

COTTON INSECT PEST MANAGEMENT

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TEXAS A&M
AGRILIFE
RESEARCH | EXTENSION

Corn & cotton share identical or similar Bt toxins and there is pest overlap

Company	1 st generation (single gene)	2 nd generation (dual gene)	3 rd generation (multi-gene)	3 rd generation (2017)
Bayer	Bollgard (Cry1Ac)	Bollgard 2 (Cry1Ac+Cry2Ab)		Bollgard 3 (Cry1Ac+Cry2Ab+Vip3Aa)
Corteva		WideStrike (Cry1Ac+Cry1F)	WideStrike 3 (Cry1Ac+Cry1F+Vip3Aa)	
BASF		TwinLink (Cry1Ab+Cry2Ae)		TwinLink Plus (Cry1Ab+Cry2Ae+Vip3Aa)



Homogeny across crops				
Crop	Cry1A	Cry1F	Cry2	Vip3Aa
Cotton	Cry1Ac, Cry1Ab	Cry1F	Cry2Ab, Cry2Ae	Vip3Aa
Corn	Cry1Ab	Cry1F	Cry2Ab2	Vip3Aa
	Cry1A.105 (Cry1Ab, Cry1Ac, Cry1F)			
Both crops	Cry1As, Cry1F, Cry2As and Vip3Aa			



BACKGROUND ON Bt RESISTANCE

SURVEY BIOASSAYS

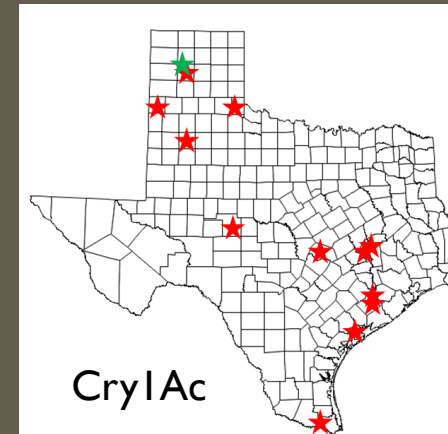
- Bollworms/corn earworm collected from the field as larvae
- Overnight delivery to lab in College Station
- Reared to F1 or F2 generation and then bioassays
- Tested for response to Cry1Ac, Cry2Ab2, Cry1F and Vip3A
- Diet overlay bioassays
 - Test 6-8 Bt concentrations and a control
 - Used 16-32 neonate larvae, replicated 4 times for each concentration; allowed to feed for 7 days
- Record number alive/dead, instar and weight of survivors
- Compare field populations to a standard laboratory strain (Benzon)
 - Dead = Actual dead larvae + 1st instar larvae
 - Dose response bioassay: Probit analysis for LC50 and their 95% CL.
 - Resistance ratio = LC50 of a field population / LC50 of the susceptible strain.



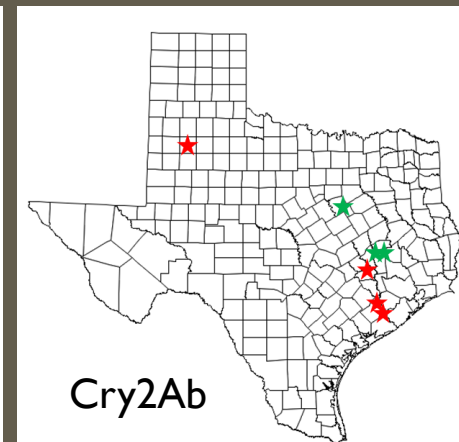
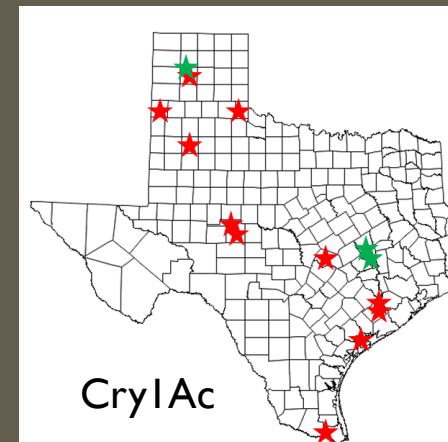
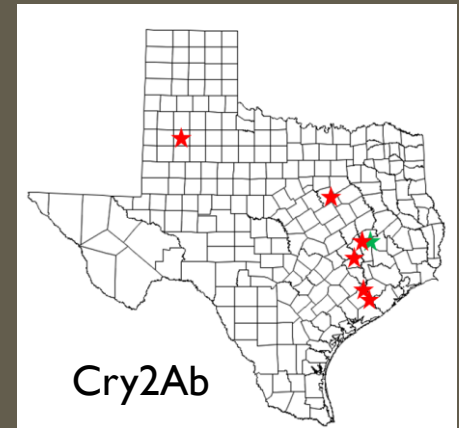
SUMMARY OF Bt RESISTANCE SURVEYS

Bt protein	Percentage of populations with RR > 10X				
	2016	2017	2018	2019	2020*
CryIAc	40%*	100%	94%	96%	100%
Cry2Ab2	80%	77%	73%	73%	100%
CryIF	ND	100%*	100%	100%	ND
Vip3Aa	0%	0%	0%	0%	0%

