superior performance of hybrid sorghums was due to a phenomenon known as “heterosis” or “hybrid vigor”, in which hybrids demonstrate markedly vigorous growth and yield as compared to their parents. The term heterosis was first used by Shull (1952). A high degree of heterosis occurs when the parents are genetically divergent or unrelated, resulting in a hybrid that presumably is heterozygous at numerous loci in the genome.

Blum et al. (1977) defined heterosis as being “the advantage of the hybrid over the best parent”. The reasons behind the phenomenon are not completely understood, but the two principal explanations are the concepts of dominance and overdominance (Crow, 1948, 1952). The dominance theory, proposed by Davenport (1908) and supported by Bruce (1910), Jones (1917) and Collins (1921), cites the effect of the dominant favorable alleles as the reason for the improved performance of hybrids. The overdominance theory, proposed independently by Shull (1908) and by East (1908), suggests that the heterozygous condition is responsible for heterosis. Complementary interaction between the recessive and dominant alleles was proposed as a possible cause of heterosis by

Quinby (1974). In recent years a consensus has grown in favor of the dominance model (Carr and Dudash, 2003). Hua et al. (2003) and Xiao et al. (1995), utilizing molecular marker techniques in rice, concluded that dominance was the major basis of heterosis. In a review of recent research, Charlesworth and Charlesworth (1999) concluded that overdominance effects were unimportant in most cases. However, the findings of some molecular marker-based studies in crops like maize (Stuber et al., 1992; Cockerham and Zeng, 1996), rice (Yu et al., 1997; Li et al., 2001; Luo et al. 2001) have suggested overdominance to be important, although the possibility of the presence of pseudo-dominance effects in these studies could not be ruled out (Carr and Dudash, 2003). These studies also showed that epistasis plays a considerable role in the phenomenon of heterosis. Lu et al. (2003), in a study of heterosis in maize, reported evidence of overdominance at the molecular marker level, but concluded that analysis at the gene level was necessary to resolve the issue. The need for this detail was mentioned years ago by Rhodes et al. (1992), who stated that only knowledge of gene location and function could decide the question of dominance versus overdominance for particular loci contributing to heterosis.

Heterosis in sorghum has been reported in the form of increased grain and forage yields, hastened flowering and maturity, increased height and larger stems and panicles (Quinby, 1963). Enhanced grain yield was reported by Kambal and Webster (1966) and by Blum (1969) to be a product of an increased number of seeds per panicle and increased seed weight.

Heterotic groups

The concept of heterotic groups evolved and developed in corn (*Zea mays* (L.)), in which the well-known heterotic groups "Reid" and "Lancaster" are, to a large extent, the basis of commercial hybrid breeding (Goodman, 1983). Parental inbreds are made by crossing lines within a group and selecting from the cross, thus avoiding a dilution of heterotic potential, an undesirable consequence of an inbred (intended as a hybrid parent) being composed of genes from both heterotic groups. Hybrids are then made by intercrossing such counterpart inbreds across the two groups, maximizing the heterotic potential between the two genetically divergent groups. The aim of widening the diversity of maize germplasm available for commercial breeding has been slowed by problems in utilizing tropical germplasm in breeding programs for temperate environments. There have been efforts to further identify heterotic patterns in maize (Pollak et al., 1991; Ordas, 1991; Vasal et al., 1992a and b).

Researchers have commented on hybrid potential between groups in sorghum. High levels of hybrid vigor were reported in hybrids of milo and hegari by Karper and Quinby (1937), especially in combination with kafir, feterita, kaoliang, sumac and broomcorn sorghums. Hybrids of more closely related parents were reported to exhibit poorer vigor. Nesbitt (1994) evaluated crosses between sorghum lines of diverse origin, and findings broadly indicated good heterosis in Kafir x Zerazera hybrids, and poor hybrid vigor in Zerazera x Kafir and Milo x Kafir hybrids. However, efforts to determine heterotic groups in sorghum have not been successful in clearly delineating any patterns (Gilbert, 1994).

Molecular marker-based studies of heterotic relationships

The phenomenon of heterosis between genetically distant or unrelated genotypes has been widely reported, and the idea of defining heterotic groups based on genotypes' genetic relatedness has fueled research to determine genetic distance between lines, based on the degree of similarity in molecular markers shared. These estimates of genetic distance can be used as indices of relatedness, and therefore as a tool for defining potential heterotic groups. This approach has been used in work on numerous crop plants.

In rice, high 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 under examination) and heterosis by Zhang et al. (1993, 1995), who also, however, reported low correlations with general heterozygosity based on all the markers. In alfalfa, Riday et al. (2003) observed no correlation of specific combining ability or mid-parent heterosis with genetic distance, and theorized that genetic distance estimates based on neutral molecular markers (not linked with genes controlling traits of interest) do not reflect heterotic potential between genotypes. Bernardo (1992) suggested a set of conditions, including high heritability and strong dominance effects, for effective prediction of hybrid performance based on molecular marker heterozygosity,

In sorghum, numerous studies have been conducted with the objective of estimating the genetic diversity of available germplasm, using a variety of molecular marker systems (Tao et al., 1993; Vierling et al., 1994; Taramino et al., 1997; Grenier et al., 2000; Smith et al., 2000; Uptmoor et al., 2003; Dillon et al., 2005), but the range of

germplasm evaluated and the extent of marker coverage in these studies was limited. The extent of marker coverage in the study by Ahnert et al. (1996) was wider, but did not examine germplasm from the World Collection. Menz et al. (2004) reported genetic similarity estimates between 50 sorghum genotypes important to hybrid sorghum breeding programs in the US, based on extensive marker coverage over the genome, using 1914 markers. In this study, B and R lines did not show a consistent genetic dissimilarity characteristic of heterotic groups, and the groupings that did appear to exist were somewhat in accordance with the working group system. The results suggested a genetic grouping of lines into five broad groups designated as: Kafir-Milo derivative males, Kafir type females, Zerazera derivative males, Zerazera derivative females and Feterita derivative males.

Some studies examined the efficacy of molecular marker-based systems in identifying phylogenetic relationships between sorghum lines, in conjunction with different methods of analysis (Vierling et al., 1994; White et al., 1995). However, these studies evaluated the ability of various approaches to yield relationship estimates that corresponded with the assumed heterotic A/B and R groups. Correlations between hybrid performance and genetic distance, in a study of Australian sorghum hybrids, were reported by Jordan et al. (2003) to be too low to be of practical value (in predicting hybrid performance), despite their being statistically significant.

CHAPTER III

MATERIALS AND METHODS

Germplasm

Two parental lines were selected from each of the five potential heterotic groups observed in the cluster analyses of lines assessed for diversity by Menz et al. (2004). Two lines were also included from the entries that did not conform to any of the five groups. These lines were chosen on the basis of their historical significance, their contribution to breeding programs and, in the case of the R-lines, their availability in an A3 cytoplasm background, facilitating their use as females in diallel crossing. Three commercial hybrid checks were also used – Pioneer 84G62, DeKalb hybrid DK53 and Sorghum Partners KS735.

The experimental material that was generated consisted of a half-diallel of the twelve parental lines (Table 1) and sixty-six hybrids. The hybrids were made by crossing the twelve parents in all possible hybrid combinations, not including reciprocal crosses. The diallel hybrids were made in the summer of 2002 in College Station, TX in a hybrid crossing block. To obtain all possible hybrid combinations, including crosses among fertility-restoring (male-fertile) genotypes, some R-line genotypes were used as females (in A3 cytoplasm) in those crosses. In addition, crosses within the A/B lines (genotypes lacking the A1 restorer gene) had to be made as A x B hybrids (Table 2). The crosses made among the R-lines, and those among the A/B lines, were sterile, and special care had to be taken to arrange the field layout in such a way that these sterile hybrids were planted next to fertile pollinators, to ensure adequate pollen supply.

Table 1. The twelve elite parental lines used in the diallel study, arranged by groups as observed by cluster analyses in the diversity study conducted by Menz et al. (2004)

LINES	PEDIGREE (race-working group in parentheses)
B lines (fertility maintainers)	
Zerazera derivatives	
1. BTx623	BTx3197 x SC170-6-4 (Kafir x Zerazera)
2. BTx635	RS/R $(C_2)S_1$-102-1 (Zerazera derivative)
Kafirs	
3. BTx3197	SA5765, Combine Kafir-60 (Kafir)
4. BTx378	Redlan (Kafir)
Unique/nonconforming lines	
5. BTx631	BTx615 x (BTx378 x SC110-9) (Kafir x Zerazera)
6. BTx642	B35, BC_1 of IS12555 (Durra)
R lines (fertility restorers)	
Zerazera derivatives	
7. RTx2817	BC_1 of IS12661 (SC170-6) (Zerazera)
8. RTAM428	BC_2 of IS12610 (SC110-9) (Zerazera)
Milo (durra)-Kafir derivatives	
9. RTx7000	SA 7000, Caprock (Kafir-Milo)
10. RTx436	(SC120-6 x Tx7000) x Tx7000 (Zerazera and Kafir-Milo)
Feterita derivatives	
11. RTx430	Tx2536 x SC170-6SC110-14E (Feterita x Zerazera)
12. RTx2737	TAM2554 x [(SA7536-1 x Tx7000) x Tx2536]

Table 2. The twelve parents in the diallel (each used as a female and as a male) and their crosses, showing parents used as females and males in the sterile hybrid combinations

		Males	1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**
		Females												
1	FR	**A3Tx430**	⊗											
2	FR	**A3Tx2737**		⊗										
3	KR	**A3Tx436**	Sterile		⊗									
4	KR	**A3Tx7000**	Hybrids	(A3 x R)		⊗								
5	ZR	**A3TAM428**					⊗							
6	ZR	**A3Tx2817**						⊗						
7	XA	**ATx642**							⊗					
8	XA	**ATx631**								⊗				
9	KA	**ATx378**			Fertile				Sterile		⊗			
10	KA	**ATx3197**			hybrids	(A x R)			hybrids	(A x B)		⊗		
11	ZA	**ATx635**											⊗	
12	ZA	**ATx623**												⊗

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Experimental procedures – field evaluation

The test, composed of 12 parents, 66 diallel hybrids and 3 hybrid checks for a total of 81 entries, was grown at each of five locations in Texas during 2003 and 2004 – at College Station, Weslaco and Halfway in the summer of 2003, and at College Station and Halfway in the summer of 2004 (Table 3). The entries were grown in a randomized complete block with three replications in each location. At each location an experimental unit was designated as two rows, with row length varying with location. The plots were combine-harvested at all locations.

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 the plot reached mid-anthesis.
2) Plant height: the average distance in centimeters from the ground to the tip of the panicle at maturity.
3) Panicle exsertion: the distance in centimeters from the flag leaf's ligule to the base of the lowest panicle branch at maturity.
4) Panicle length: the distance in centimeters from the lowest panicle branch to the tip of the panicle at maturity.
5) Number of panicles per plot: the number of panicles in each two-row plot, counted after maturity and prior to harvest.
6) 500-seed weight: the weight of 500 seeds, measured in grams, from grain samples of three panicles that were hand harvested per plot, prior to combine harvesting.
7) Grain yield: the weight of the grain harvested per plot, expressed in megagrams (metric tons) per hectare.

The plots at all locations were harvested with a JD3300 plot combine equipped with the Harvestmaster Grain Gauge System. The plot yield was converted to lbs acre^{-1}, using a conversion factor based on row width and plot length, which differed across environments. These estimates were then converted to SI units by multiplying by a conversion factor of 0.00112, to be expressed in megagrams (tons) per hectare.

In certain environments, all traits could not be evaluated. Observations on days to anthesis were not recorded at Halfway (2004), and data on panicle length was not taken at the College Station and Halfway locations in 2003. Panicle samples for estimating 500-seed weight were taken from a single replication at Halfway in 2003 and from two replications in 2004. Seed of three hybrids (ATx3197 x RTAM428, ATx378 x BTx642 and ATx623 x RTx2817) in the half-diallel were not available for planting in Halfway in 2004, and the unavailability of adequate seed (for three replications) for selected hybrids at certain locations made the use of filler lines necessary in order to maintain uniform plot competition.

Table 3. Agronomic, environmental and soil characteristics on the five environments in Texas in which the half-diallel to measure heterosis was grown

	Soil Type	Altitude (m)	Latitude	Longitude	Plot length	Row spacing	Date Planted	Date Harvested	Fertilizer regime	Irrigations	Rainfall*
College Station (2003)	Ships clay loam	96.0	30º40'N	96º21'W	18'	30"	03/25	08/07	60-40-40 lbs/ac preplant, sidedressing of 60 lbs N/ac 05/12	One- 05/07	9.75"
Weslaco (2003)	Raymondville clay loam	22.5	26º09'N	97º59'W	18'	40"	02/12	07/02	1/9: 200-500-500 preplant + Metagrow/zinc 3/19: 100-0-0	One- 04/28	8.83"
Halfway (2003)	Pullman clay loam	1071.0	34º11'N	101º57'W	17'	40"	05/21	10/14	4/30: 60-0-0 preplant	Three- 7/20, 8/5, and 8/19	8.31"
College Station (2004)	Ships clay loam	96.0	30º40'N	96º21'W	18'	30"	03/30	08/06	60-40-40 lbs/ac preplant, sidedressing of 60 lbs N/ac 05/05	None	26.4"
Halfway (2004)	Pullman clay loam	1071.0	34º11'N	101º57'W	17'	40"	05/24	10/22	80+0+0 preplant	Two- 5/27 and 8/5	19.02"

* Rainfall refers to the amount of moisture that fell during the growing season.

Statistical analysis

Analysis of variance

In each environment, data was analyzed as an RCBD (Randomized Complete Block Design), with three replications per environment. Genotypes were considered fixed effects, while replications (nested within environments) 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,

μ = 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, 3

g_j = effect of j-th genotype, j = 1, 2, …, 81

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

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

Variation due to genotypes was partitioned into variation within hybrids, diallel hybrids, parental lines and check hybrids. Contrasts were analyzed between diallel hybrids and parents, sterile and fertile hybrids, R-lines and B-lines, and between A3 x R crosses and A x B crosses. Analysis of variance across environments and for individual environments was conducted using the SPSS® statistical software. Bartlett's test for heterogeneity of error variances was conducted to assess the validity of combining the data from individual environments for a combined analysis (Little and Hills, 1978; Steel and Torrie, 1980). Results revealed heterogeneous error variances across the five environments for all traits except number of panicles per plot. In some cases, error variances were

homogeneous across selected environments. Because there were no egregious problems with the data, the data from individual environments were combined for analysis in addition to the individual analyses.

Combining ability analysis and heterosis

General combining analysis (GCA) effects of parents, specific combining ability (SCA) effects of diallel hybrids, the corresponding standard errors, and their mean squares were estimated using Griffing's Method 2 for diallel analysis (Griffing, 1956). Percent heterosis of diallel hybrids over the mid-parental value (midparent heterosis) was calculated for all traits.

Correlation estimates

Pearson's correlation coefficients between the seven traits were estimated using the SPSS 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 – and genetic similarity for diallel hybrids (between parents of a diallel hybrid), based on Menz et al. (2004). Genetic similarity estimates between the parents of each diallel hybrid were based on the number of molecular markers in common between them.

Biplot analysis

Biplot analysis is useful for analyzing diallel data in the form of a matrix, with rows representing the parental lines as testers and columns representing them as testers. Matrix elements are the grain yield means of hybrids, with parent means in the diagonal. A biplot was obtained using a Microsoft Excel add-in, with grain yield means of diallel hybrids and parents. Analysis and interpretation of the analysis was done according to the methods reported by Yan and Hunt (2002). A biplot gives a graphic representation of the relationships between parents in a diallel, highlighting the best hybrid combinations. Two principal component scores were obtained, the first explaining the highest variation, and the second a lower percentage of the variation, each successive principal component axis adding to the cumulative variation explained.

Interpretation of the biplot was done by connecting the entries furthest from the origin in the biplot in such a way that all entries are within the boundaries of the polygon. The biplot was divided into sectors by drawing perpendiculars from the origin onto the sides of the polygon. The best hybrid combination in a sector would be between the entry at the vertex of the polygon and the tester furthest from the origin. Entries and testers in the same sector represent good hybrid combinations and potential heterotic groups.

