

# Diversity Breeding within the Texas A&M Sorghum Breeding Program

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TEXAS A&M  
**AGRILIFE**  
RESEARCH

# Generating Selectable Variation - SC

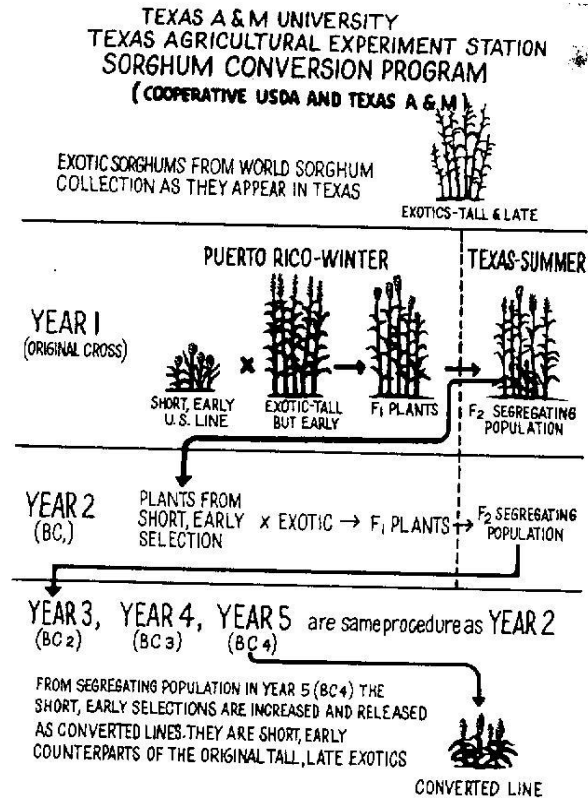
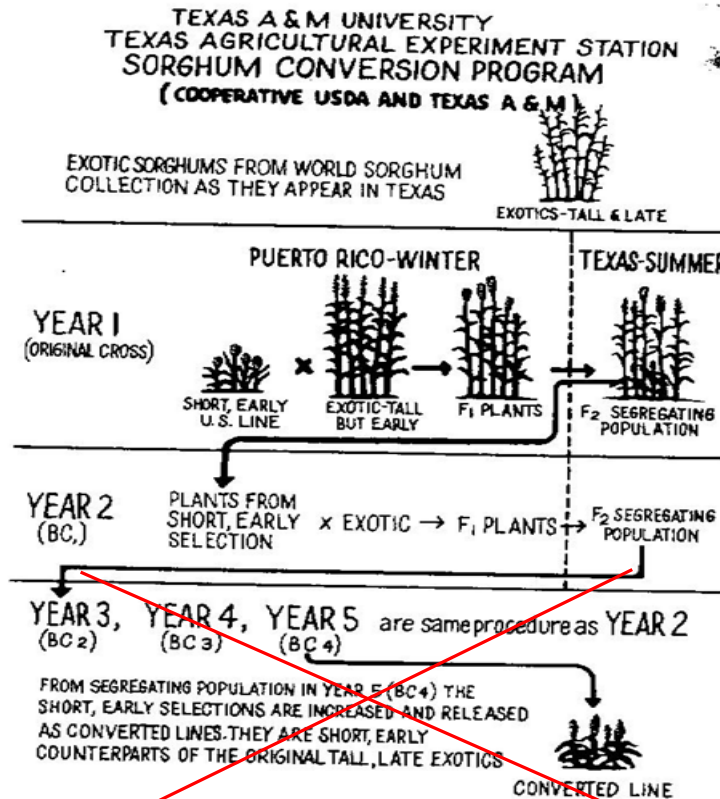


Figure 1. Procedure used in converting exotic varieties to short early types.

# TAES—USDA Sorghum Conversion Program

- 1963-2003
- ~700 were fully converted
- ~ 30-50 converted lines critical to sorghum production worldwide
- SC23
- SC33
- SC35
- SC56
- SC76
- SC77
- SC103
- SC108
- SC110
- SC120
- SC155
- SC175
- SC265
- SC303
- SC326
- SC372
- SC414
- SC599
- SC650
- SC748
- SC1079

# Reinstated Sorghum Conversion (RSC)



Markers

- F<sub>3</sub>
- Release

Markers

- BC<sub>1</sub> F<sub>2</sub>:3
- Release

- High Exotic Genome
- Medium Exotic Genome
- Low Exotic Genome
- High Exotic Genome
- Medium Exotic Genome
- Low Exotic Genome

Figure 1. Procedure used in converting exotic varieties to short early types.