2018



2019



Full range bioassay for resistance confirmation



Larval collection and rearing



Feral ♂ x Susceptible (SS) ♀



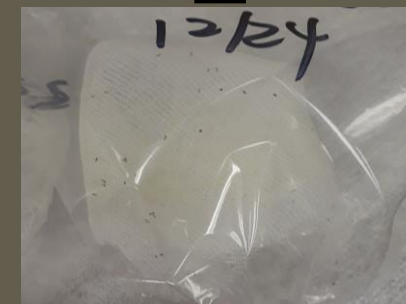
Establishing
Isoline families



F₁ family



F₁ families are reared
and Sib mated



F₂ family

F₂ screen with
discriminatory []
of Bt toxins

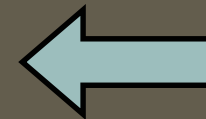
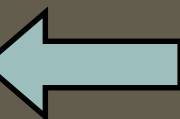


Check results
after 7 days

F₂

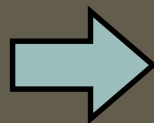
(SS) 56.25%
(RS) 37.5%
(RR) 6.25%

Assuming resistance controlled by a
single gene and recessive alleles



METHOD I: LARVAL COLLECTION METHOD F₂ SCREEN

Andow, D. A., and D. N. Alstad. 1998.



Texas *H. zea*-F₂ families surviving the diagnostic concentration of **Cry1Ac (10 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2018	Cross with SS♂	12	10	13	0.5417	(0.3507 - 0.7211)
2019	Light trap	94	89	Min: 153 Max:186	0.4069 0.4947	(0.3584 - 0.4573) (0.4445 - 0.5450)
	Totals for 2 consecutive years	106	99 (93%)	Min:166 Max:199	0.4150 0.4975	(0.3677 -0.4639) (0.4488 – 0.5463)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2018 and 2019 = 13,568 larvae

3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

Mid-South *H. zea*-F₂ families surviving the diagnostic concentration of **Cry1Ac (10 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2019	Cross with SS♀	52	48	67 74	0.6442 0.7115	(0.5486 - 0.7296) (0.6182 - 0.7898)
2020	Cross with SS♀	140	130	181 193	0.6464 0.6893	(0.5888 - 0.7001) (0.6328 - 0.7406)
	Totals for 2 consecutive years	192	178 (93%)	248 267	0.6458 0.6953	(0.5968 - 0.6920) (0.6475 - 0.7392)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2019 and 2020 = 24,576 larvae

3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

Texas *H. zea*-F₂ families surviving the diagnostic concentration of **Cry2Ab2 (10 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2018	Cross with SS♂	12	7	11	0.4583	(0.2789 - 0.6493)
2019	Light trap	108	35	39 45	0.0903 0.1042	(0.0667 - 0.1210) (0.0788 - 0.1365)
	Totals for 2 consecutive years	120	42 (35%)	50 56	0.1097 0.1228	(0.0842 – 0.1417) (0.0958 – 0.1561)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2018 and 2019 = 15,360 larvae

3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

Mid-South *H. zea*-F₂ families surviving the diagnostic concentration of **Cry2Ab2 (10 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2019	Cross with SS♀	52	18	22 25	0.2115 0.2404	(0.1441 - 0.2996) (0.1685 - 0.3308)
2020	Cross with SS♀	140	56	75 77	0.2679 0.2750	(0.2194 - 0.3226) (0.2260 - 0.3301)
	Totals for 2 consecutive years	192	74 (39%)	97 102	0.2526 0.2656	(0.2117 - 0.2984) (0.2239 - 0.3120)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2019 and 2020 = 24,576 larvae

3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

Texas *H. zea*-F₂ families surviving the diagnostic concentration of **Vip3Aa39 (3 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2018	Cross with SS♂	12	0	-	-	-
2019	Light trap	114	2	2	0.0065	(0.0014 – 0.0157)
	Totals for 2 consecutive years	126	2 (1.59%)	2	0.0042	(0.0011 – 0.0151)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2018 and 2019 = 16,128 larvae

3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

Mid-South *H. zea*-F₂ families surviving the diagnostic concentration of **Vip3Aa39 (3 µg/cm²)**

Year of collection	Method to establish the F ₂ families	Number of F ₂ families screened	Number of surviving F ₂ families ^{1,2}	Estimated number of resistance alleles ³	Estimated resistance allele frequency	Confidence Interval (95%)
2019	Cross with SS♀	52	1	1	0.0096	(0.0017 - 0.0525)
2020	Cross with SS♀	140	4	4	0.0143	(0.0056 - 0.0361)
	Totals for 2 consecutive years	192	5 (3%)	5	0.0130	(0.0056-0.0301)