CHAPTER IV

RESULTS AND DISCUSSION

Means of genotypes

Means for the traits evaluated – days to anthesis, plant height, panicle exsertion, panicle length, number of panicles per plot, 500-seed weight, and grain yield – varied across environments (Table 4). These means are averages over the five locations, barring a few traits for which data was unavailable in particular environments, as mentioned in the previous chapter. The highest grain yield average of 7.681 Mg ha^{-1} was recorded for the commercial check hybrid 84G62, and seven out of the ten highest yielding genotypes were crosses with the ATx/BTx635 and ATx631 parents.

Analysis of variance

In the combined analysis, differences among levels of effects were detected for most sources of variation (Table 5). Certain traits could not be evaluated at either every environment (days to anthesis and panicle length) or for every replication (500-seed weight), for which reason degrees of freedom are modified for those traits in the analysis of variance across environments. This is also reflected in the ANOVA tables for individual environments.

Table 4. Means of 66 diallel hybrids, 12 parental lines and 3 hybrid checks for 7 traits based on data from 5 environments – College Station, Weslaco, and Halfway in 2003, and College Station and Halfway in 2004 (ranked by yield)

Rank by yield	Genotype	Days to anthesis	Plant height (cm)	Panicle exsertion (cm)	Panicle length (cm)	Panicles per plot	500-seed weight (gm)	Grain yield (Mg/ha)
1	84G62	76.83	121.83	7.28	26.25	133.89	15.45	7.681
2	ATX635*RTX430	80	148.84	7.79	27.09	108.13	15.84	7.530
3	ATX631*RTAM428	79.92	141.22	6.77	26.81	115.13	14.97	7.496
4	DK53	79	130.89	7.11	28.79	126.27	17.33	7.479
5	ATX635*RTx7000	75.33	157.31	15.92	27.94	108.87	14.24	7.441
6	ATX635*RTx436	78.83	153.25	14.9	26.81	125.93	13.34	7.252
7	ATX378*RTx436	75.5	136.82	13.72	25.4	143.73	13.33	7.164
8	ATX623*BTx635	81.08	157.65	8.81	26.25	128.93	14.82	7.131
9	ATX635*RTAM428	80.25	149.86	7.96	26.53	101.13	13.64	7.099
10	ATX631*RTX430	77.42	139.36	8.3	30.2	116.8	15.27	7.075
11	ATX378*RTX430	74.83	143.09	10.67	26.25	128	16.01	7.040
12	ATX378*RTAM428	73.5	142.07	12.36	23.14	131.67	14.64	7.007
13	ATX3197*RTx436	74.83	136.14	13.55	25.12	127.93	13.44	6.949
14	A3TX7000*RTX2737	95.17	161.04	18.8	26.81	134.47	17.42	6.949
15	ATX378*RTX2737	74.58	142.92	16.09	22.86	144.67	15	6.893
16	ATX631*RTX2737	76.42	147.66	16.26	27.38	115.93	15.28	6.845
17	ATX635*RTx2817	82.83	155.11	8.3	30.2	113.93	13.24	6.787
18	ATX631*RTx436	79.75	143.76	12.02	30.2	101.13	15.17	6.742
19	ATX635*BTX642	81.67	157.65	13.89	27.66	113.53	15.27	6.702
20	A3TX2817*RTX430	79.42	124.8	4.74	27.66	122.8	14.84	6.682
21	A3TX2817*RTx7000	77.17	134.28	9.14	27.38	117.8	14	6.640
22	ATX642*RTX430	74.08	136.14	17.27	27.66	113.13	16.72	6.503
23	ATX623*RTx436	76.58	136.65	13.04	27.66	118.53	12.17	6.482
24	ATX631*RTx2817	74.17	136.82	6.27	29.92	108.4	13.52	6.448
25	ATX623*RTAM428	77.58	134.96	8.97	25.96	121.6	13.21	6.433
26	A3TX7000*RTX430	73.67	139.7	12.36	27.66	111.6	15.31	6.415
27	ATX623*RTX430	75.92	144.1	11.85	28.79	131.6	15.18	6.395
28	A3TX2817*RTX2737	76.42	133.27	12.87	27.09	135.8	14.75	6.389
29	ATX635*RTX2737	76.33	148.67	14.9	24.55	123.47	14.51	6.293
30	A3TX7000*RTx436	78	131.06	12.87	27.09	124.33	13.69	6.270
31	ATX642*RTX2737	76.75	130.56	21.17	25.96	131.33	15.27	6.175
32	ATX631*BTX642	80.5	145.29	14.22	28.22	116.53	16.17	6.169
33	A3TAM428*RTx436	78.58	131.4	9.65	26.81	112.13	13.71	6.164
34	ATX642*RTx7000	77.83	139.36	14.39	25.96	107.47	13.47	6.161
35	ATX623*BTx631	80.83	144.78	8.47	29.63	115.4	15.88	6.156
36	A3TX436*RTX2737	77.67	131.4	15.24	28.22	125.2	13.78	6.089
37	ATX3197*RTx2817	68.83	117.86	11.6	21.87	104.53	13.39	6.035
38	ATX3197*RTX430	72.25	138.18	11.85	26.25	134.53	16.63	6.027
39	ATX642*RTx436	80.25	139.36	20.15	27.66	112.53	14.64	6.025
40	ATX635*BTX3197	76.58	149.35	11.18	25.68	113.93	14.78	6.006
41	KS735	76.33	126.15	11.01	23.28	103.42	14.1	5.976
42	ATX623*BTx378	75.42	141.39	9.65	24.27	113.67	15.01	5.969
43	ATX378*BTX642	79.33	132.72	15.24	21.59	113.92	15.89	5.957
44	ATX623*BTX642	78.75	147.15	16.93	27.38	120.8	14.69	5.955
45	A3TX2817*RTx436	80.5	134.79	10.16	28.5	115.2	12.26	5.922

Table 4. (Cont'd)

Rank by yield	Genotype	Days to anthesis	Plant height (cm)	Panicle exsertion (cm)	Panicle length (cm)	Panicles per plot	500-seed weight (gm)	Grain yield (Mg/ha)
46	ATX642*RTAM428	78.83	125.31	14.9	23.71	132.07	12.28	5.855
47	ATX623*RTX2737	72.17	143.43	17.27	25.12	135.2	15.27	5.833
48	A3TAM428*RTx7000	76.25	137.5	11.51	25.12	106.7	13.84	5.806
49	A3TAM428*RTX2737	74.5	132.42	12.19	25.68	118.87	14.29	5.752
50	ATX642*RTx2817	80.42	114.13	9.99	26.81	127.87	13.82	5.730
51	ATX3197*RTAM428	71.83	133.56	13.12	24.13	125.42	14.28	5.692
52	ATX623*RTx2817	80.17	126.58	8.04	28.36	100.33	11.9	5.692
53	ATX3197*RTx7000	72	137.67	17.27	24.55	119.2	14.18	5.613
54	ATX3197*RTX2737	72.5	143.59	19.81	23.99	171.07	14.47	5.582
55	ATX378*RTx2817	67	133.18	8.3	21.87	108.4	13.9	5.520
56	ATX635*BTx378	79	155.62	9.31	25.96	100.8	15.83	5.499
57	A3TX2817*RTAM428	83.25	113.28	3.56	25.96	109.73	13.64	5.407
58	ATX3197*BTX642	74.5	132.08	15.92	23.71	107.73	16.15	5.393
59	ATX378*RTx7000	75.5	131.74	14.22	25.12	117.07	14.33	5.387
60	ATX631*RTx7000	77.08	137.67	14.56	26.81	102.53	14.85	5.325
61	ATX623*BTX3197	73.75	139.19	18.29	26.25	111.13	15.14	5.315
62	ATX623*RTx7000	74.08	151.38	17.95	24.55	125.87	14.12	5.313
63	ATX635*BTx631	83.33	160.02	5.76	30.76	91.87	15.63	5.311
64	A3TX436*RTX430	79.92	123.95	8.64	29.63	102.53	14.84	5.307
65	ATX3197*BTx631	79	124.8	7.11	27.66	105.8	16.13	5.260
66	ATX378*BTx631	78.17	130.22	8.64	24.55	114.93	16.2	5.241
67	A3TAM428*RTX430	77.42	132.59	6.27	27.09	97.87	13.48	5.223
68	B.TX631	82.67	135.97	7.28	30.48	103.4	14.58	5.206
69	B.TX623	78	132.93	8.97	27.09	122.73	13.04	5.117
70	R.TX7000	76.5	131.06	16.76	24.84	125.53	13.48	4.789
71	B.TX635	78.67	136.14	5.42	22.58	126.07	11.47	4.734
72	B.TX378	81.42	125.98	7.79	20.88	89.4	13.59	4.484
73	R.TX2817	83.92	102.45	0.34	26.81	97.87	13.07	4.352
74	ATX3197*BTx378	76.33	122.94	7.62	21.17	124.13	16.22	4.305
75	A3TX2737*RTX430	76.33	123.61	9.48	29.63	90.33	15.76	4.234
76	B.TX3197	76.08	123.11	9.82	19.76	134.73	13.09	4.161
77	R.TX2737	77.67	122.6	13.72	27.66	105.73	13.26	3.745
78	R.TX430	80.58	114.98	3.39	29.63	94.97	17.86	3.689
79	B.TX642	81.08	106.51	14.22	24.27	95.13	11.51	3.505
80	R.TX436	84.44	122.43	12.02	25.96	99.07	11.33	3.315
81	R.TAM428	84.13	101.09	3.39	24.27	70.67	12.9	2.787

Table 5. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents across five environments– College Station, Weslaco and Halfway in 2003 and College Station and Halfway in 2004

Source of variation	Df	GY	PH	EX	PAN	Df	DY	Df	WT	df	PL
		Mg/ha	Cm	Cm					Cm		Cm
Environment	4	606.55**	23319.31**	4217.58**	205170.85**	3	774.77**	4	347.70**	2	535.05*
Reps (Env)	10	10.37**	1561.72**	116.68**	4097.35**	8	19.66**	7	4.88**	6	70.90**
Genotype	80	16.28**	2198.23**	277.05**	3324.73**	80	119.20**	80	16.87**	80	49.10**
Hybrids	68	8.41**	1579.21**	240.87**	2707.56**	68	96.70**	68	12.69**	68	40.53**
Diallel hybrids	65	7.55**	1575.70**	238.95**	2633.63**	65	100.39**	65	12.02**	65	40.91**
Sterile vs fertile	1	79.94**	2195.78**	1345.31*	17009.82**	1	445.90**	1	51.45	1	44.93*
A3xR vs AxB	1	2.03	17224.60**	108.10	2.28	1	78.40	1	135.75*	1	94.58*
Checks	2	9.05	194.16	53.51	2741.18	2	24.11	2	23.11**	2	48.30
Diallel hybrids vs. checks	1	63.65*	4535.97*	746.49**	6858.04	1	.53	1	36.65**	1	2.62
Parents	11	8.59*	2341.18**	372.17**	5161.76**	11	126.53**	11	26.66**	11	95.78**
R-lines vs. B-lines	1	25.66	5451.60*	18.96	7465.59	1	.40	1	19.64*	1	149.34
Diallel hybrids vs. parents	1	601.56**	44400.51**	1859.38*	23287.24**	1	1541.65*	1	118.38	1	113.43*
Genotype x Env	316	2.76**	133.92**	47.64**	885.21**	239	19.33**	313	3.87**	156	7.68*
Hybrids x Env	268	2.49**	115.33**	49.26**	813.70**	204	18.18**	267	3.45**	132	7.50*
Diallel hyb. X Env	257	2.51**	112.68**	50.58**	794.77**	195	18.33**	256	3.52**	127	7.56
Ster. Vs. fert. X Env	4	2.01	76.40	64.01	128.82	3	5.57	4	8.91*	2	1.43
A3xR vs AxB x Env	4	4.66*	111.16	34.42	509.77	3	88.79**	4	9.74**	2	1.86
Checks x Env	7	2.01*	76.22	19.73	1051.12*	6	19.89**	7	1.81*	3	8.90
D.hyb. vs. checks x Env	4	3.23	351.98**	21.03	2204.54*	3	5.23	4	1.35	2	.72
Parents x Env	44	3.56**	213.51**	31.40**	1334.87**	32	22.76**	42	5.44**	22	9.09
R-lines vs. B-lines x Env	4	4.65*	333.42	21.38	3201.37*	3	6.37	4	2.63	2	7.95
D.hyb. vs. parents x Env	4	11.58**	557.74*	119.99*	852.03	3	52.85*	4	18.30**	2	3.00
Error	786	1.11	76.35	28.00	430.015	627	3.914	532	1.157	470	5.78

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

§ Separate columns for degrees of freedom for particular traits (DY, WT and PL) is due to differences in the number of replications or environments from which data was collected for those traits

Table 6. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents at College Station in 2003, with means of various categories of experimental entries

Source of variation	Df	GY	PH	EX	PAN	DY	WT	PL
		Mg/ha	Cm	Cm			gm	Cm
Reps	2	16.19**	604.83*	4.15	6258.28**	4.42	1.96	N/A
Genotype	80	7.69**	778.86**	187.32**	1280.65**	91.18**	7.12**	
Hybrids	68	5.95**	622.66**	185.74**	1130.72**	79.39**	5.92**	
Diallel hybrids	65	5.85**	595.51**	186.86**	1146.84**	81.12**	5.56**	
Sterile vs fertile	1	33.41**	430.09	67.47	2697.36*	88.31	17.17*	
A3xR vs AxB	1	0.71	5381.78**	193.84	120.18	256.71**	21.03**	
Checks	2	9.46**	54.48	83.87**	835.44*	58.78*	11.02**	
Diallel hybrids vs. checks	1	5.94	3525.11**	315.46	639.84	7.96	18.07*	
Parents	11	5.91**	639.08**	135.86**	1285.18**	93.61**	7.85**	
R-lines vs. B-lines	1	1.22	2982.25**	14.52	1144.69	4.44	3.23	
Diallel hybrids vs. parents	1	139.44**	13990.72**	940.22**	12033.72**	830.80**	74.41**	
Error	160	2.12	129.40	91.20	422.32	8.31	1.51	
Mean of genotypes		5.910	132.54	12.58	70.517	79.628	15.543	N/A
Mean of hybrids		6.233	135.57	13.35	73.332	78.800	15.789	
Mean of diallel hybrids		6.196	136.45	13.61	73.694	78.842	15.726	
Mean of sterile hybrids		5.746	134.90	13.04	70.044	79.578	16.034	
Mean of fertile hybrids		6.571	137.87	14.22	77.489	78.228	15.436	
Mean of A3 x R		5.658	127.17	11.57	68.889	77.889	15.553	
Mean of A x B		5.835	142.64	14.51	71.200	81.267	16.526	
Mean of checks		7.027	116.28	7.62	65.44	77.89	17.161	
Mean of parents		4.057	115.08	8.11	54.19	84.38	14.13	
Mean of R-lines		3.873	105.97	7.48	48.56	83.78	14.44	
Mean of B-lines		4.241	124.18	8.75	59.83	84.49	13.83	

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

Table 7. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents in College Station in 2004, with means of various categories of experimental entries

Source of variation	Df	GY	PH	EX	PAN	DY	WT	PL
		Mg/ha	cm	Cm			gm	Cm
Reps	2	3.42*	37.54	43.64*	6344.57**	68.01**	13.75**	11.84
Genotype	80	3.66**	587.14**	62.45**	1298.36**	36.99**	11.29**	19.58**
Hybrids	68	2.97**	436.13**	56.65**	1181.97**	31.01**	7.66**	15.96**
Diallel hybrids	65	2.86**	448.25**	57.92**	1162.99**	32.37**	7.63**	15.75**
Sterile vs fertile	1	8.29*	194.42	249.58**	4882.46**	171.94**	1.90	12.57
A3xR vs AxB	1	18.01**	3071.61**	5.81	36.10	.01	7.09	18.35
Checks	2	1.48	123.30	13.62	1752.78*	2.11	6.05*	30.82*
Diallel hybrids vs. checks	1	13.43**	283.38	61.10	1275.61	.22	12.83	.23
Parents	11	2.10	1003.45**	82.68**	1687.64*	37.48**	17.60**	40.71**
R-lines vs. B-lines	1	2.72	412.90	21.69	4702.85*	10.34	3.48	21.69
Diallel hybrids vs. parents	1	61.84**	6371.54**	251.16**	4618.90*	434.00**	178.24**	32.84
Error	158	.91	122.02	9.36	446.82	3.94	1.44	5.25
Mean of genotypes		3.802	144.33	12.00	113.55	76.29	12.33	27.34
Mean of hybrids		4.020	146.43	12.41	115.59	75.71	12.70	27.49
Mean of diallel hybrids		3.965	146.67	12.52	115.06	75.70	12.65	27.49
Mean of sterile hybrids		3.748	145.77	11.32	109.63	76.74	12.74	27.77
Mean of fertile hybrids		4.161	147.77	13.58	119.65	74.87	12.54	27.26
Mean of A3 x R		4.196	139.93	11.06	109.00	76.73	12.46	28.22
Mean of A x B		3.301	151.61	11.57	110.27	76.76	13.03	27.32
Mean of checks		5.221	141.11	9.88	127.22	75.89	13.86	27.66
Mean of parents		2.546	132.36	9.67	101.60	79.61	10.21	26.46
Mean of R-lines		2.271	128.98	8.89	90.56	80.09	10.52	27.23
Mean of B-lines		2.820	135.75	10.44	113.78	79.00	9.90	25.68

