



Figure 1: Tx3362 sorghum panicles—an example of the black pericarp phenotype.

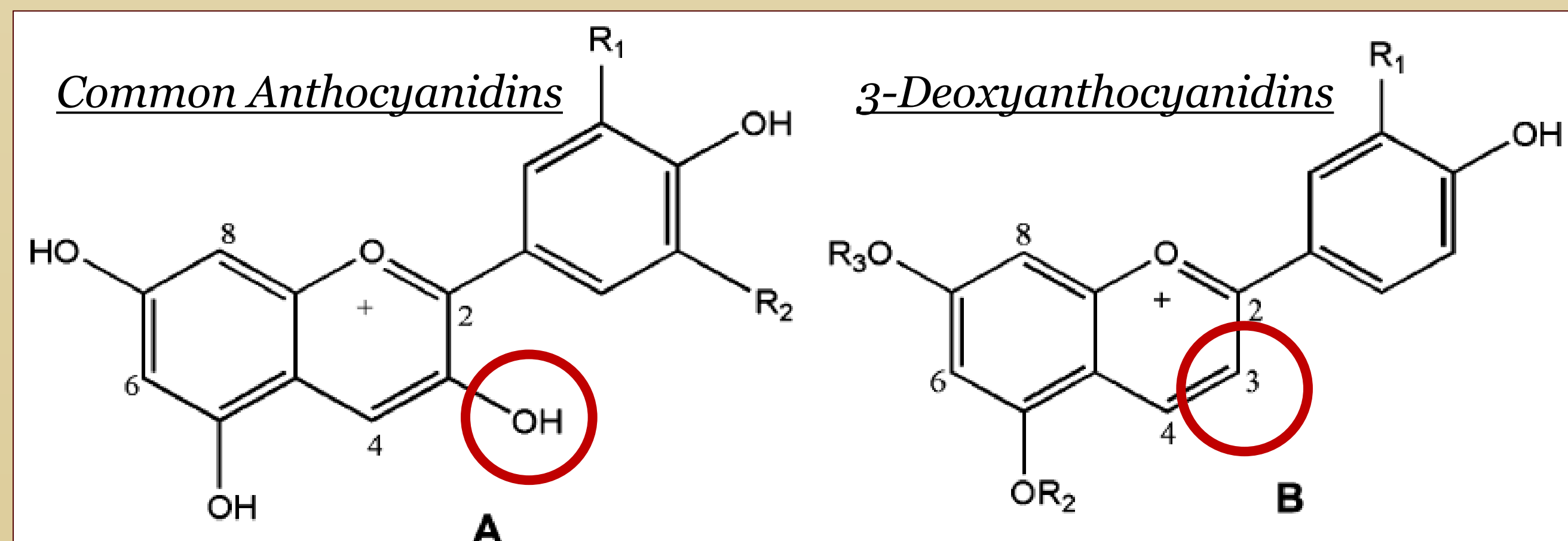


Figure 2: Comparison of common anthocyanidin molecules (A) to 3-Deoxyanthocyanidins (B). 3-DOA molecules lack a hydroxyl molecule at the 3' Carbon (Awika et al., 2004).

INTRODUCTION

- Sorghum has great potential to be specifically bred to produce high levels of different phenols (Dykes and Rooney, 2006).
- One type of phenolic compounds is anthocyanins, which are highly distributed throughout the plant kingdom. The predominant anthocyanins in sorghum are 3-deoxyanthocyanidins (3-DOA) (Awika et al., 2004a).
- Since black sorghum has unique processing properties, there is interest in adding sorghum bran to food products both as a concentrated antioxidant source and natural food colorant (Awika et al., 2004b).
- Epicarp color is determined by the *R* and *Y* genes which interact epistatically to produce red (*R_Y_*), white (*R_yy* or *rryy*), or yellow (*rrY_*) colors (Rooney, 2000).
- 'Black sorghum' is genetically red [*R_Y_*] as all *F*₁ progeny have a red phenotype. The black color must be caused by additional genetic factors which are not known (Rooney, et al. 2013).

OBJECTIVES

- Estimate the relative genetic effects (additive, dominant and epistatic) controlling the black pericarp trait using generation means.
- Determine the heritability of the black pericarp trait using defined generations.

