Development of Resistance to Multiple Adversities in Cotton

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Cotton Plant Breeder

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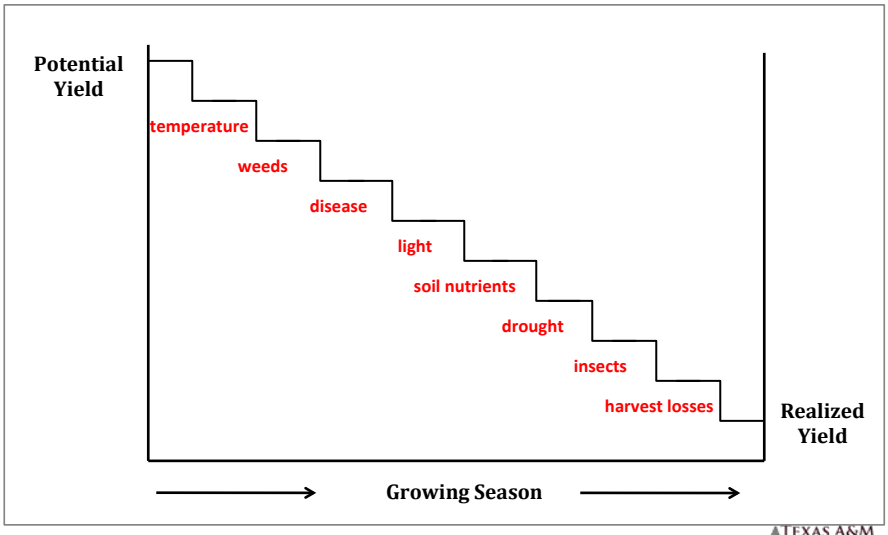
Meeting of ALIDA
Cartagena, Colombia
October 3, 2013

Yield Potential

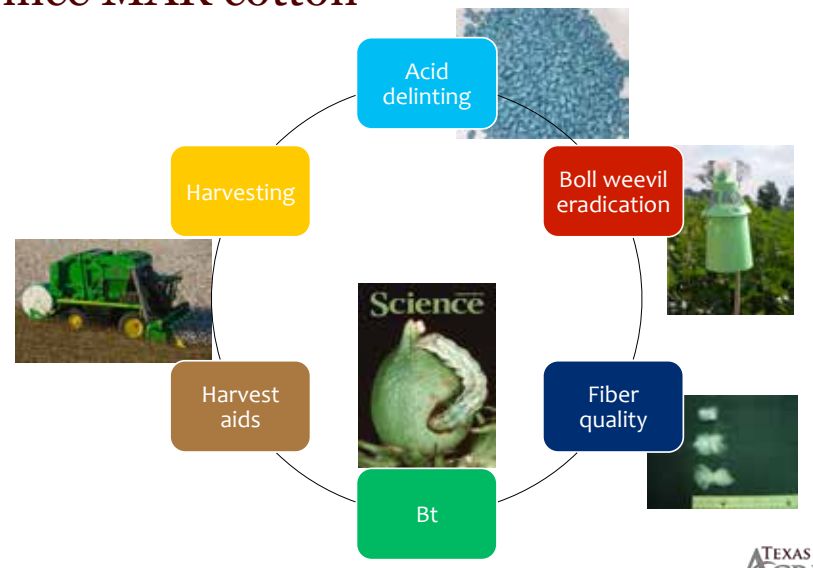


Multiple Adversity Resistance (MAR)

- Pioneered by Dr. Luther Bird, Texas A&M University
- Saved the cotton industry in the coastal region of Texas
- Based upon
  1. Earliness
  2. Bacterial blight resistance
  3. Lepidopteron and sucking insect pest resistance



Since MAR cotton



Current Situation in the USA

- Secondary insects pests are now primary pests
  - i.e. stink bugs, lygus, fleahoppers (piercing, sucking)
- Water
  - Declining in volume and quality
- High yield expectations
  - Seed costs
  - Harvest costs
  - Competition from maize and soya
- Fiber quality
- Glyphosate resistant weeds

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Breeding Objectives – Trait Discovery – Germplasm Development

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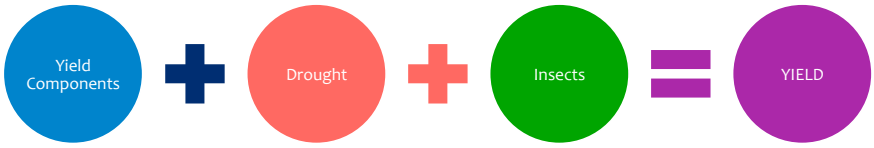

Drought Tolerance

- Definition of drought tolerance
- Seedling screening
- Leaf temperature
- Green seeker
- Root architecture
- Yield
- Fiber quality
- Recurrent selection
- Development of good parents