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

Table 8. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents in Weslaco in 2003, with means of various categories of experimental entries

Source of variation	Df	GY	PH	EX	PAN	DY	WT	PL
		Mg/ha	cm	cm			gm	Cm
Reps	2	2.81**	313.60**	11.57	4173.19**	3.57	1.13**	42.56**
Genotype	80	2.01**	437.94**	80.71**	951.27**	21.59**	6.77**	29.35**
Hybrids	68	1.24**	319.24**	56.29**	810.41**	19.85**	4.81**	26.56**
Diallel hybrids	65	1.22**	316.13**	57.29**	821.32**	20.26**	4.95**	26.84**
Sterile vs fertile	1	6.19**	254.08	162.43*	4846.75**	140.47**	.76	8.41
A3xR vs AxB	1	.74	2782.00**	4.59	749.20	54.44**	34.35**	31.61
Checks	2	.36	35.13	5.02	540.78	15.44*	1.43	30.82**
Diallel hybrids vs. checks	1	3.99**	1089.92**	93.83	728.14	1.59	2.24	.17
Parents	11	1.59**	524.93**	169.63**	1639.48**	22.20**	13.21**	47.25**
R-lines vs. B-lines	1	.49	645.16	35.13	1482.25	2.78	.02	103.23*
Diallel hybrids vs. parents	1	56.11**	7971.86**	802.18**	2773.67*	133.78**	66.52**	21.84
Error	158	.26	29.40	10.84	334.24	1.74	.47	8.07
Mean of genotypes		5.015	133.96	17.09	117.39	79.10	14.28	24.57
Mean of hybrids		5.220	136.28	17.83	118.82	78.78	14.50	24.70
Mean of diallel hybrids		5.190	136.76	17.97	118.39	78.64	14.48	24.69
Mean of sterile hybrids		5.003	135.61	16.99	113.24	79.71	14.55	24.92
Mean of fertile hybrids		5.360	137.89	18.82	123.25	78.01	14.42	24.51
Mean of A3 x R		4.913	130.05	17.22	110.33	78.93	13.93	25.51
Mean of A x B		5.093	141.17	16.76	116.13	80.49	15.16	24.33
Mean of checks		5.877	125.59	14.68	127.89	79.22	14.99	24.84
Mean of parents		3.837	120.65	12.84	109.14	80.89	13.00	23.85
Mean of R-lines		3.721	116.42	13.83	102.72	81.17	12.98	25.54
Mean of B-lines		3.954	124.88	11.85	115.56	80.61	13.02	22.15

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

Table 9. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents in Halfway in 2004, with means of various categories of experimental entries

Source of variation	Df	GY	PH	EX	PAN	DY	Df	WT	PL
		Mg/ha	Cm	Cm				gm	Cm
Reps	2	28.54**	6223.06**	464.71**	1861.26*	n/a	1	.44	158.30**
Genotype	76	7.25**	631.50**	113.84**	2565.50**		76	6.67**	17.01**
Hybrids	64	4.81**	418.12**	116.57**	2173.36**		64	6.55**	14.69**
Diallel hybrids	62	4.38**	413.43**	116.07**	2079.20**		62	6.65**	15.11**
Sterile vs fertile	1	13.72*	1264.67**	860.32**	1833.19		1	58.16**	26.39
A3xR vs AxB	1	1.04	4188.47**	15.87	479.24		1	97.07**	47.82**
Checks	1	.35	210.75*	38.71	96.00		1	2.89	.00
Diallel hybrids vs. checks	1	35.48**	916.25*	225.16*	10088.46**		1	3.81	3.06
Parents	11	8.22**	697.34**	81.12**	4402.94**		11	6.47*	25.99**
R-lines vs. B-lines	1	36.48**	2537.81**	30.29	10370.03*		1	4.44	40.32
Diallel hybrids vs. parents	1	142.20**	13994.99**	335.24**	6250.54*		1	15.40	64.59**
Error	152	1.25	64.21	18.45	424.01		64	1.33	3.92
Mean of genotypes		6.773	145.19	9.78	150.86			15.07	27.01
Mean of hybrids		7.123	148.48	10.26	153.30			15.25	27.24
Mean of diallel hybrids		7.047	148.87	10.46	152.02			15.22	27.21
Mean of sterile hybrids		6.755	146.06	8.15	148.64			16.00	27.62
Mean of fertile hybrids		7.295	151.26	12.43	154.89			14.61	26.87
Mean of A3 x R		6.861	139.36	7.73	150.91			14.68	28.34
Mean of A x B		6.642	153.25	8.59	146.21			17.31	26.85
Mean of checks		9.517	136.31	4.23	193.67			16.25	27.94
Mean of parents		4.878	127.35	7.13	137.64			14.07	25.75
Mean of R-lines		3.872	118.96	6.21	120.67			14.74	26.81
Mean of B-lines		5.885	135.75	8.04	154.61			13.74	24.69

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

§ Different degrees of freedom for reps and error in the case of 500-seed weight and panicle length are due to panicle samples (for the purpose of estimating these traits) having been taken from only two replications and not three as usual

Table 10. Mean squares of grain yield and agronomic traits in sorghum hybrids and parents in Halfway in 2003, with means of various categories of experimental entries

Source of variation	Df	GY	PH	EX	PAN	DY	WT	PL
		Mg/ha	cm	Cm			gm	cm
Reps	2	.89	629.58**	59.36**	1849.45*	2.63	n/a	n/a
Genotype	80	6.94**	334.06**	26.74**	837.01**	26.64**		
Hybrids	68	3.56**	278.04**	26.77**	732.73*	20.54**		
Diallel hybrids	65	3.41**	284.40**	26.31**	648.10	21.16**		
Sterile vs fertile	1	26.57**	336.16	246.36**	3322.26*	61.99**		
A3xR vs AxB	1	.15	2220.50**	25.88	656.10	33.61*		
Checks	2	4.60*	142.65	.72	3243.11*	7.44*		
Diallel hybrids vs. checks	1	11.08*	135.00	109.00**	1174.63	6.46		
Parents	11	4.99**	330.40**	28.48*	1450.14	41.46**		
R-lines vs. B-lines	1	3.38	207.17	2.87	2500.00	2.05		
Diallel hybrids vs. parents	1	248.19**	4280.14**	10.76	1012.71	298.30**		
Error	158	1.01	35.91	9.81	521.96	1.70		
Mean of genotypes		7.946	120.88	5.59	129.34	76.15		
Mean of hybrids		8.377	122.62	5.66	130.24	75.70		
Mean of diallel hybrids		8.328	122.79	5.82	129.74	75.66		
Mean of sterile hybrids		7.923	121.36	4.60	125.41	76.30		
Mean of fertile hybrids		8.662	123.98	6.85	133.67	75.17		
Mean of A3 x R		7.883	116.39	4.06	128.11	76.91		
Mean of A x B		7.964	126.32	5.14	122.71	75.69		
Mean of checks		9.458	118.82	2.26	141.56	76.56		
Mean of parents		5.467	110.91	5.22	124.11	78.94		
Mean of R-lines		5.160	108.51	4.94	132.44	78.67		
Mean of B-lines		5.773	113.31	5.50	115.78	79.17		

GY = Grain yield, PH = plant height, EX = panicle exsertion, PAN = number of panicles per plot, DY = days to anthesis, WT = 500-seed weight, PL = panicle length

Table 11. Means of experimental sorghum material grouped in various combination for seven traits over five environments – College Station, Weslaco and Halfway in 2003 and College Station and Halfway in 2004

	Grain Yield (Mg/ha)	Plant height (cm)	Panicle exsertion (cm)	Number of panicles per plot	Days to anthesis	500-seed weight (gm)	Panicle length (cm)
Mean of parents	**4.157**	**121.27**	**8.59**	**105.337**	**80.998**	12.945	**25.35**
Mean of diallel hybrids	**6.137**	**138.21**	**12.09**	**117.466**	**77.242**	14.484	**26.45**
Mean of checks	**7.270**	**127.00**	**7.98**	126.690	77.389	**15.557**	26.67
Mean of diallel hybrids	**6.137**	**138.21**	**12.09**	117.466	77.242	**14.484**	26.45
Mean of sterile hybrids	**5.835**	**136.74**	**10.82**	**113.395**	**78.083**	14.763	**26.77**
Mean of fertile hybrids	**6.410**	**139.75**	**13.18**	**121.792**	**76.569**	14.255	**26.21**
Mean of A3 x R	5.902	**130.58**	10.33	113.448	77.617	**14.140**	**27.36**
Mean of A x B	5.767	**142.00**	11.31	113.305	78.550	**15.392**	**26.17**
Mean of R-lines	3.779	**115.77**	8.27	98.991	80.925	**13.334**	26.53
Mean of B-lines	4.535	**126.77**	8.92	111.911	80.817	**12.691**	24.18

§ Means under comparison are joined by lines; a pair of numbers in bold, large font signify two means that are significantly different from each other at the $p < 0.05$ level

In the combined analysis, environment, reps (environment), genotype and the genotype x environment interaction were highly significant ($p<0.01$) sources of variation for almost every trait under consideration (Table 5). In individual environments, reps were a significant source of variation in grain yield at four locations – College Station (2003 and 2004), Weslaco (2003), and Halfway (2004) (Tables 6-9). Of the five environments, Halfway (2003) was the most productive environment, with an average grain yield of 7.946 Mg ha^{-1}(Table 10). In comparison, the least productive location, College Station (2004), yielded 3.802 Mg ha^{-1} (Table 7).

Highly significant differences between genotypes were recorded for all traits at all five environments (Tables 6-10), as was the case in the across - environments analysis (Table 5). In the combined analysis of the various components of the genotype term, hybrids, diallel hybrids and parents (and their interaction terms with environment) showed highly significant differences between the genotypes comprising those classes, for all traits including grain yield. The three commercial check hybrids, however, differed significantly among themselves only for seed weight, and this trend of similarity between the three checks was consistent with the results from individual environments, which showed no (or lowly) significant differences between the commercial hybrids, with the exception of the College Station (2003) environment, where 84G62 (with a yield of 9.055 Mg ha^{-1}) outyielded the other checks (and all other genotypes) by a wide margin (Table 6).

In the combined analysis within diallel hybrids, highly significant differences were seen between sterile and fertile hybrids for days to anthesis, plant height, number of panicles per plot, and grain yield (Table 5). Fertile hybrids, on an average, yielded 575 kg

ha^{-1} more than the sterile hybrids (Table 11), and this average difference was consistent across environments, albeit with lower significance levels in the 2004 environments. This trend was also manifested in SCA effects, to be discussed later in this section. Within sterile hybrids, no significant differences were observed for grain yield between A3 x R hybrids (crosses within R-lines) and A x B hybrids (crosses within the A/B lines). Despite the lack of a significant difference in grain yield, there exists a high probability that the heterotic relationships between the inbreds are confounded with the effect of the different cytoplasms (A1 and A3 cytoplasms), a possibility suggested by the findings of reduced yield in A3 hybrids compared to isocytoplasmic A1 and A2 hybrids by Moran and Rooney (2003). On average, A x B hybrids were taller by 11.42 cm (significant at the $p < 0.01$ level), and had heavier seed, although the seed weight difference was significant only at the $p < 0.05$ level (Tables 5, 11). Partitioning of the significant variation among parental inbreds into a contrast between R-lines and B-lines revealed no significant differences in grain yield between the two types in the combined analysis, and there was a significant difference in only one environment – at Halfway, TX in 2004 (Table 9).

Combined across all five environments, diallel hybrids significantly outperformed the parents (Table 5), yielding 1.980 Mg/ha more than the parents (Table 11). The hybrids were 16.94 cm taller, and had 12.13 more panicles per plot, compared to the parents. Diallel hybrids flowered 3.76 days earlier and had 3.5 cm more panicle exsertion (Table 11).

General Combining Ability (GCA) effects

GCA estimates for one environment - Halfway (2003) - could not be obtained due to the absence of three hybrids in the diallel. GCA estimates were extremely variable with location. For grain yield, over environments, BTx635 had the highest GCA, followed by BTx631. However, in individual environments, BTx623, RTx7000, BTx378, TAM428, RTx436 and RTx430 had high GCAs as well (Table 12). BTx635 was also the tallest combiner (for plant height) and the earliest (for days to anthesis) (Tables 13, 14).

Specific Combining Ability (SCA) and midparent heterosis

Grain yield

For grain yield, crosses made within a group had lower SCA and heterosis compared to all other cross types (with many of these differences also being statistically significant, as discussed in the next section dealing with comparisons) (Tables 15-18). This suggests that the grouping system adopted for this study may in fact represent actual heterotic groups. Within the across-group hybrids, averages of cross-types do not reveal any group to be particularly superior, but particular hybrids exhibiting high positive SCAs and heterosis included crosses of RTx430, RTx436, RTx7000, and RTAM 428 with the A-lines ATx635, ATx631 and ATx378.

The current grouping of germplasm appears to be justified by the lowered heterotic effects of the within-group crosses, with the exception of the two parental B-lines BTx635 and BTx623, grouped together in the “Zerazera-derivative B-lines” group. The responses of these two lines in combination with other groups differ widely from

Table 12. General Combining Ability (GCA) estimates for grain yield (Mg/ha) for each parental line in a half diallel evaluated in four environments and the combined analysis. Due to the absence of a three hybrids, GCA estimates were not reported for Halfway in 2004.

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
RTX430	-0.452	0.082	-0.101	0.480	N/A	-0.006
RTX2737	-0.546	-0.243	0.138	-0.383		-0.098
RTX436	0.602	0.049	-0.130	0.309		0.079
RTX7000	0.618	0.027	0.320	0.104		0.072
RTAM428	-0.150	-0.220	-0.726	0.457		-0.170
RTX2817	-0.162	0.011	0.149	-0.243		0.005
BTX642	-0.081	-0.182	-0.433	-0.438		-0.161
BTX631	0.292	0.499	0.247	-0.058		0.185
BTX635	0.342	0.308	0.643	0.619		0.473
BTX378	-0.745	-0.063	0.592	-0.084		-0.067
BTX3197	-0.605	-0.524	-0.654	-0.419		-0.385
BTX623	0.887	0.254	-0.046	-0.344		0.073
Standard Error	0.373	0.128	0.260	0.246		0.270

Table 13. General Combining Ability (GCA) estimates for days to anthesis for each parental line in a half diallel in each environment and the combined analysis . Data for days to anthesis were not collected in Halfway in either year.

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	-3.34	0.23	N/A	0.01	N/A	-0.91
R.TX2737	1.35	-0.27		-2.01		-0.79
R.TX436	-1.19	0.56		1.89		1.01
R.TX7000	1.35	-3.30		-1.99		-0.72
R.TAM428	0.71	0.18		0.87		0.36
R.TX2817	2.69	1.18		1.73		1.60
B.TX642	2.07	0.58		0.42		0.71
B.TX631	1.39	2.39		2.54		1.72
B.TX635	4.69	1.23		2.09		2.35
B.TX378	-3.08	-1.80		-1.46		-1.23
B.TX3197	-5.54	-0.87		-3.37		-3.17
B.TX623	-1.10	-0.11		-0.72		-0.92
Standard error	0.741	0.338		0.512		0.734

Table 14. General Combining Ability (GCA) estimates for plant height (cm) for each parental line in a half diallel in each environment and the combined analysis Due to the absence of a three hybrids, GCA estimates were not reported for Halfway in 2004.