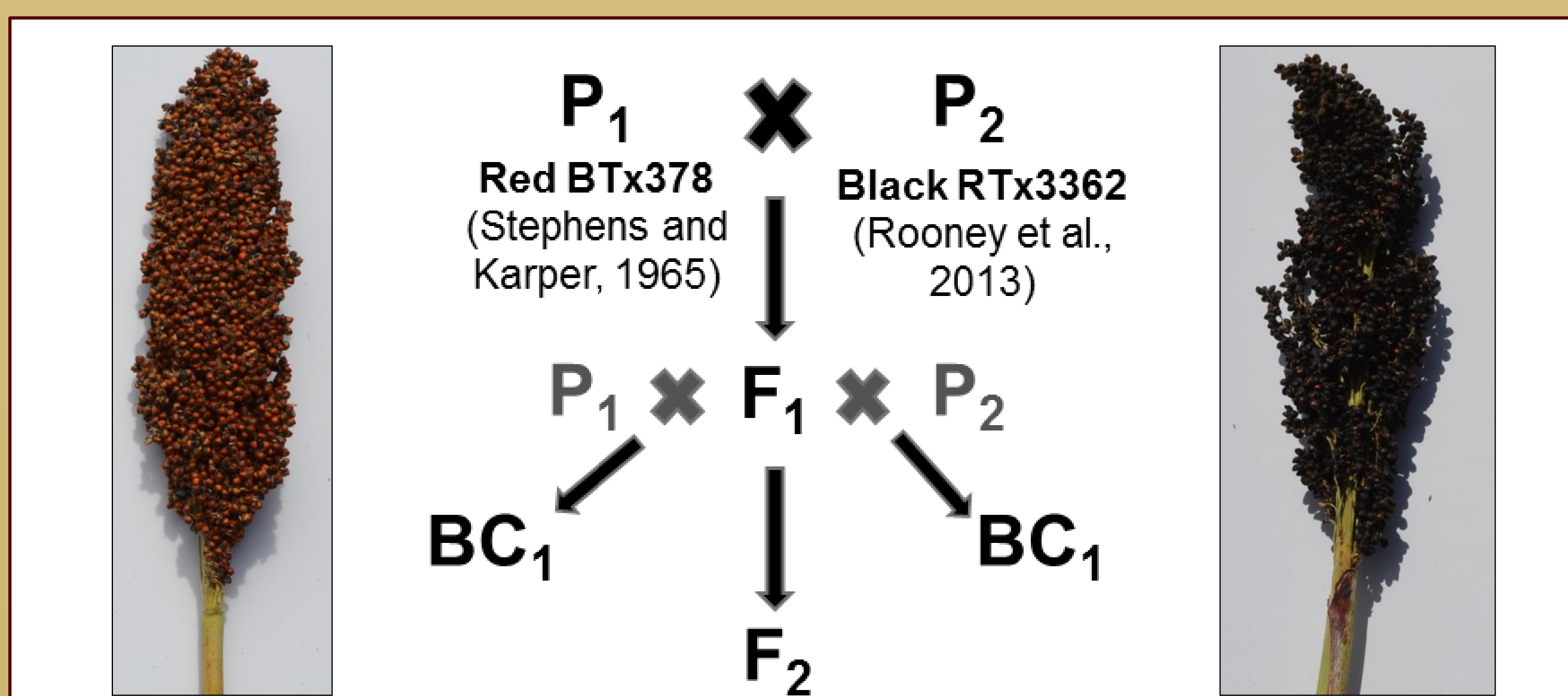


Figure 3: Comparison of divergent parents, BTx378 and RTx3362, and diagram of family structure used in the generation means analysis.

METHODS

- A generation means analysis (GMA) (Mather and Jinks, 1971) was conducted to determine the significance of different genetic effects on the inheritance of black pericarp.
- The experiment was planted in three irrigated locations in Texas in 2013—Weslaco, College Station, and Halfway.
- Whole panicles from individual plants were visually phenotyped on a 1-5 color scale; 1 representing red and 5 representing black.
- Further color measurement was quantified using a CR-410 Colorimeter (Konica Minolta Sensing Americas, Inc.; Ramsey, NJ). Measurements are expressed in accordance with the Commission Internationale de l'Eclairage (2004) as *L*^{*}, *a*^{*}, *b*^{*} values. *L*^{*} is a lightness value (0 = black, 100 = white); *a*^{*} indicates green or red (-*a*^{*} = greenness, +*a*^{*} = redness); *b*^{*} indicates blue or yellow (-*b*^{*} = blueness, +*b*^{*} = yellowness).
- A joint scaling test was performed on a three-parameter model in order to estimate midparent [*m*], additive effects [*a*], and dominance effects [*d*] with the genetic value of the *i*th generation being $\mu_i = m + [a]x_{i1} + [d]x_{i2}$ (Kearsey and Pooni, 1996).
- Lack of fit of the three-parameter model indicates the existence of epistatic effects, thus a six-parameter model was employed to estimate epistatic effects, including additive x additive gene interaction [*aa*], dominance x dominance interaction [*dd*], and additive x dominance interaction [*ad*], written as $\mu_i = m + [a]x_{i1} + [d]x_{i2} + [aa]x_{i1}^2 + [dd]x_{i2}^2 + [ad]x_{i1}x_{i2}$ (Kearsey and Pooni, 1996).
- Broad sense heritability is the ratio between total genetic variation to total phenotypic variation and was estimated as $H^2(F_2) = \frac{V_G}{(V_G + V_E)}$ (Fehr, 1987).