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Whiteflies

- Honeydew contamination
- Yield and fiber decline
- Passive breeding
- Rio Grande Valley (far South Texas)
- Smooth leaf plant types

Whiteflies on underside of leaf

Adult whitefly and nymphs (dark colored)

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Resistance to cotton fleahopper
(*Pseudatomoscelis seriatus*) (Hemiptera: Miridae)

Framework for Public Cotton Breeding

Texas A&M AgriLife Research

Trait Discovery **Germplasm Development**

Phenotyping **Genotyping** **Assembly**

Fleahoppers

Texas A&M AgriLife Research

- Regional pest in Texas
- Host range
  - Highly polyphagous
    - >160 plants
- Piecing-sucking mouthpart
- Facultatively predaceous
  - Noctuid eggs

- Cotton pest
  - Overwinters in wild hosts as eggs
    - Woolly croton
    - Hatching: February-March (College Station)
  - Migration from wild hosts to cotton in spring/early summer
    - Cotton squaring
  - Feeds on squares
    - Blasting
      - Delayed maturity
      - Whip-like growth

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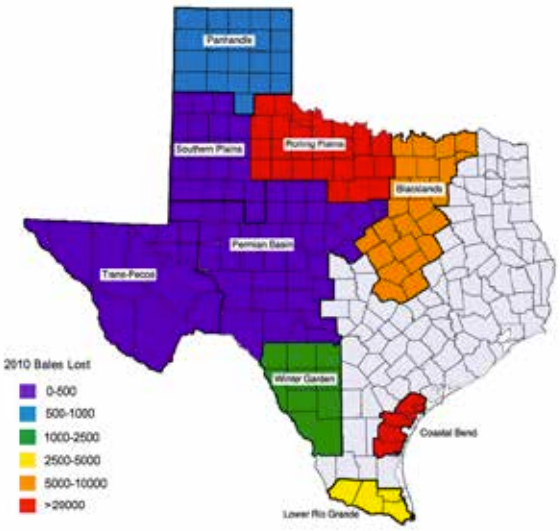

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What is known…

- Cotton Leaf Pubescence
  - Hirsute
    - Higher hopper numbers
    - Less hopper damage
    - Greater Resistance
  - Glabrous
    - Lower hopper numbers
    - More hopper damage
    - Greater Susceptibility
  - Type of Resistance?

Screening methods

- Potential Elite Parents (High Yielding—Susceptible)
  - TAM 07V-45: Smooth
  - TAM 06WE-14: Hairy
- Potential Trait Parents (Fleahopper Resistant)
  - 18 lines (F_3 IPS seed)
    - Partitioned into three isolines (smooth, hairy, and pilose)
- Resistance Screening
  - Two locations (College Station and Corpus Christi)
  - Sprayed and unsprayed
  - Counted insects, feeding damage, and yield

2012- Insects per Plant

Source of Variation	Mean Squares
Location	118.76*
Location*Rep	7.32
Treatment	88.10*
Location*Treatment	27.32*
Genotype	84.04**
Location*Genotype	19.50*
Treatment*Genotype	7.97
Location*Trt*Rep	3.67
Location*Geno*Rep	3.94
Location*Geno*Trt	4.53

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2012 Insects per Plant

College Station			Corpus Christi		
Genotype	CFH/Plant		Genotype	CFH/Plant	
07V45	1.05	A	07V45	1.11	A
06WE14	1.90	A	06WE14	1.70	AB
GH02	3.67	B	GH07	2.24	BC
GH04	4.36	B	GH02	2.42	BC
GH07	4.50	B	GH04	2.60	C

*Levels not connected by the same letter are significantly different

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2012 Percent Square Loss

Source of Variation	Mean Squares
Location	0.129
Location*Rep	0.061*
Treatment	0.184*
Location*Treatment	0.002
Genotype	1.116**
Location*Genotype	0.028
Treatment*Genotype	0.129*
Location*Trt*Rep	0.019
Location*Geno*Rep	0.017
Location*Geno*Trt	0.019

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2012 Percent Square Loss

Percent Square Loss by Genotype: Treated vs. Untreated

Treated			Untreated		
Genotype	Percent Sq Loss		Genotype	Percent Sq Loss	
07V45	0.4126	A	07V45	0.5785	A
06WE14	0.3261	B	06WE14	0.3272	B
GH07	0.2479	C	GH02	0.2504	BC
GH04	0.2260	CD	GH04	0.2472	BC
GH02	0.1605	D	GH07	0.1930	C