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	-7.31	-1.06	-1.56	-2.00	N/A	-3.02
R.TX2737	6.96	-0.27	-6.15	6.47		1.23
R.TX436	-3.50	-3.54	1.16	-3.51		-1.65
R.TX7000	8.53	2.15	0.20	5.20		3.88
R.TAM428	-7.31	-4.63	-3.31	-6.48		-6.44
R.TX2817	-12.30	-8.19	-3.04	-15.09		-9.83
B.TX642	-5.38	-5.41	-2.04	-2.24		-3.84
B.TX631	6.29	4.51	2.56	5.07		4.07
B.TX635	14.28	13.82	15.07	15.84		14.22
B.TX378	-1.36	-2.15	-0.35	0.06		-0.14
B.TX3197	-4.23	-2.09	-3.89	-5.24		-3.22
B.TX623	5.33	6.86	1.35	1.93		4.75
Standard error	2.938	1.386	1.550	2.849		2.473

Table 15. Specific Combining Ability (SCA) values of 66 diallel hybrids for grain yield (Mg/ha), based on combined data from five environments- College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-1.50												FR
3	KR	**A3Tx436**	-0.60	0.27											KR
4	KR	**A3Tx7000**	0.51	1.14	0.28										KR
5	ZR	**A3TAM428**	-0.44	0.18	0.42	0.07									ZR
6	ZR	**A3Tx2817**	0.85	0.64	0.00	0.73	-0.27								ZR
7	XA	**ATx642**	0.83	0.60	0.27	0.41	0.35	0.05							XA
8	XA	**ATx631**	1.06	0.92	0.64	-0.77	1.64	0.42	0.31						XA
9	KA	**ATx378**	1.28	1.22	1.31	-0.46	1.41	-0.26	0.35	-0.71					KA
10	KA	**ATx3197**	0.58	0.23	1.42	0.09	0.41	0.58	0.10	-0.38	-1.08				KA
11	ZA	**ATx635**	1.22	0.08	0.86	1.06	0.96	0.47	0.55	-1.18	-0.75	0.08			ZA
12	ZA	**ATx623**	0.49	0.02	0.49	-0.67	0.69	-0.22	0.21	0.06	0.13	-0.21	0.75		ZA

Standard Error = 0.366

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 16. Simplified SCA table for grain yield (Mg/ha), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal; numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-1.50												FR
3	KR	**A3Tx436**	0.33	(0.72)											KR
4	KR	**A3Tx7000**			0.28										KR
5	ZR	**A3TAM428**	0.31	(0.57)	0.30	(0.34)									ZR
6	ZR	**A3Tx2817**					-0.27								ZR
7	XA	**ATx642**	0.85	(0.19)	0.14	(0.62)	0.62	(0.70)							XA
8	XA	**ATx631**							0.31						XA
9	KA	**ATx378**	0.83	(.051)	0.59	(0.92)	0.53	(0.68)	-0.16	(0.48)					KA
10	KA	**ATx3197**									-1.08				KA
11	ZA	**ATx635**	0.45	(0.55)	0.44	(0.77)	0.47	(0.51)	-0.09	(0.76)	-0.19	(0.40)			ZA
12	ZA	**ATx623**											0.75		ZA

Table 17. Midparent heterosis values of diallel hybrids for grain yield (Mg/ha), based on combined data from five environments-College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	13.9												FR
3	KR	**A3Tx436**	51.6	72.5											KR
4	KR	**A3Tx7000**	51.3	62.8	54.7										KR
5	ZR	**A3TAM428**	61.3	76.1	102.0	53.3									ZR
6	ZR	**A3Tx2817**	66.2	57.8	54.5	45.3	51.5								ZR
7	XA	**ATx642**	80.8	70.3	76.7	48.6	86.1	45.8							XA
8	XA	**ATx631**	59.1	52.9	58.2	6.5	87.6	34.9	41.6						XA
9	KA	**ATx378**	72.3	67.5	83.7	16.2	92.7	24.9	49.1	8.2					KA
10	KA	**ATx3197**	53.5	41.2	85.9	25.4	63.8	41.8	40.7	12.3	-0.4				KA
11	ZA	**ATx635**	78.8	48.5	80.2	56.3	88.8	49.4	62.7	6.9	19.3	35.0			ZA
12	ZA	**ATx623**	45.2	31.7	53.8	7.3	62.8	20.2	38.1	19.3	24.3	14.6	44.8		ZA

Standard error = 8.739

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 18. Simplified midparent heterosis table for grain yield (Mg/ha), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal; numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	13.9												FR
3	KR	**A3Tx436**	59.6	(10.2)											KR
4	KR	**A3Tx7000**			54.7										KR
5	ZR	**A3TAM428**	65.4	(8.0)	63.8	(25.8)									ZR
6	ZR	**A3Tx2817**					51.5								ZR
7	XA	**ATx642**	65.8	(12.3)	47.5	(29.7)	63.6	(27.2)							XA
8	XA	**ATx631**							41.6						XA
9	KA	**ATx378**	58.6	(14.1)	52.8	(37.2)	55.8	(29.3)	27.6	(20.4)					KA
10	KA	**ATx3197**									-0.4				KA
11	ZA	**ATx635**	51.0	(19.9)	49.4	(30.5)	55.3	(28.5)	31.7	(24.3)	23.3	(8.8)			ZA
12	ZA	**ATx623**											44.8		ZA

each other, and the ATx623 x BTx635 hybrid combination, contrary to the trend characteristic of hybrids made within a group, showed high specific combining ability and heterosis for grain yield across environments (Tables 15, 17) and ranked 8th for yield among the diallel hybrids (Table 4). The possibility of this heterotic response being due to the high general combining ability of BTx635 (the best general combiner of all the parental lines) was considered (Table 12), but this particular within-group hybrid combination was superior in yield specific combining ability and actual grain yield to six other across-group crosses involving BTx635. These observations suggest that BTx635 and BTx623 would be better considered as members of separate groups, despite the high genetic similarity (GS) value between them (Table 19). The reason for the differences between the two supposedly closely related lines may be BTx623's partial Kafir pedigree (Table 1), a possibility supported by the fact that the heterotic response of BTx635 with Kafir males, like RTx7000 and RTx436, was highly superior to that of BTx623 with the same Kafir males.

The hybrid combination of BTx635 with the Feterita-derivative male RTx430 was the highest-yielding diallel hybrid, with very high SCA effects and heterosis, but the other ZA x FR crosses exhibited much lower heterosis. The Zerazera B-lines BTx635 and BTx623 exhibited good heterotic response in combination with one Zerazera-derivative male, RTAM428, but moderate to low SCA and heterosis with the other male, RTx2817. BTx635 and BTx623 showed poor heterotic response with all the other B-line groups, with the exception of BTx642, in combination with which BTx635 had moderate SCA effects. This was consistent with the trend observed in all the other hybrid combinations between B-lines, all of which showed moderately low heterotic effects.

Differential responses of members of a group with other lines was observed - Zerazera derivative male Tx2817 combined moderately well with both Feterita derivative males Tx430 and Tx2737, whereas hybrids of those lines with the other Zerazera derivative male, TAM428, exhibited low positive and negative SCA effects.

Interactions between zerazera derivative males and milo (durra) - kafir males were also selectively heterotic – Tx2817 x Tx7000 and TAM428 x Tx436 (both ZR x KR hybrids) had moderate SCA effects and heterosis, but the other combinations had low heterotic expression.

The heterotic relationship between the milo (durra)-kafir males and the feterita derivative male lines seems to be clearly explained by the data, where the Tx7000 (KR) showed very high SCA effects in combination with Tx2737 (FR). Tx436 x Tx430, conversely, had negative SCA effects, and the other across-group combinations were intermediate in SCA effects and heterosis.

The within-group crosses in the R-lines were uniformly poor in heterotic expression, with low positive and negative SCA effects, supporting the hypothesis of the groups being potential heterotic groups.

A-line x R-line hybrids, in general, were superior in heterosis to sterile crosses, but differential heterotic responses were observed, including those of the zerazera-derivative B-lines BTx635 and BTx623 with various R-line groups, discussed earlier in this section. Hybrids of both Kafir females, ATx3197 and ATx378, with the milo (durra) – kafir male RTx436, were highly heterotic, whereas negative SCA effects were exhibited by their hybrids with the other milo (durra) – kafir male, RTx7000.

ATx378 x RTAM428, with very high SCA effects and heterosis, was the only such superior Kafir female x Zerazera-derivative male hybrid, the other combinations expressing moderate levels of heterosis. The Kafir female ATx378 had a highly heterotic relationship with both Feterita-derivative males, RTx430 and RTx2737, but the hybrids of these two males with the other kafir female, ATx3197, showed moderate and low SCA effects, respectively.

ATx631 and ATx642, being in the same group solely by virtue of both of them not conforming to any other group, were considered as separate, unrelated, lines.
ATx631 showed excellent heterotic response in hybrid combination with all R-lines in the diallel with the exception of RTx7000, a milo (durra) – kafir male, with which it had negative SCA effects.

ATx642 combined well with both Feterita-derivative males, RTx430 and RTx2737, showing moderately high SCA effects, but its hybrid combinations with the other R-line groups were poor in heterotic effects. ATx642 is an early generation backcross derivative of SC35 from the sorghum conversion program. The exotic parent is genetically an R-line and the maintainer status of BTx642 was derived from the donor parent in the conversion process. Thus, this line is somewhat unique in possessing an R-line type genome which accounts for the poor performance with some R-line groups, but it also indicates significant heterosis with other groups of R-lines. Regardless of whether or not this heterosis is due to retention of additional B-line germplasm from the donor parent, it clearly indicates that there are different responses of material to groups within the R-lines.

Significantly higher grain yields for fertile (A x R) hybrids as compared to those of the sterile diallel hybrids (A3 x R and A x B crosses, i.e. crosses made among R-lines, and among A/B lines, respectively), as mentioned before in the discussion on the analysis of variance, are reflected in similar large differences in grain yield SCA estimates (Tables 15, 16). Midparent heterosis values, however, were low only for A x B hybrids and not for the A3 x R crosses (Tables 17, 18). Field examination of the sterile hybrids revealed good levels of seed set, confirming that fertile hybrids did not have a phenotypic seed set advantage over the sterile diallel hybrids. The yield contrast seems to indicate a heterotic relationship between the B- and R-lines, and this variation is likely to be a product of decades of selecting and breeding elite B- and R-lines, a process designed to produce mutually heterotic parental lines, rather than a result of the two groups being phylogenetically divergent. This is supported by the observation by Menz et al. (2004) that diversity analyses based on molecular markers did not reveal consistent divergence between B- and R- lines. Consistent with that hypothesis is the observation, in this study, that sterile hybrids within the R-lines (A3 x R crosses) were not as low-performing as the A x B hybrids, in terms of SCA effects and heterosis levels(Table 20). This difference is enhanced when BTx642 crosses are excluded from the comparison, that B-line parent possessing an R-line type genome, as previously mentioned.This could be a result of the fact that R-lines have a broader genetic base than do B-lines, reflected by the differences in genetic similarity estimates in the two groups (Table 19). An examination of these GS estimates also shows that BTx642 is genetically different from the other B-lines. Selective R x R (A3 x R) combinations showed moderate to high heterosis and SCA

effects – Tx7000 x Tx2737 (KR x FR), a superior hybrid combination, ranked 14th in yield (Table 4) and was 8th in SCA effects (Table 15).

Another important aspect to consider in comparing these hybrids is the fact that they are not uniform in their cytoplasmic background. Given the knowledge that A3 cytoplasm hybrids have been shown to suffer yield reductions in comparison with isocytoplasmic A1 and A2 hybrids (Moran and Rooney, 2003), there exists a very real possibility that the evaluation of heterotic potential expressed in yield is being confounded with the effect of non-uniform cytoplasm in the set of diallel hybrids, since the hybrids made within the R-lines are all A3 hybrids, while the others are A1-based. However, if cytoplasm alone were the cause of the reduction, then the A x B hybrids should not have lower yields as they yielded the same as A3 x R.

Other traits

For days to anthesis, plant height and panicle exsertion, crosses made within a group had lower SCA and heterosis compared to all other cross types, echoing the situation seen in the case of grain yield (Tables 21-32). Many of these differences were statistically significant (Tables 33-40). For days to anthesis, A x R hybrids had lower SCAs and heterosis values than the A3 x R and A x B hybrids, as a higher degree of heterotic action is associated with hastened flowering and maturity (Tables 21, 22). For 500-seed weight, within-group crosses had higher or comparable SCA effects compared to those of the across-group crosses (Tables 41, 42). Another manifestation of this slight anomaly was in the form of low positive correlation of SGD (Specific Genetic Distance) with SCA and midparent heterosis for 500-seed weight (Table 43).

Table 19. Genetic Similarity estimates (calculated and expressed using a Dice coefficient of similarity, a function of the proportion of markers common to two lines) between the 12 elite parental lines based on 1814 AFLP and 100 SSR markers (Menz, unpublished)

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	0.667												FR
3	KR	**A3Tx436**	0.717	0.573											KR
4	KR	**A3Tx7000**	0.558	0.545	0.672										KR
5	ZR	**A3TAM428**	0.583	0.498	0.639	0.587									ZR
6	ZR	**A3Tx2817**	0.650	0.481	0.639	0.561	0.683								ZR
7	XA	**ATx642**	0.558	0.519	0.563	0.609	0.617	0.539							XA
8	XA	**ATx631**	0.522	0.524	0.532	0.514	0.624	0.559	0.555						XA
9	KA	**ATx378**	0.507	0.521	0.572	0.711	0.567	0.494	0.587	0.650					KA
10	KA	**ATx3197**	0.533	0.540	0.571	0.699	0.579	0.508	0.585	0.649	0.890				KA
11	ZA	**ATx635**	0.554	0.515	0.594	0.661	0.681	0.615	0.592	0.624	0.743	0.771			ZA
12	ZA	**ATx623**	0.583	0.486	0.626	0.646	0.706	0.745	0.569	0.626	0.703	0.755	0.783		ZA

Table 20. Grain yield SCA (Specific Combining Ability) and MPH (midparent heterosis) averages of A3 x R and A x B hybrids, with significance levels at which they are statistically different

Type of sterile hybrid (none excluded)	**SCA**	**Sig.**	**MPH**	**Sig.**
A3 x R	0.152		58.33	
		.244		.000
A x B	-0.119		27.77	
Excluding crosses with BTx642[§]				
A3 x R	0.152		58.33	
		.078		.000
A x B	-0.330		18.43	

§ BTx642 is derived from SC35, an R-line, and retains a R-line type genome

Table 21. Specific Combining Ability (SCA) values of diallel hybrids for days to anthesis, based on combined data from four environments - College Station, Weslaco and Halfway in 2003, and College Station in 2004.