# Reinstated Sorghum Conversion (RSC) Program

- 2009-2015
  - 136 unadapted “partially” converted
  - Released early generation material ( $F_{2:4}$  &  $BC_1F_2$ )
  - Partially converted lines of potential value to forage and grain production
- **RSC08**
  - **RSC17**
  - **RSC22**
  - RSC35
  - **RSC37**
  - RSC40
  - RSC53
  - RSC62
  - RSC66
  - RSC68
  - **RSC73**
  - RSC74
  - **RSC76**
  - RSC77
  - RSC93
  - RSC94
  - RSC105
  - RSC111
  - RSC112
  - **RSC114**
  - RSC116
  - RSC119
  - RSC124
  - RSC130
  - RSC132
  - RSC133
  - **RSC135**
  - RSC124

# Objectives

- ⊙ Relationship between % exotic genome and agronomic performance
- ⊙ Performance of partially converted lines across testers



# RSC Marker-assisted Breeding Scheme

- Genotype By Sequencing
  - (GBS), ~2,000 SNPs spanning 10 chromosomes
- Each line testcrossed to three testers

% Exotic Genome Recovered (% Ex.Gen.)				
Population	# Lines	Low	Medium	High
RSC 08	2	0.24	0.30	0.33
RSC 17	2	0.32	0.35	0.40
RSC 22	2	0.28	0.33	0.37
RSC 37	2	0.26	0.28	0.34
RSC 73	2	0.33	0.38	0.49
RSC 76	2	0.31	0.46	0.53
RSC 114	2	0.22	0.28	0.32
RSC 135	2	0.26	0.32	0.35

# Materials & Methods - Genotypes

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RSC Population	Country of Origin	Race	Fert. R.x.
8	Ethiopia	Durra	R
17	Mali	Durra	R
22	USA	Caudatum	B
37	Sudan	Caudatum	R
73	Sudan	Caudatum	R
76	Sudan	Caudatum-Durra	R
114	Ethiopia	Durra	R
135	Ethiopia	Durra	R

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Tester	Height/Maturity	Zone	
Tx436	3-dwf/medium	Temp/Tropical	R
Tx2928	3-dwf/early	Temp. Adapt.	B
Tx645	3-dwf/med-late	Sub.Tropical	B

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# Materials & Methods (2015)

Test	Num. Plots	Reps	YD (t/ha)	Height (cm)	DY
RSC022	72	4	4.24	73	66
RSC135	72	4	4.54	64	68
RSC114	36	2	5.01	71	68
RSC076	48	2	5.28	59	67
RSC073	60	2	5.43	58	66
RSC017	35	2	5.79	59	64
RSC008	30	2	5.89	65	67
RSC037	36	2	6.30	66	64
Average			5.31	64	66

# Materials & Methods (2016-2017)

2016				
Location	RSC017	RSC037	RSC114	RSC135
College Station, TX	x	x	x	x
Corpus Christi, TX		x		x
Halfway, TX	x		x	x
Weslaco, TX	x	x	x	
2017				
College Station, TX		x	x	x
Corpus Christi, TX				x
Halfway, TX				
Weslaco, TX				
Number of entries	30	30	30	30
Replications	4	4	4	4
Years Observed	1	2	2	2
Total observations	120	240	240	240

# Results & Discussion – Level

Yield (t/ha) 2016-2017

% Ex. Gen	RSC 17		RSC 37		RSC 114		RSC 135		Average	
High	3.85	A	4.54	A	4.40	A	3.88	AB	4.32	A
Medium	3.54	A	4.39	A	3.72	B	3.58	B	4.09	AB
Low	.	.	3.19	B	4.49	A	4.39	A	3.84	B

\*Levels not connected by the same letter are significantly different within Population (RSC) using T-test at alpha 0.05

- ⊙ High % exotic recovery yields higher for two populations
- ⊙ Low % exotic recovery yields higher for two populations
- ⊙ Across all populations, high % exotic yields the best

# Results & Discussion – Tester

Yield (t/ha) 2016-2017

Tester	RSC 17		RSC 37		RSC 114		RSC 135		Average	
A3Tx436	3.62	A	3.93	B	3.30	C	2.94	C	3.49	B
ATx2928	3.67	A	4.60	A	4.06	B	4.02	B	4.22	A
ATx645	4.02	A	4.38	AB	4.88	A	4.69	A	4.54	A

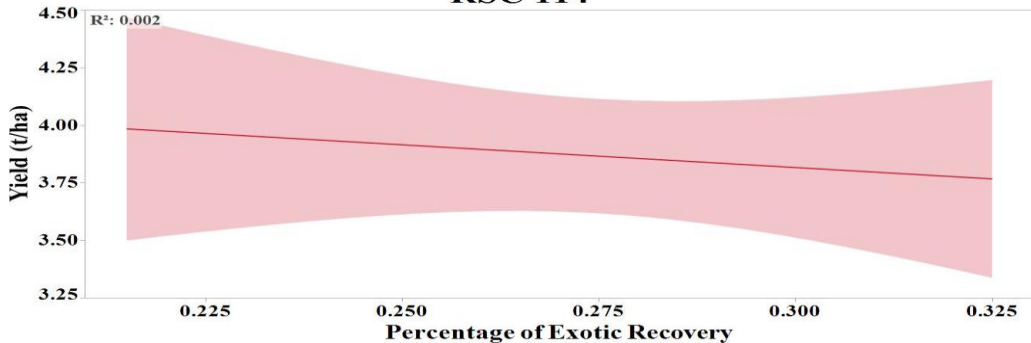
\*Levels not connected by the same letter are significantly different within Population (RSC) using T-test at alpha 0.05