*Levels not connected by the same letter are significantly different

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2012 Percent Square Loss

Untreated

Smooth			Hairy			Very Hairy		
07V45	0.5785	A	06WE14	0.3272	A	GH04	0.1639	A
GH02	0.4413	B	GH02	0.1726	AB	GH02	0.1575	A
GH07	0.3399	BC	GH07	0.1592	B	GH07	0.1332	A
GH04	0.3217	C	GH04	0.1397	B			

Treated

Smooth			Hairy			Very Hairy		
07V45	0.4126	A	06WE14	0.3261	A	GH07	0.2187	A
GH04	0.3517	AB	GH04	0.1599	B	GH02	0.1351	A
GH07	0.3383	AB	GH07	0.1563	B	GH04	0.1242	A
GH02	0.2712	B	GH02	0.1194	B			

*Levels not connected by the same letter are significantly different

AGRILIFE RESEARCH

2012 Yield

Source of Variation	Mean Squares
Location	55,9975*
Location*Rep	8,340
Treatment	12,328
Location*Treatment	1,126
Genotype	54,544**
Location*Genotype	59,506**
Treatment*Genotype	5,612
Location*Trt*Rep	9,106
Location*Geno*Rep	3,819
Location*Geno*Trt	2,210

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2012 Yield

College Station			Corpus Christi		
Genotype	Lbs/Acre		Genotype	Lbs/Acre	
06WE14	593	A	07V45	346	A
07V45	569	A	GH07	330	AB
GH07	395	B	GH02	282	ABC
GH04	383	B	GH04	271	BC
GH02	363	B	06WE14	238	C

*Levels not connected by the same letter are significantly different

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2013

	F -Value			
Genotype	**Date 1**	**Date 2**	**Date 3**	**Date 4**
GENO	0.0005**	<0.0001**	<0.0001**	0.0003**
TRT	0.4396	0.1613	0.0084**	<0.0001**
GENO*TRT	<0.0001**	0.0897	0.2047	0.5007

**Highly significant at α=0.05

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2013 Percent Square Set

DATE 2

GENO	% SQ SET	TUKEY
F	97.4	A
E	97.3	A
A	97.3	A
C	96.7	A
B	95.8	A
D	95.5	A
H	94.5	A
G	89.1	B

DATE 3

GENO	% SQ SET	TUKEY
D	98.8	A
B	98.1	A
E	97.9	A
C	97.5	A
A	97.4	A
F	97.1	AB
H	95.2	AB
G	93.5	B

DATE 4

GENO	% SQ SET	TUKEY
E	96.3	A
D	95.7	AB
C	95.4	AB
A	94.8	AB
B	94.6	AB
H	92.9	AB
F	92.7	B
G	92.6	B

*Levels not connected by the same letter are significantly different

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RNA Sequencing

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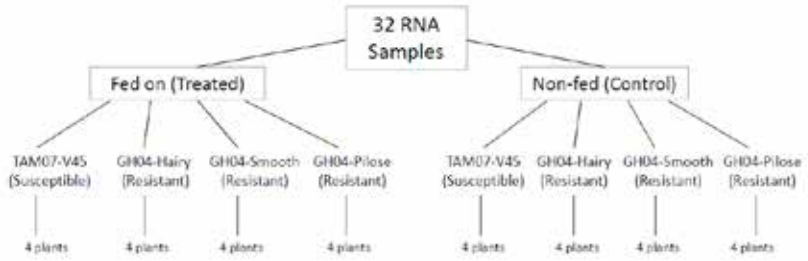
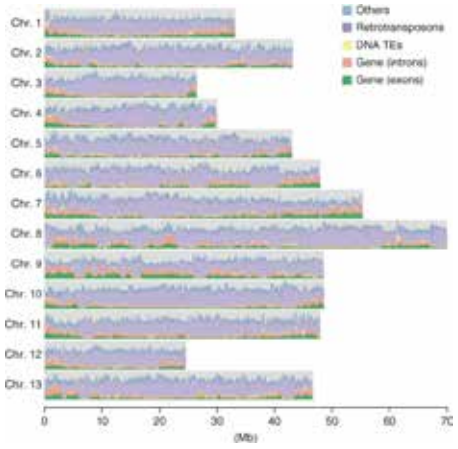
- **Resistance versus Susceptible**
  - **Response from caged feeding insects**
  - **Ethylene response elements**

Illumina Hi-Seq



The draft genome of a diploid cotton *Gossypium raimondii*.
Nature Genetics (2012) Volume: 44, Pages: 1098–1103 Year published: (2012)



D subgenome + A subgenome = *G. hirsutum* and *barbadense*

Trait discovery (e.g. fleahopper resistance)

Marker –assisted breeding

Lower cost, more effective breeding

Future

Diversity

Native traits

Trait discovery and integration

Uncover Quantitative Trait Interactions