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-0.1												FR
3	KR	**A3Tx436**	1.7	-0.6											KR
4	KR	**A3Tx7000**	-2.8	18.6	-0.4										KR
5	ZR	**A3TAM428**	-0.1	-3.2	-0.9	-1.5									ZR
6	ZR	**A3Tx2817**	0.6	-2.5	-0.2	-1.8	3.2								ZR
7	XA	**ATx642**	-3.8	-1.3	0.4	-0.2	-0.3	0.0							XA
8	XA	**ATx631**	-1.5	-2.6	-1.1	-2.0	-0.2	0.1	0.0						XA
9	KA	**ATx378**	-1.1	-1.5	-2.4	-0.6	-3.7	-5.5	1.8	-0.4					KA
10	KA	**ATx3197**	-1.8	-1.6	-1.1	-2.2	-3.4	-1.4	-1.1	2.4	2.6				KA
11	ZA	**ATx635**	0.5	-3.3	-2.6	-4.4	-0.5	0.8	0.5	1.2	-0.2	-0.7			ZA
12	ZA	**ATx623**	-0.3	-4.2	-1.6	-2.4	0.1	1.4	0.9	1.9	-0.5	-0.3	1.6		ZA

Standard error = 0.998

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 22. Simplified SCA table for days to anthesis, with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-0.1												FR
3	KR	**A3Tx436**	4.2	(9.8)											KR
4	KR	**A3Tx7000**			-0.4										KR
5	ZR	**A3TAM428**	-1.3	(1.8)	-1.1	(0.7)									ZR
6	ZR	**A3Tx2817**					3.2								ZR
7	XA	**ATx642**	-2.3	(1.2)	-0.7	(1.1)	-0.1	(0.2)							XA
8	XA	**ATx631**							0.0						XA
9	KA	**ATx378**	-1.5	(0.3)	-1.6	(0.8)	-3.5	(1.7)	0.6	(1.7)					KA
10	KA	**ATx3197**									2.6				KA
11	ZA	**ATx635**	-1.9	(2.3)	-2.7	(1.2)	0.4	(0.9)	1.1	(0.6)	-0.4	(0.2)			ZA
12	ZA	**ATx623**											1.6		ZA

Table 23. Specific Combining Ability (SCA) values of diallel hybrids for plant height (cm), based on combined data from five environments- College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-10.49												FR
3	KR	**A3Tx436**	-7.27	-4.06											KR
4	KR	**A3Tx7000**	2.95	20.04	-7.05										KR
5	ZR	**A3TAM428**	6.16	1.75	3.61	4.18									ZR
6	ZR	**A3Tx2817**	1.75	5.98	10.38	4.34	-6.33								ZR
7	XA	**ATx642**	7.12	-2.72	8.97	3.44	-0.30	-8.09							XA
8	XA	**ATx631**	2.42	6.47	5.46	-6.17	7.71	6.69	9.17						XA
9	KA	**ATx378**	10.35	5.94	2.72	-7.89	12.76	7.26	0.81	-9.61					KA
10	KA	**ATx3197**	8.52	9.69	5.12	1.12	7.33	-4.99	3.25	-11.95	-9.60				KA
11	ZA	**ATx635**	1.75	-2.66	4.79	3.33	6.20	14.83	11.39	5.84	5.65	2.46			ZA
12	ZA	**ATx623**	6.48	1.56	-2.34	6.86	0.76	-4.24	10.35	0.07	0.89	1.76	2.79		ZA

Standard Error = 3.360

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 24. Simplified SCA table for plant height (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-10.49												FR
3	KR	**A3Tx436**	2.92	(12.19)											KR
4	KR	**A3Tx7000**			-7.05										KR
5	ZR	**A3TAM428**	3.91	(2.49)	5.63	(3.18)									ZR
6	ZR	**A3Tx2817**					-6.33								ZR
7	XA	**ATx642**	3.32	(4.53)	2.92	(6.48)	1.50	(7.32)							XA
8	XA	**ATx631**							9.17						XA
9	KA	**ATx378**	8.62	(1.95)	0.27	(5.68)	5.59	(7.51)	-4.37	(7.52)					KA
10	KA	**ATx3197**									-9.60				KA
11	ZA	**ATx635**	1.78	(3.73)	3.16	(3.94)	4.39	(8.16)	6.91	(5.16)	2.69	(2.07)			ZA
12	ZA	**ATx623**											2.79		ZA

Table 25. Specific combining ability (SCA) values of diallel hybrids for panicle exsertion (cm), based on combined data from five environments - College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-3.27												FR
3	KR	**A3Tx436**	-1.72	-1.23											KR
4	KR	**A3Tx7000**	0.25	0.57	-2.96										KR
5	ZR	**A3TAM428**	-0.24	-0.42	-0.57	-0.46									ZR
6	ZR	**A3Tx2817**	-0.31	1.71	1.40	-1.37	-1.35								ZR
7	XA	**ATx642**	4.45	2.23	3.61	-3.90	2.21	-1.24							XA
8	XA	**ATx631**	1.16	3.01	1.17	1.95	-0.23	0.72	0.90						XA
9	KA	**ATx378**	2.21	1.52	1.54	0.30	4.04	1.43	0.60	-0.32					KA
10	KA	**ATx3197**	1.57	3.42	-0.45	1.52	2.98	2.91	-0.55	-3.67	-4.48				KA
11	ZA	**ATx635**	0.18	1.18	3.57	2.84	0.48	2.28	0.09	-2.35	-0.11	-0.08			ZA
12	ZA	**ATx623**	2.26	1.57	-0.27	2.89	-0.48	0.05	1.16	-1.62	-1.75	5.06	-1.75		ZA

Standard Error = 2.041

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 26. Simplified SCA table for panicle exsertion (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-3.27												FR
3	KR	**A3Tx436**	-0.53	(1.12)											KR
4	KR	**A3Tx7000**			-2.96										KR
5	ZR	**A3TAM428**	0.18	(1.02)	-0.25	(1.17)									ZR
6	ZR	**A3Tx2817**					-1.35								ZR
7	XA	**ATx642**	2.71	(1.38)	0.71	(3.24)	0.37	(1.47)							XA
8	XA	**ATx631**							0.90						XA
9	KA	**ATx378**	2.18	(0.88)	0.73	(0.98)	2.84	(1.07)	-0.99	(1.86)					KA
10	KA	**ATx3197**									-4.48				KA
11	ZA	**ATx635**	1.30	(0.87)	2.26	(1.72)	0.58	(1.20)	-0.68	(1.60)	0.78	(2.96)			ZA
12	ZA	**ATx623**											-1.75		ZA

Table 27. Midparent heterosis values of diallel hybrids for days to anthesis, based on combined data from four environments - College Station, Weslaco and Halfway in 2003, and College Station in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-3.5												FR
3	KR	**A3Tx436**	-3.1	-4.2											KR
4	KR	**A3Tx7000**	-6.2	23.5	-3.1										KR
5	ZR	**A3TAM428**	-6.0	-7.9	-6.8	-5.1									ZR
6	ZR	**A3Tx2817**	-3.4	-5.4	-4.4	-3.8	-0.9								ZR
7	XA	**ATx642**	-8.4	-3.3	-3.0	-1.2	-4.6	-2.5							XA
8	XA	**ATx631**	-5.2	-4.7	-4.6	-3.1	-4.2	-2.2	-1.7						XA
9	KA	**ATx378**	-7.6	-6.2	-9.0	-4.4	-11.2	-11.7	-2.4	-4.7					KA
10	KA	**ATx3197**	-7.8	-5.7	-6.8	-5.6	-10.3	-6.1	-5.2	-0.5	-3.1				KA
11	ZA	**ATx635**	-4.2	-7.0	-7.7	-7.5	-5.9	-2.7	-2.5	-1.4	-5.9	-5.7			ZA
12	ZA	**ATx623**	-4.3	-7.3	-5.7	-4.1	-4.3	-1.0	-1.0	0.6	-5.4	-4.3	-1.4		ZA

Standard Error = 5.434

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 28. Simplified midparent heterosis table for days to anthesis, with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-3.5												FR
3	KR	**A3Tx436**	2.5	(14.0)											KR
4	KR	**A3Tx7000**			-3.1										KR
5	ZR	**A3TAM428**	-5.7	(1.8)	-5.0	(1.3)									ZR
6	ZR	**A3Tx2817**					-0.9								ZR
7	XA	**ATx642**	-5.4	(2.1)	-3.0	(1.4)	-3.4	(1.2)							XA
8	XA	**ATx631**							-1.7						XA
9	KA	**ATx378**	-6.8	(1.0)	-6.4	(2.0)	-9.8	(2.6)	-3.2	(2.2)					KA
10	KA	**ATx3197**									-3.1				KA
11	ZA	**ATx635**	-5.7	(1.7)	-6.3	(1.7)	-3.5	(2.1)	-1.1	(1.3)	-5.3	(0.7)			ZA
12	ZA	**ATx623**											-1.4		ZA

Table 29. Midparent heterosis values of diallel hybrids for plant height (cm), based on combined data from five environments-College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	4.1												FR
3	KR	**A3Tx436**	4.4	7.3											KR
4	KR	**A3Tx7000**	13.6	27.0	3.4										KR
5	ZR	**A3TAM428**	22.7	18.4	17.6	18.5									ZR
6	ZR	**A3Tx2817**	14.8	18.4	19.9	15.0	11.3								ZR
7	XA	**ATx642**	22.9	14.0	21.7	17.3	20.7	9.2							XA
8	XA	**ATx631**	11.1	14.2	11.3	3.1	19.1	14.8	19.8						XA
9	KA	**ATx378**	18.8	15.0	10.2	2.5	25.1	16.6	14.2	-0.6					KA
10	KA	**ATx3197**	16.1	16.9	10.9	8.3	19.1	11.5	15.0	-3.7	-1.3				KA
11	ZA	**ATx635**	18.5	14.9	18.5	17.7	26.3	30.0	29.9	17.6	18.7	15.2			ZA
12	ZA	**ATx623**	16.3	12.3	7.0	14.7	15.3	7.6	22.9	7.7	9.2	8.7	17.2		ZA

Standard Error = 5.389

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 30. Simplified midparent heterosis table for plant height (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	4.1												FR
3	KR	**A3Tx436**	13.1	(10.0)											KR
4	KR	**A3Tx7000**			3.4										KR
5	ZR	**A3TAM428**	18.6	(3.2)	17.7	(2.1)									ZR
6	ZR	**A3Tx2817**					11.3								ZR
7	XA	**ATx642**	15.5	(5.1)	13.4	(8.1)	16.0	(5.1)							XA
8	XA	**ATx631**							19.8						XA
9	KA	**ATx378**	16.7	(1.6)	8.0	(3.8)	18.1	(8.7)	6.2	(9.8)					KA
10	KA	**ATx3197**									-1.3				KA
11	ZA	**ATx635**	15.5	(2.6)	14.5	(5.3)	19.8	(10.3)	19.5	(9.4)	13.0	(4.8)			ZA
12	ZA	**ATx623**											17.2		ZA

Table 31. Midparent heterosis values of diallel hybrids for panicle exsertion (cm), based on combined data from five environments-College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	10.9												FR
3	KR	**A3Tx436**	12.1	18.4											KR
4	KR	**A3Tx7000**	22.7	23.3	-10.6										KR
5	ZR	**A3TAM428**	85.0	42.6	25.3	14.3									ZR
6	ZR	**A3Tx2817**	154.5	83.1	64.4	6.9	90.9								ZR
7	XA	**ATx642**	96.2	51.5	53.5	-7.1	69.2	37.2							XA
8	XA	**ATx631**	55.6	54.8	24.6	21.1	27.0	64.4	32.3						XA
9	KA	**ATx378**	90.9	49.6	38.5	15.9	121.2	104.2	38.5	14.6					KA
10	KA	**ATx3197**	79.5	68.3	24.0	29.9	98.7	128.3	32.4	-16.8	-13.5				KA
11	ZA	**ATx635**	76.9	55.8	70.9	43.5	80.8	188.2	41.4	-9.3	41.0	46.7			ZA
12	ZA	**ATx623**	91.8	52.2	24.2	39.5	45.2	72.7	46.0	4.2	15.2	94.6	22.4		ZA

Standard Error = 20.478

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 32. Simplified midparent heterosis table for panicle exsertion (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	10.9												FR
3	KR	**A3Tx436**	19.1	(5.2)											KR
4	KR	**A3Tx7000**			-10.6										KR
5	ZR	**A3TAM428**	91.3	(46.5)	27.7	(25.6)									ZR
6	ZR	**A3Tx2817**					90.9								ZR
7	XA	**ATx642**	64.5	(21.2)	23.0	(24.8)	49.5	(20.6)							XA
8	XA	**ATx631**							32.3						XA
9	KA	**ATx378**	72.1	(17.6)	27.1	(9.5)	113.1	(14.0)	17.2	(24.8)					KA
10	KA	**ATx3197**									-13.5				KA
11	ZA	**ATx635**	69.2	(18.6)	44.5	(19.4)	96.7	(62.9)	20.5	(27.3)	49.4	(33.1)			ZA
12	ZA	**ATx623**											22.4		ZA

Table 33. Grain yield SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	-0.302 [a]	-0.330 [a]	-0.654 [a]	0.055 [ab]	N/A	-0.364 [a]
KA x KR	0.199 [a]	0.244[abc]	1.294 [c]	0.240 [b]		0.591 [bc] (.040)
KR x FR	0.372 [a]	-0.013 [ab]	0.536 [bc]	0.211 [b]		0.329[abc] (.130)
ZR x KR	0.032 [a]	0.300[abc]	0.077 [ab]	0.149 [ab]		0.303[abc] (.145)
ZA x KR	0.756 [a]	0.032[abc]	1.230 [c]	0.064 [ab]		0.436[abc] (.082)
KA x FR	1.106 [a]	0.705 [c]	0.870 [bc]	0.395 [b]		0.826 [c] (.012)
KA x ZR	0.720 [a]	0.143[abc]	0.597 [bc]	0.655 [b]		0.535 [abc] (.052)
ZA x KA	0.003 [a]	0.046[abc]	0.078 [ab]	-0.792 [a]		-0.188[ab] (.695)
ZR x FR	0.233 [a]	0.165[abc]	0.565 [bc]	0.257 [b]		0.308[abc] (.141)
ZA x FR	0.332 [a]	0.561 [bc]	0.447 [bc]	0.567 [b]		0.454 [abc] (.076)
ZA x ZR	0.893 [a]	0.307[abc]	0.631 [bc]	0.505 [b]		0.475 [abc] (.069)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 34. Grain yield MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	39.99 [a]	20.27 [a]	35.25 [a]	53.17 [b]	39.34 [ab]	32.90[ab]
KA x KR	44.42[ab]	18.94 [a]	81.78 [ab]	32.86 [ab]	77.30[abc]	52.81[abc] (.217)
KR x FR	52.55[abc]	26.33 [ab]	67.23 [ab]	84.30 [bc]	88.77 [bc]	59.56 [bc] (.101)
ZR x KR	46.64[abc]	33.29[abc]	63.55 [ab]	71.93 [bc]	135.12 [c]	63.77 [bc] (.059)
ZA x KR	49.08[abc]	24.16 [a]	85.94 [b]	36.28 [ab]	48.64 [ab]	49.38[abc] (.305)
KA x FR	114.60 [c]	48.38 [bc]	55.51 [ab]	56.81 [bc]	47.79 [ab]	58.64 [bc] (.113)
KA x ZR	106.40[bc]	33.13[abc]	52.67 [ab]	67.87 [bc]	57.57[abc]	55.83[abc] (.156)
ZA x KA	49.04[abc]	26.50 [ab]	44.99 [ab]	-13.14 [a]	5.97 [a]	23.32[a] (.549)
ZR x FR	83.77[abc]	50.09 [c]	54.88 [ab]	111.35 [c]	60.01[abc]	65.37 [c] (.048)
ZA x FR	58.32[abc]	54.93 [c]	55.38 [ab]	69.33 [bc]	31.60 [ab]	51.03[abc] (.260)
ZA x ZR	80.16[abc]	47.31 [bc]	62.46 [ab]	64.85 [bc]	44.74 [ab]	55.30[abc] (.166)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 35. Days to anthesis SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	0.84 [ab]	1.84 [e]	N/A	2.27 [e]	N/A	1.39 [bc]
KA x KR	-1.91 [a]	-0.89 [bcd]		-2.61 [ab]		-1.58 [ab] (.170)
KR x FR	15.44 [b]	0.64 [de]		-0.36 [cd]		4.22 [c] (.191)
ZR x KR	-4.25 [a]	0.18 [cd]		-0.07 [d]		-1.09 [ab] (.250)
ZA x KR	-5.01 [a]	-2.45 [ab]		-2.45 [abc]		-2.74 [ab] (.059)
KA x FR	-2.17 [a]	-0.98 [bc]		-1.99 [abcd]		-1.50 [ab] (.181)
KA x ZR	-4.66 [a]	-3.10 [a]		-3.29 [a]		-3.51 [a] (.027)
ZA x KA	-0.96 [ab]	0.27 [cd]		-0.50 [bcd]		-0.42 [ab] (.398)
ZR x FR	-3.18 [a]	-1.00 [bc]		-0.29 [d]		-1.28 [ab] (.216)
ZA x FR	-3.61 [a]	-0.63 [cd]		-0.92 [bcd]		-1.85 [ab] (.135)
ZA x ZR	1.70 [ab]	0.42 [cde]		0.04 [d]		0.42 [abc] (.651)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 36. Days to anthesis MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	-3.69 [a]	-0.34 [e]	N/A	-1.94 [d]	N/A	-2.39 [bc]
KA x KR	-7.70 [a]	-4.00 [bc]		-8.99 [a]		-6.43 [ab] (.186)
KR x FR	19.70 [b]	-2.42 [cde]		-5.67 [bc]		2.48 [c] (.113)
ZR x KR	-9.01 [a]	-2.88 [bcd]		-4.62 [cd]		-5.00 [ab] (.391)
ZA x KR	-7.62 [a]	-5.06 [ab]		-7.83 [ab]		-6.26 [ab] (.205)
KA x FR	-8.49 [a]	-4.16 [bc]		-7.99 [ab]		-6.83 [ab] (.148)
KA x ZR	-14.49 [a]	-6.72 [a]		-8.91 [a]		-9.83 [a] (.018)
ZA x KA	-8.05 [a]	-1.45 [de]		-5.62 [bc]		-5.32 [ab] (.336)
ZR x FR	-8.23 [a]	-4.36 [bc]		-4.64 [cd]		-5.69 [ab] (.279)
ZA x FR	-6.42 [a]	-2.88 [bcd]		-5.70 [bc]		-5.67 [ab] (.281)
ZA x ZR	-3.66 [a]	-1.52 [de]		-3.82 [cd]		-3.47 [abc] (.720)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 37. Plant height SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