1. 5 survivors with at least 1 larva ≥ 3rd instar

2. Based on 128 larvae per bioassay/F₂ family: Total insects assayed 2019 and 2020 = 24,576 larvae

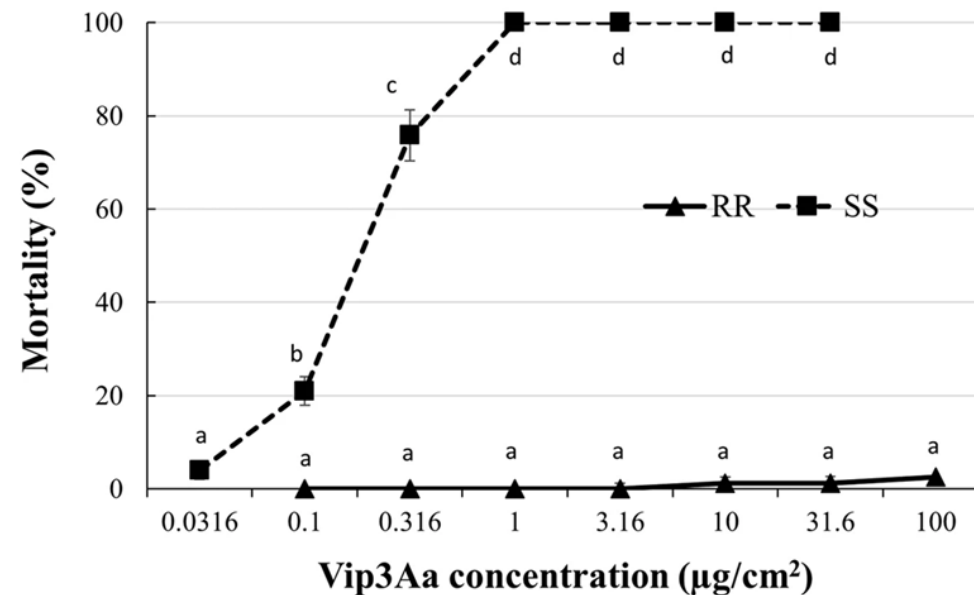
3. Number of resistant alleles based on results from simple monogenic inheritance models

($\chi^2 < 3.841$ with 1 df, $p > 0.05$)

OPEN First documentation of major Vip3Aa resistance alleles in field populations of *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae) in Texas, USA

Fei Yang^{1,7*}, José C. Santiago González^{1,7}, Nathan Little², Dominic Reisig³, Gregory Payne⁴, Rafael Ferreira Dos Santos⁵, Juan Luis Jurat-Fuentes⁵, Ryan Kurtz⁶ & David L. Kerns^{1*}

Susceptibility of SS and RR populations of *H. zea* to Vip3Aa39 protein



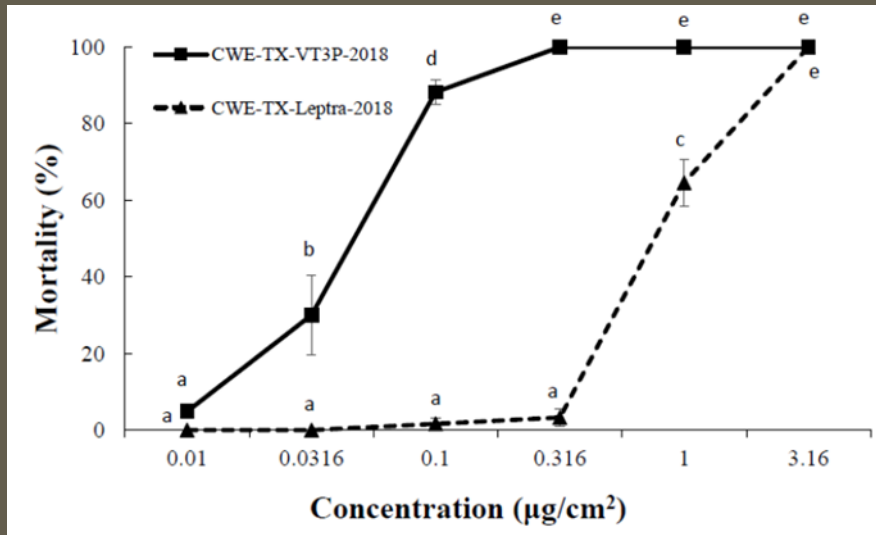
Concentration-larval mortality response of the SS and RR strains of *Helicoverpa zea* to Vip3Aa39 protein. Mean percentage mortality values followed by a different letter are significantly different (Tukey's HSD test, $\alpha = 0.05$).