RESULTS

Figure 4. Mean and standard error (SE) of visual score, *L*^{*}, *a*^{*}, and *b*^{*} values in parents, *F*₁, *F*₂, *BC*₁*P*₁, and *BC*₁*P*₂ generations grown in three environments in Texas in 2013.

Location	Generation	N	Means ± SE			
			Visual score	<i>L</i> [*]	<i>a</i> [*]	<i>b</i> [*]
College Station	P1	25	1.00 ± 0.00	50.45 ± 0.44	13.88 ± 0.15	25.53 ± 0.21
	P2	25	5.00 ± 0.00	28.95 ± 0.19	5.46 ± 0.18	4.16 ± 0.24
	F1	25	2.00 ± 0.00	40.23 ± 0.48	14.57 ± 0.17	19.89 ± 0.35
	BC1P1	75	1.24 ± 0.05	42.99 ± 0.36	16.25 ± 0.15	22.42 ± 0.28
	BC1P2	75	2.25 ± 0.07	36.11 ± 0.34	13.11 ± 0.18	14.17 ± 0.36
	F2	150	1.75 ± 0.05	42.17 ± 0.34	14.02 ± 0.12	20.50 ± 0.28
Halfway	P1	25	1.00 ± 0.00	54.91 ± 0.29	14.98 ± 0.16	29.59 ± 0.16
	P2	25	5.00 ± 0.00	32.56 ± 0.44	7.89 ± 0.22	9.65 ± 0.50
	F1	25	2.00 ± 0.00	43.42 ± 0.29	15.43 ± 0.15	23.96 ± 0.23
	BC1P1	75	1.23 ± 0.05	47.83 ± 0.52	15.34 ± 0.15	26.83 ± 0.32
	BC1P2	75	2.13 ± 0.20	42.53 ± 0.46	14.77 ± 0.16	21.46 ± 0.40
	F2	150	1.55 ± 0.12	45.51 ± 0.32	14.45 ± 0.13	23.99 ± 0.22
Weslaco	P1	50	1.00 ± 0.00	46.43 ± 0.23	15.88 ± 0.11	25.25 ± 0.21
	P2	50	5.00 ± 0.00	30.03 ± 0.23	6.85 ± 0.15	6.71 ± 0.31
	F1	49	2.00 ± 0.00	36.44 ± 0.15	14.49 ± 0.13	17.17 ± 0.15
	BC1P1	150	1.39 ± 0.05	40.43 ± 0.30	15.76 ± 0.11	21.05 ± 0.26
	BC1P2	150	2.93 ± 0.10	35.63 ± 0.17	12.16 ± 0.12	13.71 ± 0.19
	F2	299	2.05 ± 0.06	38.39 ± 0.20	14.32 ± 0.09	18.06 ± 0.20

Figure 5. Broad (*H*²) sense heritability estimates of the black pericarp trait in sorghum. The estimates were made using generation means analysis of generations from the cross ATx378 x RTx3362, grown in College Station, Halfway, and Weslaco, Texas in 2013, and evaluated by visual score rating, *L*^{*}, *a*^{*}, and *b*^{*} values.

Location	Broad (<i>H</i> ²) sense heritability estimates			
	Visual Score	<i>L</i> [*]	<i>a</i> [*]	<i>b</i> [*]
College Station	1.00	0.88	0.71	0.90
Halfway	1.00	0.79	0.63	0.72
Weslaco	1.00	0.78	0.61	0.72

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RESULTS (CONT'D.)

Figure 6: Estimates of mid-parent [*m*], additive [*a*], dominance [*d*] and epistatic effects [*a x a*, *a x d*, *d x d*] (and their standard errors) from the joint scaling test for visual score, *L*^{*}, *a*^{*}, and *b*^{*} values in parents (*P*₁ and *P*₂) and their *F*₁, *F*₂, *BC*₁*P*₁, and *BC*₁*P*₂ crosses grown in College Station (CS), Halfway (HW), and Weslaco, (WE) Texas in 2013.