	ENVIRONMENTS					
Type of cross	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	-8.88 [a]	-5.07 [a]	-2.53 [ab]	7.07 [a]	N/A	-6.14 [a]
KA x KR	0.45 [ab]	1.27 [abc]	-1.87 [ab]	1.22 [abc]		0.27 [ab] (.115)
KR x FR	23.02 [b]	-1.24 [ab]	-3.52 [a]	3.81 [ab]		2.92 [b] (.029)
ZR x KR	4.92 [ab]	4.92 [bc]	2.15[abc]	6.67 [c]		5.63 [b] (.005)
ZA x KR	3.30 [ab]	0.45 [abc]	3.26[abc]	2.45 [bc]		3.16 [b] (.025)
KA x FR	10.76 [ab]	7.37 [c]	6.69 [c]	5.76 [c]		8.63 [b] (.001)
KA x ZR	-0.46 [ab]	5.71 [bc]	8.23 [c]	4.91 [bc]		5.59 [b] (.006)
ZA x KA	5.01 [ab]	0.81 [abc]	3.09[abc]	4.40 [bc]		2.69 [b] (.033)
ZR x FR	4.44 [ab]	4.89 [bc]	1.61[abc]	6.12 [c]		3.91 [b] (.016)
ZA x FR	-0.36 [ab]	3.38 [bc]	-0.89 [ab]	-0.21 [abc]		1.78 [ab] (.054)
ZA x ZR	7.37 [ab]	5.74 [bc]	4.57 [bc]	3.70 [bc]		4.39 [b] (.012)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 38. Plant height MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	10.67 [a]	6.86 [ab]	6.42 [abc]	3.18 [a]	8.39 [a]	6.94 [a]
KA x KR	16.14 [ab]	5.58 [a]	2.03 [ab]	6.73 [ab]	9.71 [a]	7.97 [ab] (.806)
KR x FR	44.94 [b]	6.11 [ab]	1.59 [a]	2.64 [a]	14.53 [ab]	13.05 [abc] (.153)
ZR x KR	23.51[ab]	15.44 [bcd]	9.19[abcd]	16.05 [bc]	24.66 [c]	17.73 [c] (.014)
ZA x KR	20.05 [ab]	10.79 [abc]	10.58[abcd]	11.09 [abc]	20.06 [bc]	14.50 [abc] (.080)
KA x FR	30.13 [ab]	13.71[abcd]	13.45 [cd]	9.13 [abc]	19.54 [bc]	16.68 [c] (.026)
KA x ZR	14.57 [ab]	16.74 [cd]	17.62 [d]	14.23 [bc]	21.28 [bc]	16.35 [bc] (.031)
ZA x KA	17.30 [ab]	11.62 [abc]	13.16 [cd]	12.05 [abc]	11.29 [a]	12.98[abc] (.158)
ZR x FR	28.48 [ab]	19.32 [cd]	12.91 [cd]	14.26 [bc]	19.62 [bc]	18.59 [c] (.009)
ZA x FR	21.46 [ab]	16.44 [cd]	10.98 [bcd]	8.25 [abc]	21.38 [bc]	15.50 [bc] (.049)
ZA x ZR	22.41 [ab]	23.12 [d]	18.43 [d]	16.82 [c]	25.76 [c]	19.81 [c] (.004)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 39. Panicle exsertion SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	-3.01 [a]	-3.72 [a]	2.51 [ab]	-0.72 [a]	N/A	-2.76 [a]
KA x KR	0.56 [ab]	-0.71 [ab]	4.99 [bcd]	1.03[ab]		0.73 [bcd] (.001)
KR x FR	2.61 [ab]	-1.00 [ab]	8.43 [d]	-1.42 [a]		-0.53 [b] (.024)
ZR x KR	-0.83 [ab]	0.47 [bc]	7.01 [cd]	-0.57 [a]		-0.25 [b] (.012)
ZA x KR	3.13 [ab]	1.27 [bc]	5.05 [bcd]	3.36 [b]		2.26 [de] (.000)
KA x FR	2.34 [ab]	1.31 [bc]	4.71 [bcd]	2.88 [b]		2.18 [cde] (.000)
KA x ZR	2.28 [ab]	3.31 [c]	3.93 [abc]	2.67 [b]		2.84 [e] (.000)
ZA x KA	7.73 [b]	0.62 [bc]	0.06 [a]	-1.87 [a]		0.78 [bcd] (.001)
ZR x FR	1.80 [ab]	1.65 [bc]	4.20[abcd]	0.43[ab]		0.19 [bc] (.004)
ZA x FR	-2.50 [a]	3.51 [c]	5.83 [bcd]	0.55[ab]		1.30[bcde] (.000)
ZA x ZR	0.20 [ab]	1.37 [bc]	4.20 [bcd]	-0.93 [a]		0.58 [bcd] (.001)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 40. Panicle exsertion MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	37.77 [a]	42.87[abc]	-35.24 [a]	31.48 [ab]	-37.36 [a]	20.02 [a]
KA x KR	74.97 [a]	2.78 [a]	-3.51 [a]	25.51 [ab]	52.97[bcd]	27.07 [ab] (.744)
KR x FR	71.61 [a]	9.11 [a]	-11.94 [a]	21.72 [ab]	4.86 [bc]	19.13 [a] (.967)
ZR x KR	43.05 [a]	35.38[abc]	-1.60 [a]	23.68 [ab]	37.92[bcd]	27.72 [ab] (.722)
ZA x KR	92.41 [a]	27.30 [ab]	-0.33 [a]	47.21[abc]	56.88[bcd]	44.51 [ab] (.262)
KA x FR	227.24 [a]	38.87[abc]	39.94 [a]	69.86 [bc]	100.00 [d]	72.09[bcd] (.021)
KA x ZR	163.39 [a]	112.28 [c]	72.12 [a]	70.83 [bc]	231.57 [e]	113.11 [d] (.000)
ZA x KA	192.20 [a]	46.53[abc]	39.92 [a]	0.36 [a]	-0.15 [ab]	49.36[abc] (.181)
ZR x FR	25597.09 [b]	95.72 [bc]	-26.36 [a]	88.67 [c]	70.65 [cd]	91.31 [cd] (.002)
ZA x FR	51.87 [a]	72.13[abc]	97.46 [ab]	39.74[abc]	98.10 [d]	69.17[bcd] (.028)
ZA x ZR	502.50 [a]	113.93 [c]	270.00 [ab]	18.38 [a]	84.15 [d]	96.73 [d] (.001)

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns;¶ numbers in parentheses denote significance level at which within-group crosses differ from other cross combinations (FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 41. Specific combining ability (SCA) values of diallel hybrids for 500-seed weight (gm), based on combined data from five environments- College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-0.3												FR
3	KR	**A3Tx436**	0.1	0.0											KR
4	KR	**A3Tx7000**	-0.3	2.7	0.4										KR
5	ZR	**A3TAM428**	-1.5	0.2	1.0	0.2									ZR
6	ZR	**A3Tx2817**	0.0	0.8	-0.3	0.5	0.8								ZR
7	XA	**ATx642**	1.0	0.5	1.3	-0.9	-1.5	0.3							XA
8	XA	**ATx631**	-1.2	-0.3	1.0	-0.3	0.5	-0.8	1.0						XA
9	KA	**ATx378**	-0.1	-0.2	-0.5	-0.5	0.5	-0.1	1.0	0.6					KA
10	KA	**ATx3197**	0.7	-0.6	-0.2	-0.4	0.3	-0.4	1.5	0.7	1.1				KA
11	ZA	**ATx635**	0.4	0.0	0.2	0.1	0.1	-0.1	1.1	0.7	1.2	0.3			ZA
12	ZA	**ATx623**	-0.3	0.8	-0.9	0.1	-0.2	-1.4	0.6	1.0	0.4	0.7	0.9		ZA

Standard Error = 0.517

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table 42. Simplified SCA table for 500-seed weight (gm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal. Numbers in parentheses denote standard deviation of the averages

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-0.3												FR
3	KR	**A3Tx436**	0.6	(1.4)											KR
4	KR	**A3Tx7000**			0.4										KR
5	ZR	**A3TAM428**	-0.1	(1.0)	0.4	(0.5)									ZR
6	ZR	**A3Tx2817**					0.8								ZR
7	XA	**ATx642**	0.0	(1.0)	0.3	(1.0)	-0.4	(0.9)							XA
8	XA	**ATx631**							1.0						XA
9	KA	**ATx378**	-0.1	(0.5)	-0.4	(0.1)	0.1	(0.4)	0.9	(0.4)					KA
10	KA	**ATx3197**									1.1				KA
11	ZA	**ATx635**	0.2	(0.5)	-0.1	(0.5)	-0.4	(0.7)	0.8	(0.3)	0.7	(0.4)			ZA
12	ZA	**ATx623**											0.9		ZA

Pairwise comparisons

Based on SCA and midparent heterosis, across-group type crosses are compared with each other and against within-group crosses, with all of the latter lumped into one category.

The within-group crosses had consistently and significantly lower SCAs for grain yield than the other cross types, and lower heterosis levels in most cases as well, strengthening the possibility of the groups being mutually heterotic (Tables 33, 34). The KA x FR, ZR, KR hybrids (Kafir females x Feterita-derivative, Zerazera-derivative, and milo (durra)-kafir derivative males) had significantly higher SCA effects in comparison with the within-group crosses, as did the ZA x FR, ZR hybrids (Zerazera-derivative females x Feterita-derivative and Zerazera-derivative males) (Table 33). The lower heterosis estimates of the within-group crosses were, however, statistically significant only at reduced levels of significance (Table 34). Significant differences between the various types of across-group crosses were few and inconsistent.

Comparisons between across-group hybrids (not taking within-group crosses into consideration) revealed highly significant differences in SCA effects between the across-group sterile and fertile hybrids. Similar differences in heterosis, although statistically significant only at lower significance levels, are observed (Table 44). These differences between sterile and fertile across-group hybrids prove that the similar contrast seen in the complete set of hybrids is not solely due to the effect of the within-group crosses.

A similar comparison between sterile hybrids showed quite consistent differences, although significant only at lower significance levels, between the across-group and within-group hybrids, the latter exhibiting lower SCA effects and heterosis (Table 45).

Table 43. Pearson correlation coefficients between Genetic Similarity (GS) of a cross (between parents of the diallel hybrid) and the corresponding Specific Combining Ability (SCA), midparent heterosis (MPH) for 7 traits, and with the trait itself, for the set of 66 diallel hybrids, based on combined data from five environments – College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

	Correlation of Genetic Similarity (GS) with		
Trait	**SCA**	**MPH**	**Trait per se**
Grain yield	-.396**	-.365**	-.322**
Plant height	-.380**	-.320**	-.049
Panicle exsertion	-.417**	-.249*	.131
Panicle number/plot	-.323**	-.349**	-.264*
Days to anthesis	.241*	.119	-.087
500-seed weight	.057	.050	-.031
Panicle length	.268*	-.358**	-.319**

*Significant at the p = 0.05 level (1-tailed)
**Significant at the p = 0.01 level (1-tailed)

Table 44. Mean values of specific combining ability (SCA) and heterosis (for grain yield) for across-group diallel hybrids, contrasting across group fertile hybrids against across group sterile hybrids, with the significance levels associated with the differences (for five individual environments and a combined analysis)

Environments		SCA	Sig.	MPH	Sig.
College Station 2003	Across-group fertile crosses	0.658	.048	69.47	.088
	Across-group sterile crosses	0.004		48.78	
Weslaco 2003	Across-group fertile crosses	0.361	.035	40.72	.208
	Across-group sterile crosses	0.094		34.22	
Halfway 2003	Across-group fertile crosses	0.779	.002	62.44	.161
	Across-group sterile crosses	0.172		50.83	
College Station 2004	Across-group fertile crosses	0.401	.034	68.83	.347
	Across-group sterile crosses	-0.012		56.37	
Halfway 2004	Across-group fertile crosses	N/A	N/A	55.99	.946
	Across-group sterile crosses			55.03	
Combined environments	Across-group fertile crosses	0.547	.004	55.54	.098
	Across-group sterile crosses	0.092		45.08	

SCA = Specific combining ability

MPH = Midparent heterosis

Table 45. Mean values of specific combining ability (SCA) and heterosis (for grain yield) for sterile diallel hybrids, contrasting within-group sterile hybrids against across-group sterile hybrids, with the significance levels associated with the differences (for five individual environments and a combined analysis)

Environments		SCA	Sig.	MPH	Sig.
College Station 2003	Within-group sterile crosses	-0.302	.638	39.99	.627
	Across-group sterile crosses	0.004		48.78	
Weslaco 2003	Within-group sterile crosses	-0.330	.115	20.27	.182
	Across-group sterile crosses	0.094		34.22	
Halfway 2003	Within-group sterile crosses	-0.654	.037	35.25	.279
	Across-group sterile crosses	0.172		50.83	
College Station 2004	Within-group sterile crosses	0.055	.865	53.17	.901
	Across-group sterile crosses	-0.012		56.37	
Halfway 2004	Within-group sterile crosses	N/A	N/A	39.34	.612
	Across-group sterile crosses			55.03	
Combined environments	Within-group sterile crosses	-0.364	.141	32.90	.306
	Across-group sterile crosses	0.092		45.08	

SCA = Specific combining ability

MPH = Midparent heterosis

Correlations between grain yield and other agronomic traits

Seed weight and number of panicles per plot were positively correlated with grain yield in the combined analysis across environments (Table 46). Panicle exsertion and days to anthesis had a significant negative correlation with grain yield. In the analysis for hybrid entries, plant height was significantly and negatively correlated with grain yield.

Correlation of genetic similarity estimates with SCA and heterosis

Genetic similarity estimates were significantly and negatively correlated with yield (-.322**), and with yield GCA (- 0.396**) and midparent heterosis (-0.365**) (Table 43). These levels of correlation, while not high enough to be valuable in parental selection for hybrid breeding or for prediction of hybrid performance, do show a pattern of correspondence between molecular-marker based genetic similarity and heterotic effects for grain yield.

Similar findings of insufficiently high (for hybrid performance prediction) correlation between genetic similarity and heterosis were reported in a study of Australian sorghum hybrids by Jordan et al. (2003) and in rice by Zhang (1993, 1995).

Other researchers have reported little to no correlation between genetic distance and heterozygosity, and have proposed reasons for the lack of correlation, including neutral markers that are unrelated to the trait of interest (Riday et al., 2003). This explanation is in agreement with the conclusions reached by Zhang (1993, 1995), where specific marker heterozygosity (solely considering markers exhibiting significant effects on the traits involved) was highly correlated with heterosis, but general marker heterozygosity (based on all markers used) had a low correlation with phenotypically expressed heterosis.

The only examples of non-significant correlation between genetic similarity estimates and the traits (and their associated SCA and heterosis estimates) were in the case of seed weight, and with days to anthesis (for the trait per se and heterosis), (Table 43).

Table 46. Pearson correlation coefficients among grain yield and agronomic traits based on data from five environments – College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004, presented separately for the set of 12 parental lines, 69 hybrid entries, and for the whole set of 81 entries

Parents

	Panicle length	500-seed weight	Days-to-anthesis	Panicles plot^{-1}	Panicle exsertion	Plant height
500-seed weight	-.030					
Days to anthesis	.230*	.024				
Panicles/plot	-.179*	-.152*	-.460**			
Panicle exsertion	-.170*	-.190*	-.281**	.109		
Plant height	.177*	-.072	-.081	.240**	.364**	
Grain yield	-.129	.390**	-.091	.458**	-.104	.073

Diallel hybrids and hybrid checks

	Panicle length	500-seed weight	Days to anthesis	Panicles/plot	Panicle exsertion	Plant height
500-seed weight	-.235**					
Days to anthesis	.195**	.086*				
Panicles/plot	-.175**	-.100*	-.348**			
Panicle exsertion	-.264**	.020	-.120**	-.030		
Plant height	.292**	-.082*	.050	.088*	.292**	
Grain yield	.064	.317**	-.006	.333**	-.238**	-.100**

Total

	Panicle length	500-seed weight	Days to anthesis	Panicles/plot	Panicle exsertion	Plant height
500-seed weight	-.143**					
Days to anthesis	.160**	-.002				
Panicles/plot	-.155**	-.072*	-.386**			
Panicle exsertion	-.215**	-.009	-.174**	.007		
Plant height	.292**	.018	.071*	.149**	.330*	
Grain yield	.071*	.378**	-.107**	.365**	-.159**	.043

* Correlation significant at the p = 0.05 level (1-tailed)
** Correlation significant at the p = 0.01 level (1-tailed)

Biplot analysis

The biplot is based on grain yield averages over five environments of sixty-six hybrids in a diallel consisting of 12 parents and it provides a graphic representation of the heterotic relationship between the genotypes in the diallel (Fig. 2). The first two principal component axes explain 52.75 % and 15.27 % of the total variation, respectively.