CORN EARWORM FEEDING IN LEPTRA CORN TX & MS -2019

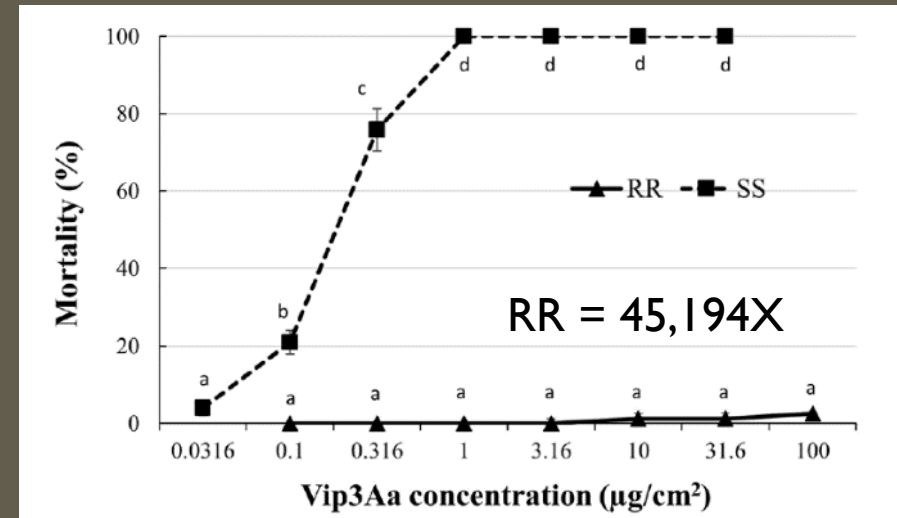


COMPARISON OF VIP3A RESISTANT STRAINS

STRAIN ESTABLISHED FROM LEPTRA CORN COLLECTION

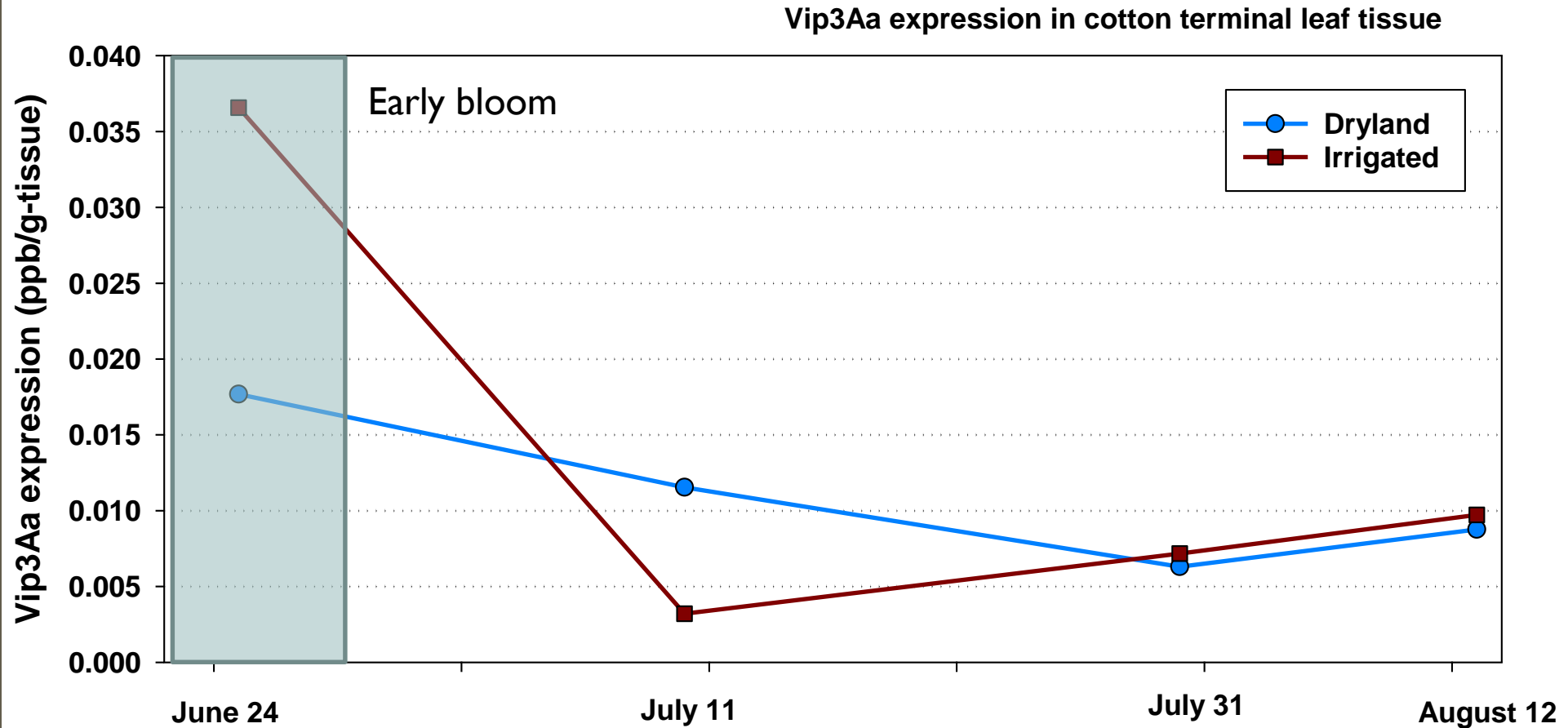


STRAIN ESTABLISHED FROM F_2 SCREEN



Bollgard 3 with unexpected bollworm injury
Probably due to combination of low level
resistance and poor Bt expression

Bt EXPRESSION IN COTTON



TESTING FOR GENETIC INHERITANCE AND DOMINANCE



HOW MANY GENES ARE INVOLVED?

-TEST FOR MONOGENICITY-

- Conformity to a Mendelian monogenic model
 - H_0 was that resistance is controlled by one locus with two alleles
 - A backcross between RS and RR, Expected = 50% RR and 50% RS
 - A backcross between RS and SS, Expected = 50% SS and 50% RS
 - The F_2 mating, Expected = 25% RR, 50% RS and 25% SS
- Chi-square (χ^2) tests for goodness of fit was used to evaluate whether the inheritance of resistance fits a the Mendelian monogenic model
 - $\chi^2 = (O - E)^2 / np(1 - p)$
 - Where O is the observed number of dead larvae of the F_2 or backcross populations at a given Cry2Ab2 concentration, E is the expected number of dead larvae, n is the number of total larvae tested and p is the expected mortality
 - We utilized 4 Cry2Ab2 concentrations of purified protein and lyophilized corn leaf powder
 - The χ^2 value was compared with the χ^2 distribution with one degree of freedom
 - Where $P < 0.05$, the null hypothesis of monogenic resistance could be rejected

TEST FOR MONOGENETICITY CRY2Ab2

Table 6 Test for monogenic inheritance for resistance to Cry2Ab2 by comparing expected and observed mortalities of the F₂ backcross populations between F₁ and SS and between F₁ and RR at different Cry2Ab2 concentrations