Trait	Model ^a	Environment			
		CS	HW	WE	
Visual score	Three parameter	843.24**	746.45**	194.93**	
	χ^2				
	Six parameter				
	<i>m</i>	3.03 ± 0.27**	2.47 ± 0.63**	2.58 ± 0.32**	
	<i>a</i>	2.00 ± 0.00**	2.00 ± 0.00**	1.99 ± 0.01**	
	<i>d</i>	-4.06 ± 0.66**	-3.21 ± 1.57	-1.53 ± 0.81	
	<i>a x a</i>	-0.03 ± 0.27	0.53 ± 0.63**	0.43 ± 0.32	
	<i>a x d</i>	-1.97 ± 0.17**	-2.18 ± 0.42**	-0.91 ± 0.22**	
	<i>d x d</i>	3.03 ± 0.40**	2.74 ± 0.97**	0.95 ± 0.50	
	<i>L</i> [*]	Three parameter	92.99**	95.77**	144.03**
		χ^2			
		Six parameter			
<i>m</i>		50.18 ± 1.69**	45.06 ± 1.91**	39.67 ± 1.07**	
<i>a</i>		10.75 ± 0.24**	11.18 ± 0.27**	8.20 ± 0.16**	
<i>d</i>		-22.09 ± 4.09**	3.43 ± 4.96	-1.87 ± 2.66	
<i>a x a</i>		-10.48 ± 1.67**	-1.33 ± 1.89	-1.44 ± 1.05	
<i>a x d</i>		-7.75 ± 1.09**	-11.76 ± 1.48**	-8.79 ± 0.76**	
<i>d x d</i>		12.15 ± 2.61**	-5.08 ± 3.15	-1.36 ± 1.66	
<i>a</i> [*]		Three parameter	306.88**	223.93**	165.20**
		χ^2			
		Six parameter			
	<i>m</i>	7.03 ± 0.68**	9.03 ± 0.68**	12.79 ± 0.49**	
	<i>a</i>	4.21 ± 0.12**	3.54 ± 0.14**	4.52 ± 0.09**	
	<i>d</i>	20.43 ± 1.73**	15.30 ± 1.72**	4.42 ± 1.25**	
	<i>a x a</i>	2.64 ± 0.67**	2.40 ± 0.67**	-1.42 ± 0.48**	
	<i>a x d</i>	-2.14 ± 0.51**	-5.94 ± 0.52**	-1.83 ± 0.38**	
	<i>d x d</i>	-12.89 ± 1.12**	-8.90 ± 1.09**	-2.71 ± 0.82**	
	<i>b</i> [*]	Three parameter	110.12**	117.80**	70.82**
		χ^2			
		Six parameter			
<i>m</i>		23.69 ± 1.46**	19.00 ± 1.37**	18.68 ± 1.04**	
<i>a</i>		10.68 ± 0.16**	9.97 ± 0.26**	9.27 ± 0.19**	
<i>d</i>		-8.93 ± 3.59**	14.98 ± 3.63**	-0.98 ± 2.57	
<i>a x a</i>		-8.85 ± 1.45**	0.62 ± 1.35	-2.69 ± 1.02**	
<i>a x d</i>		-4.87 ± 0.96**	-9.21 ± 1.15**	-3.86 ± 0.75**	
<i>d x d</i>		5.13 ± 2.27**	-10.02 ± 2.34**	-0.52 ± 1.60	

*, ** indicate terms are significant at 5% and 1% levels of probability, respectively.
^a*m* = mid-parent effect, *a* = additive effect, *d* = dominance effect, *a x a* = additive x additive effect, *a x d* = additive x dominance effect, and *d x d* = dominance x dominance effect.

DISCUSSION & CONCLUSIONS

- In all traits (visual score, *L*^{*}, *a*^{*}, *b*^{*}) and across all environments (College Station, Weslaco, Halfway), the three-parameter model was not sufficient to explain inheritance. Therefore, the six parameter model was employed due to the presence of significant epistatic interactions.
- Additive and additive x dominance genetic effects were consistently detected for each trait across all environments.
- Effects due to dominance, additive x additive, and dominance x dominance interactions were variable across traits and environments.
- Visual scores, *L*^{*}, *a*^{*} and *b*^{*} ratings are highly heritable in each environment.
- The creation of high yielding hybrids with elite agronomic traits and high levels of phenolic compounds should be possible through recurrent selection or backcross breeding methods.

FUTURE RESEARCH

- Estimate the relative genetic effects (additive, dominant and epistatic) controlling the black pericarp trait using generation means from a cross between white and black pericarp sorghum parental lines.
- Combining *L*^{*}, *a*^{*}, and *b*^{*} values as a single, whole picture estimate of grain pericarp color.
- Analysis of samples via near-infrared spectroscopy (NIR) to estimate the relative genetic effects (additive, dominant and epistatic), as well as the heritability estimate and minimum number of genes controlling the concentration of beneficial phenolic compounds.
- Genetic dissection of black pericarp trait through QTL analysis.