The entries furthest from the origin - RTx430, RTx2737, BTx635, BTx 378, RTx7000, RTx2817 and RTAM428 - form a polygon, constructed so as to contain all entries within its perimeter. The sides of this polygon are bisected, wherever possible, by perpendiculars (A, B, C, and D) drawn from the origin. These perpendiculars divide the graph into sectors, good combinations being between entries and testers within a sector, the sector separation being open to interpretation. The best hybrid combinations are between the vertex entries (the entries at the vertices of the polygon) and testers furthest from the origin in the same sector, although sector boundaries are not rigidly observed, the sectors merely being tools for interpretation. The heterotic relationships discussed earlier (in the section on grain yield SCA and heterosis) are reflected in the biplot, which accurately highlights the best hybrid combinations such as RTAM428 with ATx631, ATx635 and ATx378; RTx430 with ATx631, ATx635 and ATx378; RTx2737 with ATx378 and A3Tx7000; and the hybrids of RTx436 with both ATx3197 and ATx378. It may be noted that one of these most heterotic combinations, of RTx2737 and A3Tx7000, was between R-lines.

This graphical representation of the heterotic relationships, while reflecting the same heterotic combinations observed in the examination of CA and heterosis estimates, does not, however, define distinct heterotic groups.

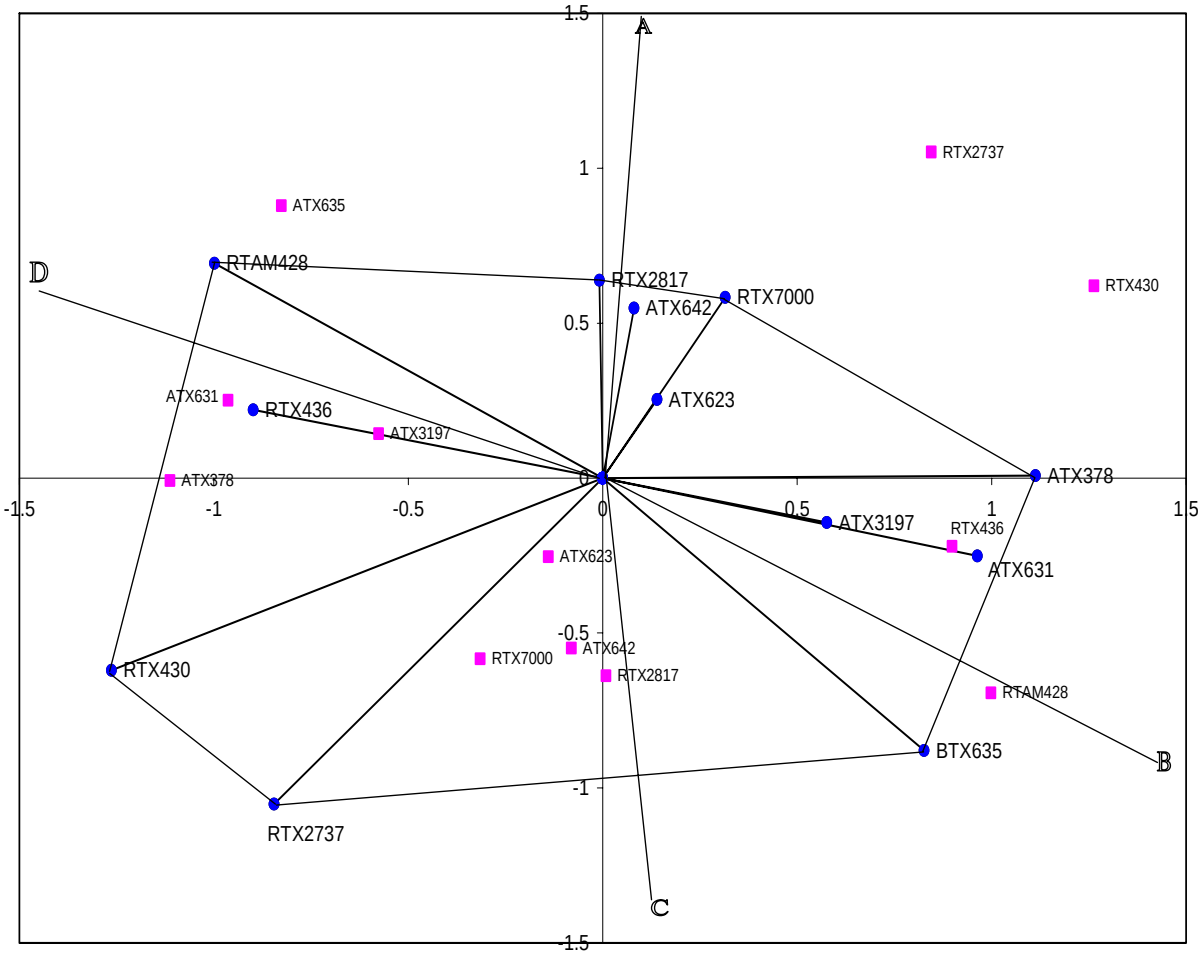

Figure 2. Biplot representation of the relationships between the 12 parental lines in hybrid combination with each other in the diallel (based on grain yield across five environments). Solid blue circles denote entries, solid pink squares denote testers

§ A, B, C and D are perpendiculars drawn from the origin, bisecting the sides of the polygon (formed by connecting the outermost entries), wherever possible
‡ The perpendiculars bisect the graph into sectors, and the best hybrid combinations in each sector are between the entry at the vertex and the tester furthest from the origin in the same sector (e.g. Tx635 x TAM428 in the BC sector)

CHAPTER V

CONCLUSIONS

The objective of this study was to determine whether a heterotic relationship exists between the groups of genotypes observed by cluster analyses in the molecular marker-based diversity study by Menz et al. (2004).

Within-group crosses (hybrids of members of the same group) were numerically inferior in SCA effects and heterosis for grain yield compared to across-group crosses (crosses made between members of different groups). Many of these numerical differences were statistically significant as well, and these trends across environments were consistent in individual environments, and in other traits like plant height and days to anthesis. These results indicate that a heterotic response is detectable across these groups, but they do not clearly prove that all of these groups are distinct heterotic groups.

Hybrids among R-lines and among B-lines, all of which were sterile, were significantly lower in yield compared to fertile hybrids. Since molecular marker data provide no proof of consistent genetic dissimilarity between the two groups (A/B lines and R lines), the yield performance differences (and corresponding heterotic response) are most likely to be the result of concerted breeding efforts of the last fifty years, which have developed lines within the mutually separated groups, thus maximizing the heterotic interactions between them. This possibility is supported by the fact that this trend was much less evident in the R-lines, which, in general, have a wider genetic base than the B-lines, and whose development involves less breeding pressure.

Even though no significant differences existed for grain yield between the crosses among the R-lines (A3 x R hybrids) and those among the A/B lines (A x B hybrids), there

exists a high probability that the heterotic relationships between the inbreds are confounded with the effect of the different cytoplasmic backgrounds (A1, A3) of the various diallel hybrids, previous studies having shown yield reduction effects in A3 genotypes (Moran and Rooney, 2003). One method of addressing the issue would be for further studies to utilize A3 females for all the hybrids in a diallel, thus obtaining a complete set of uniformly-A3 hybrids, and avoiding the confounding effect of non-uniform cytoplasmic background.

The question of whether the poor heterosis observed in the sterile hybrids compared to the fertile hybrids is a result of the effect of the within-group crosses (all of which are sterile) is answered by the comparisons within across-group hybrids (not taking within-group crosses into consideration). These comparisons reveal highly significant differences in SCA effects between the across-group sterile and fertile hybrids. This persistent contrast between sterile and fertile hybrids even in the absence of the yield average-reducing effect of any within-group crosses showed that this difference was not merely a result of the within-group crosses reducing the yield average of the sterile crosses in general. Conversely, a similar difference between within- and across-group sterile crosses showed that the poorer heterosis of within-group crosses was not solely due to their sterility.

Based on the observation of consistently and significantly inferior heterotic expression of within-group crosses in comparison with across-group crosses, and that of significant correlation of genetic similarity estimates with grain yield SCA and heterosis, the grouping system suggested by molecular data seems to reflect a pattern of phenotypically expressed heterotic responses. An examination of the heterotic effects

manifested in individual hybrid combinations reveals a pattern of interactions, which, while broadly in agreement with the hypothesis, also reveals differential responses which make it impossible to define distinct heterotic groups.

Apart from the consistent observations of low heterosis in within-group crosses and sterile hybrids, generalized conclusions regarding the relative superiority of particular inter-group hybrid combinations over others were difficult to draw due to the differential heterotic responses between individual members of groups. Our study was limited in the number of genotypes per group it was feasible to evaluate in five environments, and an illumination of the larger picture of the heterotic relationships hinted at by the molecular marker-based diversity study (Menz et al., 2004) may be made possible by similar field experiments with an expanded range of genotypes.

Although the significant correlations (much higher, in fact, than those observed in numerous similar studies, as mentioned in the Discussion) between genetic similarity and yield heterosis indices were not high enough to be reliably used for parental selection in hybrid breeding, or for prediction of hybrid performance, they do support the hypothesis that the pattern of heterotic relationships suggested by the molecular data represents a system of heterotic groups.

While distinct heterotic groups could not be defined, this proof of the existence of a pattern of heterotic responses across the groups suggests that efforts to clearly define the heterotic groups would be beneficial, allowing breeding efforts to fully realize the apparent latent heterotic potential. However, at the present time, the inability to define distinct groups would suggest the continued use of the B- and R-lines as heterotic groups, until clearer distinctions can be made between the alternate heterotic groups.

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APPENDIX

Table A1. General Combining Ability (GCA) estimates for panicle exsertion (cm) for each parental line in a half diallel in each environment and the combined analysis

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	-3.66	-1.07	-1.37	-3.10	N/A	-2.47
R.TX2737	4.75	5.94	-0.34	3.73		3.64
R.TX436	1.66	0.50	0.99	1.98		1.25
R.TX7000	5.11	2.92	1.17	3.19		3.00
R.TAM428	-3.54	-3.55	-0.04	-2.68		-2.61
R.TX2817	-7.11	-3.40	-1.79	-4.31		-4.06
B.TX642	1.78	2.31	3.47	3.85		3.71
B.TX631	-1.30	-2.77	-0.28	-2.14		-1.97
B.TX635	-4.69	0.50	-1.25	-1.17		-1.50
B.TX378	-0.57	-0.35	-0.52	0.58		-0.65
B.TX3197	5.35	-1.29	1.17	-0.20		1.17
B.TX623	2.21	0.26	-1.19	0.28		0.48
Standard error	2.481	0.848	0.807	0.788		1.502

Table A2. General Combining Ability (GCA) estimates for number of panicles per plot for each parental line in a half diallel in each environment and the combined analysis

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	-6.99	-7.36	1.96	-7.36	N/A	-4.23
R.TX2737	1.77	9.10	14.35	3.69		9.38
R.TX436	8.10	-0.19	-0.49	-6.43		0.06
R.TX7000	8.46	3.51	1.56	5.69		1.46
R.TAM428	-3.04	-9.89	-2.01	-4.66		-6.63
R.TX2817	-7.60	-6.44	-2.44	-2.28		-3.28
B.TX642	-3.28	-0.19	-1.37	-0.52		-1.38
B.TX631	-1.87	-4.17	-10.27	-8.57		-6.80
B.TX635	-6.30	9.24	-1.08	-9.97		-1.70
B.TX378	-2.49	-0.40	-4.56	5.50		0.95
B.TX3197	5.52	1.73	5.49	16.05		7.74
B.TX623	7.74	5.07	-1.13	8.86		4.43
Standard error	5.312	4.683	5.880	5.389		6.039

Table A3. General Combining Ability (GCA) estimates for panicle length (cm) for each parental line in a half diallel in each environment and the combined analysis

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	N/A	2.17	N/A	1.53	N/A	1.84
R.TX2737		0.17		0.08		0.09
R.TX436		1.20		0.56		0.97
R.TX7000		-0.61		-0.77		-0.20
R.TAM428		-0.37		-0.71		-0.85
R.TX2817		0.17		0.93		0.56
B.TX642		-0.80		0.38		-0.47
B.TX631		2.77		2.20		2.26
B.TX635		0.90		0.20		0.23
B.TX378		-3.22		-2.67		-2.68
B.TX3197		-2.85		-2.19		-2.25
B.TX623		0.47		0.44		0.50
Standard error		0.739		0.595		0.647

Table A4. General Combining Ability (GCA) estimates for 500-seed weight (gm) for each parental line in a half diallel in each environment and the combined analysis

Parents	College Station (2003)	Weslaco (2003)	Halfway (2003)	College Station (2004)	Halfway (2004)	Combined locations
R.TX430	1.15	0.55	N/A	1.03	N/A	1.30
R.TX2737	0.98	0.10		0.97		0.35
R.TX436	-1.04	-1.11		-0.47		-1.02
R.TX7000	0.33	1.10		-0.13		-0.07
R.TAM428	-0.65	-0.97		-0.43		-0.68
R.TX2817	-0.74	-1.01		-1.35		-0.85
B.TX642	0.33	-0.03		-1.63		0.00
B.TX631	0.69	0.28		1.19		0.78
B.TX635	-0.23	-0.63		0.14		-0.23
B.TX378	-0.26	1.44		1.16		0.44
B.TX3197	-0.49	0.45		0.28		0.26
B.TX623	-0.06	-0.16		-0.76		-0.28
Standard error	0.319	0.174		0.310		0.380

Table A5. Specific Combining Ability (SCA) values of diallel hybrids for number of panicles per plot, based on combined data from five environments- College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-30.7												FR
3	KR	**A3Tx436**	-9.2	-0.1											KR
4	KR	**A3Tx7000**	-1.5	7.7	6.9										KR
5	ZR	**A3TAM428**	-7.2	0.2	2.8	-4.0									ZR
6	ZR	**A3Tx2817**	14.4	13.8	2.5	3.7	3.8								ZR
7	XA	**ATx642**	2.9	7.4	-2.0	-8.5	24.2	16.6							XA
8	XA	**ATx631**	11.9	-2.5	-8.0	-8.0	12.7	2.6	8.8						XA
9	KA	**ATx378**	15.4	18.5	26.8	-1.2	21.5	-5.2	-1.5	4.9					KA
10	KA	**ATx3197**	15.1	38.1	4.2	-5.9	8.4	-15.8	-14.5	-11.0	-0.4				KA
11	ZA	**ATx635**	-1.8	-0.1	11.7	-6.8	-6.4	3.0	0.7	-15.5	-14.3	-8.0			ZA
12	ZA	**ATx623**	15.5	5.5	-1.8	4.1	7.9	-16.7	1.9	1.9	-7.6	-16.9	10.3		ZA

Standard Error = 8.206

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A6. Simplified SCA table for number ofg panicles per plot, with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-30.7												FR
3	KR	**A3Tx436**	-0.8												KR
4	KR	**A3Tx7000**			6.9										KR
5	ZR	**A3TAM428**	5.3		1.3										ZR
6	ZR	**A3Tx2817**					3.8								ZR
7	XA	**ATx642**	4.9		-6.6		14.0								XA
8	XA	**ATx631**							8.8						XA
9	KA	**ATx378**	21.8		6.0		2.2		-5.5						KA
10	KA	**ATx3197**									-0.4				KA
11	ZA	**ATx635**	4.8		1.8		-3.0		-2.8		-11.7				ZA
12	ZA	**ATx623**											10.3		ZA