Cry2Ab2 protein	Strain [†]	Concentration (μg cm ⁻²)	N [‡]	Observed dead (O)	Expected dead (E)	χ ²	P-Value
Corn leaf powder	Pooled BCS: F ₁ *SS	1	256	13.8	92.7	105.15	<0.05
		3.16	256	50.9	116.7	68.16	<0.05
		10	256	124.4	174.7	45.62	<0.05
		31.6	256	251.9	223.5	28.45	<0.05
	Pooled BCR: F ₁ *RR	1	256	5.9	14.8	5.74	<0.05
		3.16	256	8.96	23.6	9.96	<0.05
		10	256	49.9	72.7	9.97	<0.05
		31.6	256	204.0	145.4	54.71	<0.05
	Pooled F ₂ : F ₁ *F ₁	1	128	12.2	26.9	10.20	<0.05
		3.16	128	27.4	35.1	2.32	0.13
		10	128	49.8	61.9	4.56	<0.05
		31.6	128	60.9	92.2	38.00	<0.05
Solubilized	Pooled BCS: F ₁ *SS	1	256	23.0	96.3	89.25	<0.05
		3.16	256	96.0	175.0	112.63	<0.05
		10	256	226.3	235.6	4.66	<0.05
		31.6	256	247.8	252.9	8.64	<0.05
	Pooled BCR: F ₁ *RR	1	256	1.0	19.1	18.45	<0.05
		3.16	256	27.4	82.6	54.41	<0.05
		10	256	80.4	143.9	63.96	<0.05
		31.6	256	209.9	227.3	11.90	<0.05
	Pooled F ₂ : F ₁ *F ₁	1	128	2.9	28.8	30.01	<0.05
		3.16	128	18.0	64.4	67.09	<0.05
		10	128	71.0	94.9	23.17	<0.05
		31.6	128	102.0	120.1	43.76	<0.05

[†]F₁: progeny from crosses between the parental resistant (RR) and susceptible (SS) insects; Pooled BCS: progeny from crossing F₁ with SS; Pooled BCR: progeny from crossing F₁ with RR; Pooled F₂: progeny from crossing F₁ with F₁.

[‡]Total number of neonates assayed.

TEST FOR MONOGENETICITY VIP3A_a

Table 4. Test for fitting a Mendelian monogenic model for Vip3Aa resistance in *Helicoverpa zea*

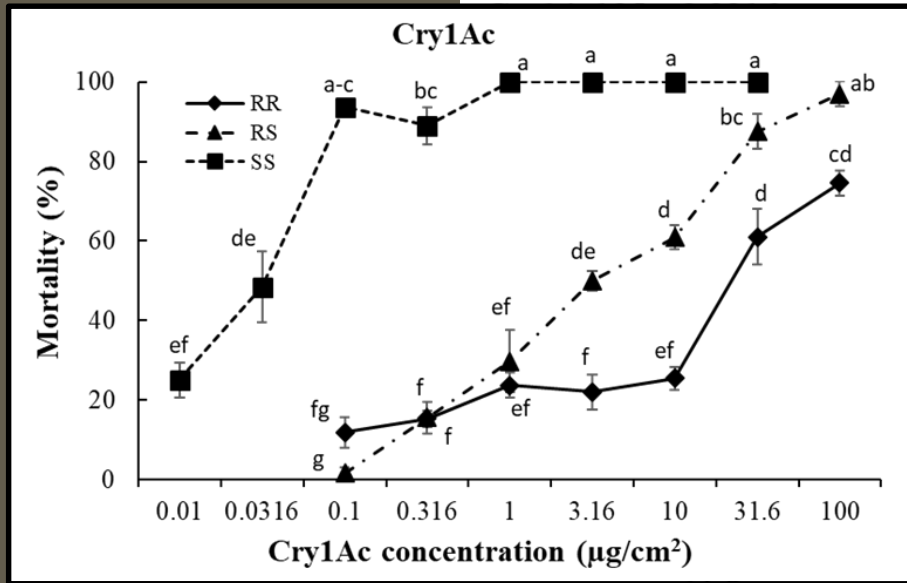
Vip3Aa39 concentration	Insect strain	N*	Observed dead (O)	Expected dead (E)	χ^2	P-value
3.16 $\mu\text{g cm}^{-2}$	Pooled backcross	256	119.8	128.0	1.049	0.306
	Pooled F ₂	128	94.7	96.0	0.068	0.794
10 $\mu\text{g cm}^{-2}$	Pooled backcross	256	130.3	129.7	0.006	0.938
	Pooled F ₂	128	91.8	96.4	0.907	0.341

*Total number of neonates assayed.