- ⊙ A3Tx436 has lowest yield across populations
- ⊙ ATx645 tends to be the highest yielding across populations
- ⊙ Across all populations, ATx645 yields the highest

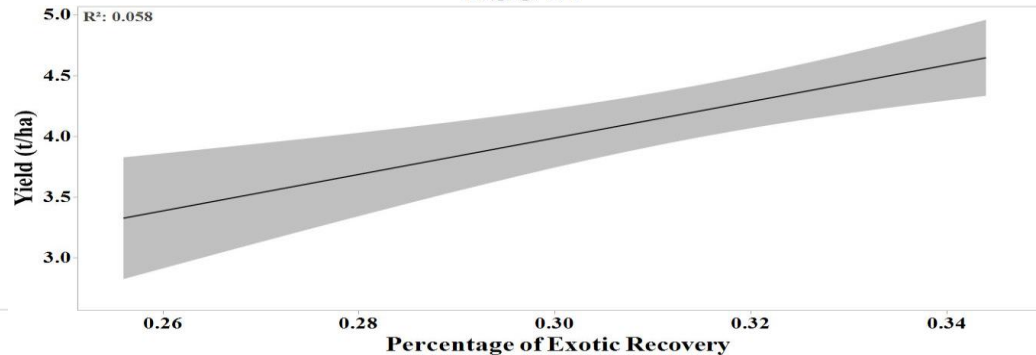
# Pearson Correlations

		RSC37		RSC114		RSC135		
% Ex.Gen	Tester	Ht	Yield	Ht	Yield	Ht	Yield	
Low	A3Tx436	DY	0.55	-0.37	0.24	-0.85	0.30	-0.65
		Ht	.	0.22	.	-0.60	.	-0.13
	ATx2928	DY	0.65	0.20	0.82	0.34	0.40	-0.29
		Ht	.	0.56	.	0.40	.	0.26
	ATx645	DY	0.73	0.52	0.25	0.11	0.92	-0.17
		Ht	.	0.81	.	-0.46	.	-0.19
Medium	A3Tx436	DY	0.91	-0.64	0.84	-0.77	0.39	-0.56
		Ht	.	-0.46	.	-0.52	.	-0.27
	ATx2928	DY	0.88	0.35	0.67	0.45	0.11	-0.57
		Ht	.	0.19	.	0.51	.	-0.07
	ATx645	DY	0.89	-0.09	0.82	0.74	0.53	0.09
		Ht	.	0.15	.	0.64	.	0.11
High	A3Tx436	DY	0.65	-0.50	0.53	-0.85	0.40	-0.57
		Ht	.	-0.28	.	-0.76	.	-0.49
	ATx2928	DY	0.82	0.41	0.74	-0.57	0.44	0.37
		Ht	.	0.26	.	-0.10	.	0.02
	ATx645	DY	0.17	-0.12	0.90	-0.66	0.96	-0.37
		Ht	.	0.06	.	-0.75	.	-0.57

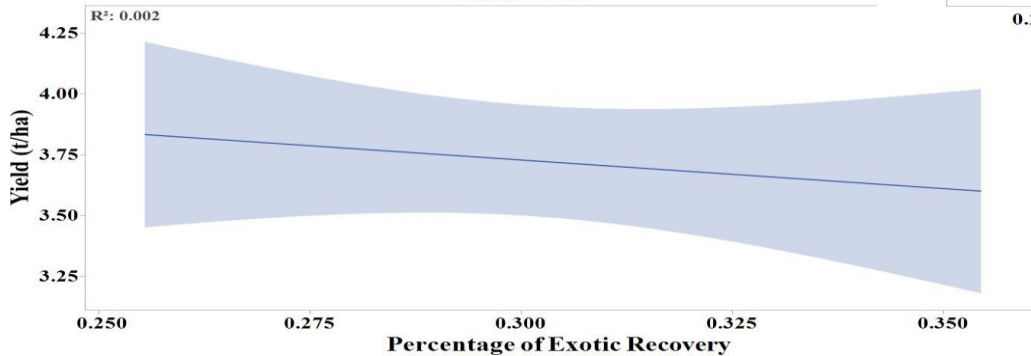
**RSC 114**



**RSC 37**



**RSC 135**



# Conclusions

- ⊙ No clear relationship between % exotic genome recovered and agronomic performance
- ⊙ Testcross performance varies from population to population
  - ⊙ Race of exotic parent helps determine combining performance with different testers
- ⊙ Cross R lines with R lines and B lines with B lines
- ⊙ If markers are to be used, a weighted system of individual markers is more beneficial (genomic selection)

# RSC Line Selections: Potential for International Distribution

- ⊙ Evaluated 375 RSC ( $F_3$  &  $BC_1F_3$ ) lines in 2016
  - ⊙ Breeding value estimated by Dr. Fred R. Miller
- ⊙ RSC lines (33) advanced based on estimated breeding value
- ⊙ Testcross hybrid trial evaluation (2018)
  - ⊙ Multi-location yield trials (6)
    - ⊙ Two testers – TxARG-1, Tx2928
    - ⊙ David Horne, Dr. Nikhil Patil



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