Table A7. Specific Combining Ability (SCA) values of diallel hybrids for panicle length (cm), based on combined data from three environments- Weslaco in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	1.45												FR
3	KR	**A3Tx436**	0.56	0.90											KR
4	KR	**A3Tx7000**	-0.25	0.66	0.05										KR
5	ZR	**A3TAM428**	-0.16	0.19	0.43	-0.10									ZR
6	ZR	**A3Tx2817**	-1.00	0.19	0.71	0.75	-0.01								ZR
7	XA	**ATx642**	0.02	0.08	0.89	0.37	-1.24	0.46							XA
8	XA	**ATx631**	-0.17	-1.24	0.70	-1.52	-0.86	0.83	0.17						XA
9	KA	**ATx378**	0.82	-0.81	0.84	1.73	0.41	-2.27	-1.53	-1.30					KA
10	KA	**ATx3197**	0.40	-0.11	0.13	0.74	0.97	-2.70	0.17	1.38	-0.17				KA
11	ZA	**ATx635**	-1.24	-2.02	-0.65	1.65	0.89	3.15	1.64	2.01	2.15	1.45			ZA
12	ZA	**ATx623**	0.19	-1.73	-0.08	-2.01	0.05	1.04	1.08	0.61	0.19	1.74	-0.74		ZA

Standard Error = 0.879

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A8. Simplified SCA table for panicle length (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	1.45												FR
3	KR	**A3Tx436**	0.47												KR
4	KR	**A3Tx7000**			0.05										KR
5	ZR	**A3TAM428**	-0.20		0.45										ZR
6	ZR	**A3Tx2817**					-0.01								ZR
7	XA	**ATx642**	-0.32		0.11		-0.20								XA
8	XA	**ATx631**							0.17						XA
9	KA	**ATx378**	0.07		0.86		-0.90		-0.32						KA
10	KA	**ATx3197**									-0.17				KA
11	ZA	**ATx635**	-1.20		-0.27		1.28		1.33		1.38				ZA
12	ZA	**ATx623**											-0.74		ZA

Table A9. Midparent heterosis values of diallel hybrids for number of panicles per plot, based on combined data from five environments- College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-10.0												FR
3	KR	**A3Tx436**	5.7	22.3											KR
4	KR	**A3Tx7000**	1.2	16.3	10.7										KR
5	ZR	**A3TAM428**	18.2	34.8	32.1	8.8									ZR
6	ZR	**A3Tx2817**	27.4	33.4	17.0	5.5	30.2								ZR
7	XA	**ATx642**	19.0	30.8	15.9	-2.6	59.3	32.5							XA
8	XA	**ATx631**	17.8	10.9	-0.1	-10.4	32.3	7.7	17.4						XA
9	KA	**ATx378**	38.9	48.3	52.5	8.9	64.5	15.8	23.5	19.2					KA
10	KA	**ATx3197**	17.1	42.3	9.4	-8.4	22.1	-10.1	-6.3	-11.1	10.8				KA
11	ZA	**ATx635**	-2.2	6.5	11.9	-13.5	2.8	1.8	2.7	-19.9	-6.4	-12.6			ZA
12	ZA	**ATx623**	20.9	18.4	6.9	1.4	25.7	-9.0	10.9	2.1	7.2	-13.7	3.6		ZA

Standard Error = 6.825

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A10. Simplified midparent heterosis table for number of panicles per plot, with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	-10.0												FR
3	KR	**A3Tx436**	11.4												KR
4	KR	**A3Tx7000**			10.7										KR
5	ZR	**A3TAM428**	28.4		15.8										ZR
6	ZR	**A3Tx2817**					30.2								ZR
7	XA	**ATx642**	19.6		0.7		33.0								XA
8	XA	**ATx631**							17.4						XA
9	KA	**ATx378**	36.6		15.6		23.1		6.3						KA
10	KA	**ATx3197**									10.8				KA
11	ZA	**ATx635**	10.9		1.7		5.3		-1.1		-6.4				ZA
12	ZA	**ATx623**											3.6		ZA

Table A11. Midparent heterosis values of diallel hybrids for panicle length (cm), based on combined data from three environments-Weslaco in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	3.4												FR
3	KR	**A3Tx436**	6.6	5.3											KR
4	KR	**A3Tx7000**	1.6	2.2	6.7										KR
5	ZR	**A3TAM428**	0.5	-1.1	6.7	2.3									ZR
6	ZR	**A3Tx2817**	-2.0	-0.5	8.0	6.0	1.7								ZR
7	XA	**ATx642**	2.6	0.0	10.1	5.7	-2.3	5.0							XA
8	XA	**ATx631**	0.5	-5.8	7.0	-3.1	-2.1	4.4	3.1						XA
9	KA	**ATx378**	3.9	-5.8	8.4	9.9	2.5	1.8	-4.4	-4.4					KA
10	KA	**ATx3197**	6.3	1.2	9.9	10.1	9.6	6.1	7.7	10.1	4.2				KA
11	ZA	**ATx635**	3.8	-2.2	10.5	17.9	13.3	22.3	18.1	16.0	19.5	21.3			ZA
12	ZA	**ATx623**	1.5	-8.2	4.3	-5.4	1.1	5.2	6.6	2.9	1.2	12.0	5.7		ZA

Standard Error = 4.935

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A12. Simplified midparent heterosis table for panicle length (cm), with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	3.4												FR
3	KR	**A3Tx436**	3.9												KR
4	KR	**A3Tx7000**			6.7										KR
5	ZR	**A3TAM428**	-0.8		5.8										ZR
6	ZR	**A3Tx2817**					1.7								ZR
7	XA	**ATx642**	-0.7		4.9		1.3								XA
8	XA	**ATx631**							3.1						XA
9	KA	**ATx378**	1.4		9.6		5.0		2.3						KA
10	KA	**ATx3197**									4.2				KA
11	ZA	**ATx635**	-1.3		6.8		10.5		10.9		13.5				ZA
12	ZA	**ATx623**											5.7		ZA

Table A13. Midparent heterosis values of diallel hybrids for 500-seed weight (gm), based on combined data from five environments-College Station, Weslaco and Halfway in 2003, and College Station and Halfway in 2004

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	1.3												FR
3	KR	**A3Tx436**	1.6	12.1											KR
4	KR	**A3Tx7000**	-2.3	30.3	10.3										KR
5	ZR	**A3TAM428**	-12.4	9.3	13.1	4.9									ZR
6	ZR	**A3Tx2817**	-4.0	12.1	0.5	5.5	5.0								ZR
7	XA	**ATx642**	13.8	23.3	28.2	7.7	0.6	12.4							XA
8	XA	**ATx631**	-5.9	9.8	17.1	5.8	8.9	-2.2	23.9						XA
9	KA	**ATx378**	1.8	11.7	6.9	5.9	10.5	4.3	26.6	15.0					KA
10	KA	**ATx3197**	7.4	9.8	10.0	6.7	9.9	2.4	31.2	16.6	21.6				KA
11	ZA	**ATx635**	8.0	17.4	17.0	14.1	11.9	7.9	32.9	20.0	26.3	20.4			ZA
12	ZA	**ATx623**	-1.8	16.1	-0.2	6.5	1.8	-8.8	19.7	15.0	12.7	15.9	21.0		ZA

Standard Error = 13.988

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A14. Simplified midparent heterosis table for 500-seed weight, with averages of the four hybrids comprising each cross-combination type provided in each shaded/unshaded block, and within-group crosses in the diagonal

			1 FR **RTx430**	2 FR **RTx2737**	3 KR **RTx436**	4 KR **RTx7000**	5 ZR **RTAM428**	6 ZR **RTx2817**	7 XA **BTx642**	8 XA **BTx631**	9 KA **BTx378**	10 KA **BTx3197**	11 ZA **BTx635**	12 ZA **BTx623**	
1	FR	**A3Tx430**													FR
2	FR	**A3Tx2737**	1.3												FR
3	KR	**A3Tx436**	10.4												KR
4	KR	**A3Tx7000**			10.3										KR
5	ZR	**A3TAM428**	1.2		6.0										ZR
6	ZR	**A3Tx2817**					5.0								ZR
7	XA	**ATx642**	10.3		14.7		4.9								XA
8	XA	**ATx631**							23.9						XA
9	KA	**ATx378**	7.7		7.4		6.8		22.3						KA
10	KA	**ATx3197**									21.6				KA
11	ZA	**ATx635**	9.9		9.4		3.2		21.9		18.8				ZA
12	ZA	**ATx623**											21.0		ZA

Table A15. Panicle number per plot SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	-5.77 [a]	-9.21 [a]	-10.19 [a]	1.74 [ab]	N/A	-2.03 [ab]
KA x KR	0.77 [a]	2.43 [ab]	14.14 [c]	14.54 [bc]		5.99 [bc]
KR x FR	13.39 [a]	-2.28 [a]	-4.55 [ab]	-1.77 [ab]		-0.77 [ab]
ZR x KR	1.68 [a]	0.46 [a]	-7.50 [ab]	-3.55 [ab]		1.27 [ab]
ZA x KR	4.47 [a]	4.85 [ab]	7.38 [bc]	0.70 [ab]		1.79 [ab]
KA x FR	22.41 [a]	23.64 [b]	6.86[abc]	28.50 [c]		21.76 [c]
KA x ZR	4.83 [a]	-0.87 [a]	0.07[abc]	-1.94 [ab]		2.23 [ab]
ZA x KA	-8.26 [a]	-11.40 [a]	-4.72 [ab]	-18.44 [a]		-11.71 [a]
ZR x FR	8.49 [a]	4.21 [ab]	3.05[abc]	5.17 [b]		5.33 [b]
ZA x FR	-3.22 [a]	7.98 [ab]	9.59 [bc]	6.67 [bc]		4.78 [b]
ZA x ZR	4.99 [a]	-1.07 [a]	-1.53[abc]	-3.86 [ab]		-3.04 [ab]

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A16. Panicle number per plot MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	30.01 [a]	-0.88 [a]	-4.57 [ab]	15.47[abc]	25.66[abcd]	9.07 [abc]
KA x KR	46.49[ab]	1.34 [ab]	17.77 [b]	28.94 [bc]	3.78 [abc]	15.63[abcd]
KR x FR	69.19[ab]	4.57 [ab]	-1.93 [ab]	25.92 [bc]	2.02 [abc]	11.37 [abc]
ZR x KR	42.53 [a]	6.75 [ab]	-6.52 [a]	8.49[abc]	48.16 [d]	15.84[abcd]
ZA x KR	13.45 [a]	2.13 [ab]	9.48 [ab]	-2.68 [ab]	-6.11 [ab]	1.67 [ab]
KA x FR	152.27 [b]	34.24 [c]	11.94 [ab]	63.76 [d]	19.62[abcd]	36.64 [d]
KA x ZR	105.55[ab]	12.98[abc]	6.24 [ab]	14.48[abc]	41.54 [cd]	23.07 [bcd]
ZA x KA	10.43 [a]	-7.67 [a]	4.27 [ab]	-13.47 [a]	-12.75 [a]	-6.39 [a]
ZR x FR	97.12[ab]	25.93 [bc]	4.45 [ab]	37.03 [cd]	32.66 [bcd]	28.43 [cd]
ZA x FR	13.86 [a]	17.49[abc]	12.72 [ab]	18.09[abc]	0.90 [abc]	10.91 [abc]
ZA x ZR	26.42 [a]	8.42[abc]	2.93 [ab]	-6.60 [a]	20.48[abcd]	5.32 [abc]

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A17. Panicle length SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	N/A	0.89 [bc]	N/A	-0.74 [ab]	N/A	0.12[abc]
KA x KR		1.25 [bc]		0.39[abc]		0.86 [bc]
KR x FR		-0.20[abc]		0.54[abc]		0.47[abc]
ZR x KR		0.64 [bc]		0.81 [bc]		0.45[abc]
ZA x KR		-0.35[abc]		-0.88 [ab]		-0.27 [ab]
KA x FR		0.80 [bc]		-0.52 [ab]		0.07[abc]
KA x ZR		-2.17 [a]		0.60[abc]		-0.90 [a]
ZA x KA		0.86 [bc]		1.66 [c]		1.38 [c]
ZR x FR		-1.29 [ab]		0.11[abc]		-0.20 [ab]
ZA x FR		-1.44 [ab]		-0.94 [a]		-1.20 [a]
ZA x ZR		1.73 [c]		1.23 [c]		1.28 [c]

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(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A18. Panicle length MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	N/A	6.29 cd	N/A	1.48abc	5.88abc	4.32 abc
KA x KR		10.25 cd		9.21bcd	9.52 bc	9.58 bcd
KR x FR		0.01abcd		2.32abc	9.41 bc	3.89 abc
ZR x KR		3.47abcd		9.90 cd	4.16abc	5.77abcd
ZA x KR		5.67 bcd		2.72abc	12.44 bc	6.79abcd
KA x FR		3.75abcd		-1.50 ab	2.46 ab	1.39 ab
KA x ZR		-9.23 a		9.98 cd	-5.20 a	-0.56 a
ZA x KA		11.27 d		13.82 d	15.39 c	13.51 d
ZR x FR		-7.09 ab		0.89abc	3.98abc	-0.77 a
ZA x FR		-2.63 abc		-3.57 a	2.76 ab	-1.31 a
ZA x ZR		10.42 cd		10.66 cd	12.92 bc	10.47 cd

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A19. 500-seed weight SCA (Specific Combining Ability) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	0.63 [ab]	0.03 [a]	N/A	0.22 [ab]	N/A	0.57 [b]
KA x KR	-0.19 [a]	0.40 [a]		0.02 [ab]		-0.40 [a]
KR x FR	2.88 [b]	-0.19 [a]		0.44 [ab]		0.64 [b]
ZR x KR	-0.60 [a]	0.09 [a]		0.34 [ab]		0.36 [ab]
ZA x KR	-0.91 [a]	0.30 [a]		0.54 [ab]		-0.14 [ab]
KA x FR	-0.15 [a]	0.19 [a]		-0.04 [ab]		-0.07 [ab]
KA x ZR	-0.33 [a]	0.69 [a]		1.21 [b]		0.06 [ab]
ZA x KA	0.95 [ab]	0.34 [a]		-0.50 [a]		0.68 [b]
ZR x FR	0.05 [a]	0.60 [a]		0.30 [ab]		-0.13 [ab]
ZA x FR	-0.24 [a]	0.20 [a]		0.91 [b]		0.22 [ab]
ZA x ZR	0.09 [a]	-0.31 [a]		-0.44 [a]		-0.39 [a]

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

Table A20. 500-seed weight MPH (midparent heterosis) averages of potential heterotic groups, with all within-group crosses considered as one category, for five individual environments and a combined analysis

Type of Cross	ENVIRONMENTS					
	College Station 2003	Weslaco 2003	Halfway 2003	College Station 2004	Halfway 2004	Combined environments
Combined (within-group crosses)	14.15 [ab]	9.48 [a]	N/A	19.62[a]	15.97 [b]	11.83 [ab]
KA x KR	12.25 [ab]	13.26 [a]		16.07[a]	6.21 [ab]	7.38 [ab]
KR x FR	3.97 [b]	5.20 [a]		19.87[a]	2.80 [ab]	10.41 [ab]
ZR x KR	1.99 [a]	6.97 [a]		20.41[a]	2.41 [ab]	6.01 [a]
ZA x KR	7.10 [a]	10.30 [a]		25.92[a]	5.00 [ab]	9.36 [ab]
KA x FR	10.98 [a]	12.62 [a]		13.14[a]	12.56 [b]	7.69 [ab]
KA x ZR	2.29 [a]	17.87 [a]		26.15[a]	4.32 [ab]	6.76 [a]
ZA x KA	18.96 [ab]	15.61 [a]		13.24[a]	33.52 [c]	18.83 [b]
ZR x FR	5.92 [a]	14.07 [a]		18.19[a]	-3.39 [a]	1.24 [a]
ZA x FR	10.52 [a]	11.42 [a]		25.97[a]	6.31 [ab]	9.94 [ab]
ZA x ZR	5.59 [a]	7.54 [a]		14.21[a]	1.00 [ab]	3.20 [a]

§ Values followed by the same letter are not significantly different from each other at the 0.05 level (LSD) – comparisons are made within columns

(FR = Feterita derivative males, KR = Milo(durra)-kafir derivative males, ZR = Zerazera derivative males
XA = Unique/nonconforming females, KA = Kafir females, ZA = Zerazera derivative females)

VITA

Name:	Krishnamoorthy Gabriel
Place and date of birth:	New Delhi, 1977
Permanent address:	45-B, D.D.A. Flats, Masjid Moth, Phase-I, New Delhi – 110048. India
Email address:	kgabk@yahoo.co.in
Education:	B.Sc (Ag), Acharya N.G. Ranga Agricultural University, 1999 M.Sc (Ag), Plant Breeding and Genetics, Maharana Pratap University of Agriculture and Technology, 2001 Ph.D, Plant Breeding, Texas A&M University, 2005