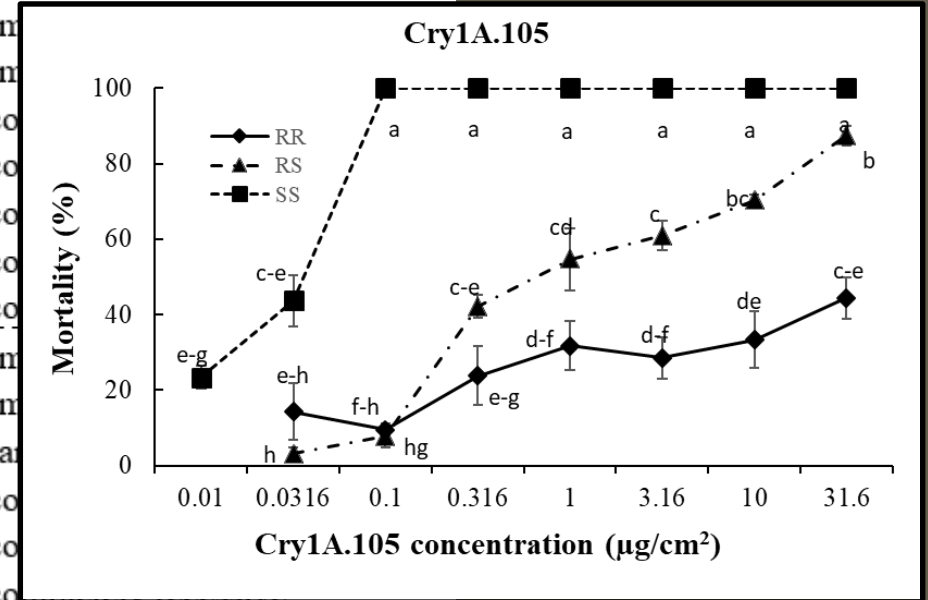
IS THE TRAIT DOMINANT OR RECESSIVE? -DOMINANCE OF RESISTANCE-

- **Effective Dominance ' D_{ML} ' - Bourguet et al. (2000)**
 - Based on a series of single concentrations; we used 4 concentrations
 - $D_{ML} = (ML_{RS} - ML_{SS}) / (ML_{RR} - ML_{SS})$
 - Where ML_{SS} , ML_{RR} , and ML_{RS} are the mortality of the SS, RR, and F_1 (RS) strains at a given Cry2Ab2 concentration
 - The values of D_{ML} range from 0 to 1, where $D_{ML} = 0$ indicates completely recessive resistance and $D_{ML} = 1$ means resistance is completely dominant

DOMINANCE IN CRYIA PROTEINS



Bt protein	Concentration (µg/cm²)	Effective dominance (DML)	Result
RR	0.01	1.37	Com
RR	0.0316	1.02	Com
RR	0.1	0.76	Inco
RR	0.316	0.66	Inco
RR	1	0.55	Inco
RR	3.16	0.45	Inco
RR	10	0.22	Inco
RR	31.6	1.13	Com
RR	100	1.00	Com
RS	0.01	0.92	Near
RS	0.0316	0.64	Inco
RS	0.1	0.52	Inco
RS	0.316	0.32	Inco
RS	1	0.32	Inco
RS	3.16	0.32	Inco
RS	10	0.32	Inco
RS	31.6	0.32	Inco
RS	100	0.32	Inco
SS	0.01	0.32	Inco
SS	0.0316	0.32	Inco
SS	0.1	0.32	Inco
SS	0.316	0.32	Inco
SS	1	0.32	Inco
SS	3.16	0.32	Inco
SS	10	0.32	Inco
SS	31.6	0.32	Inco
SS	100	0.32	Inco

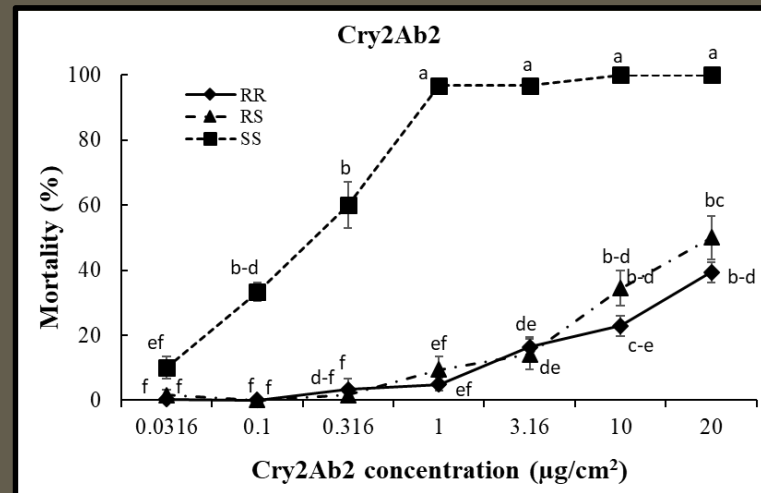


Values closer to 1.0 indicate dominance

DOMINANCE CRY2Ab2

Cry2Ab2	0.0316	0.88	Incompletely dominant
	0.1	1.00	Completely dominant
	0.316	1.03	Completely dominant
	1	0.95	Nearly completely dominant
	3.16	1.03	Completely dominant
	10	0.85	Incompletely dominant
	20	0.82	Incompletely dominant

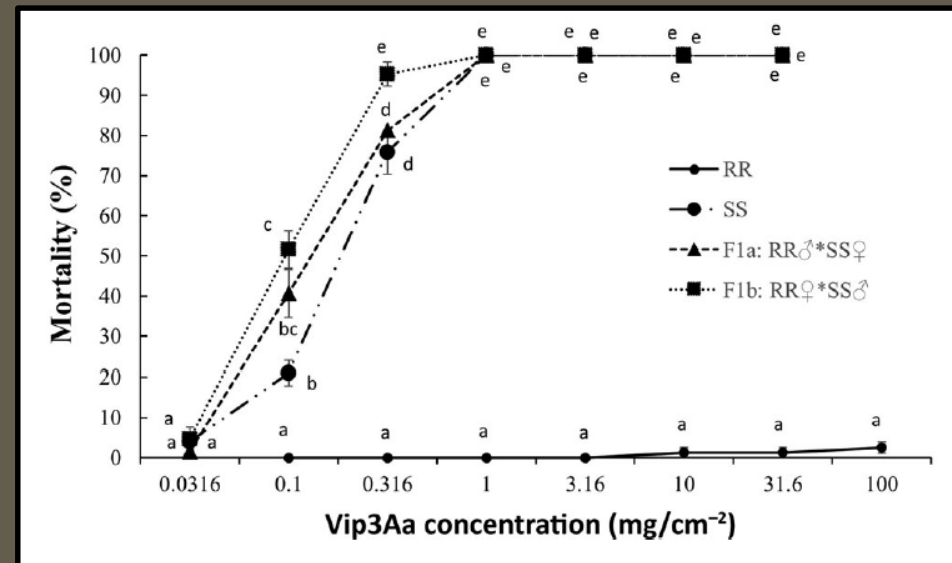
Values closer to 1.0 indicate dominance



DOMINANCE VIP3Aa

Vip3Aa39	0.0316	0.05	Nearly completely recessive
	0.1	-0.11	Completely recessive
	0.316	-9.52	Completely recessive
	1	/	Completely recessive
	3.16	/	Completely recessive
	10	/	Completely recessive

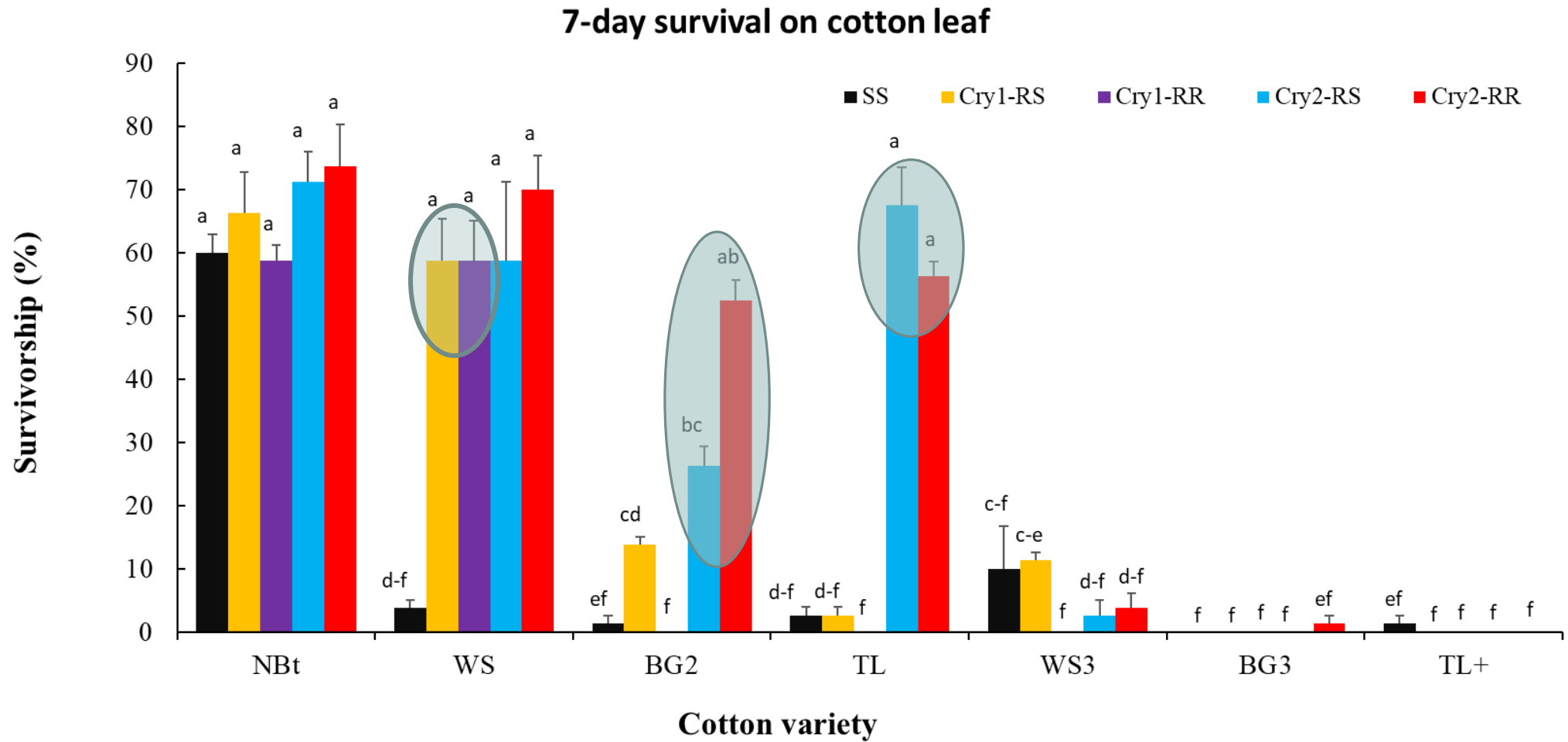
Values closer to 1.0 indicate dominance



SUMMARY OF RESISTANCE INHERITANCE TESTS AND F2 SCREEN ALLELE FREQUENCIES FOR *H. zea* TO Bt PROTEINS

<i>Bt</i> protein	Inheritance characterization			Mid-South 2019-2020 Allele frequency	
	Sex linkage	Genes	Functional dominance		
CryIAc	Autosomal	Polygenic	RS & RR	(0.65-0.70)	Very high
Cry2Ab2	Autosomal	Polygenic	RS & RR	(0.25-0.27)	High
CryIF	ND	ND	ND	ND	
Vip3Aa	Autosomal	Monogenic	Completely recessive	0.0130	Low but not rare

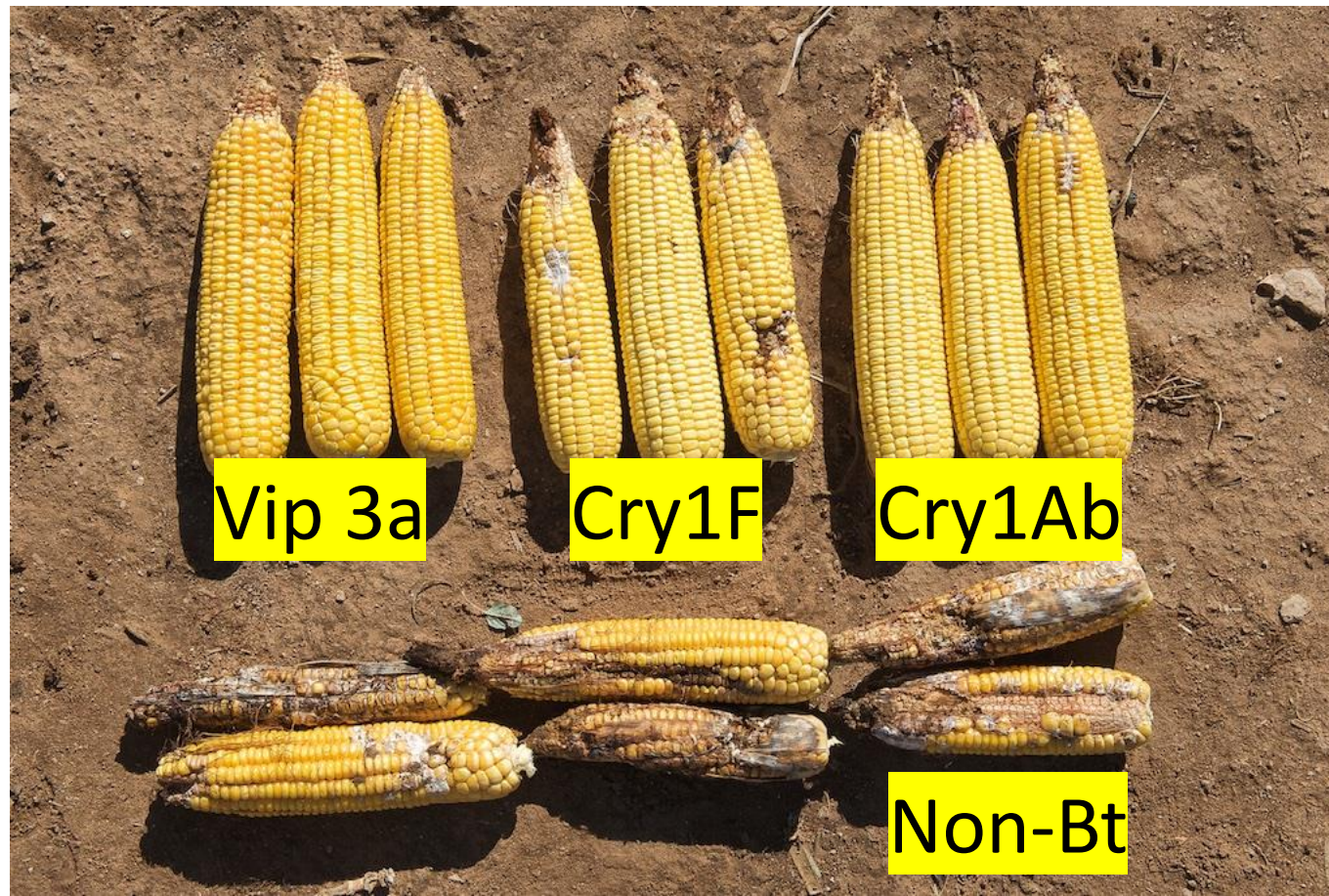
SURVIVAL OF DIFFERENT B_t RESISTANT GENOTYPES ON VARIOUS B_t TECHNOLOGIES



Preserving VIP is a priority of the public sector entomologists!



2014, Texas, before resistance to single toxin Bts



www.nature.com/scientificreports

**SCIENTIFIC
REPORTS**
nature research

OPEN First documentation of major Vip3Aa resistance alleles in field populations of *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae) in Texas, USA

Fei Yang^{1,7*}, José C. Santiago González^{1,7}, Nathan Little², Dominic Reisig³, Gregory Payne⁴, Rafael Ferreira Dos Santos⁵, Juan Luis Jurat-Fuentes⁵, Ryan Kurtz⁶ & David L. Kerns^{1*}

The corn earworm, *Helicoverpa zea*, is a major target pest of the insecticidal Vip3Aa protein used in pyramided transgenic Bt corn and cotton with Cry1 and Cry2 proteins in the U.S. The widespread resistance to Cry1 and Cry2 proteins in *H. zea* will challenge the long-term efficacy of Vip3Aa technology. Determining the frequency of resistant alleles to Vip3Aa in field populations of *H. zea* is critically important for resistance management. Here, we provided the first F₂ screen study to estimate the resistance allele frequency for Vip3Aa in *H. zea* populations in Texas, U.S. In 2019, 128 *H. zea* neonates per isofamily for a total of 114 F₂ families were screened with a diagnostic concentration of 3.0 µg/cm² of Vip3Aa39 protein in diet-overlay bioassays. The F₂ screen detected two families carrying a major Vip3Aa resistance allele. The estimated frequency of major resistance alleles against Vip3Aa39 in *H. zea* in Texas from this study was 0.0065 with a 95% CI of 0.0014–0.0157. A Vip3Aa-resistant strain (RR) derived from the F₂ screen showed a high level of resistance to Vip3Aa39 protein, with a resistance ratio of >588.0-fold relative to a susceptible population (SS) based on diet-overlay bioassays. We provide the first documentation of a major resistance allele conferring high levels of Vip3Aa resistance in a field-derived strain of *H. zea* in the U.S. Data generated from this study contribute to development of management strategies for the sustainable use of the Vip3Aa technology to control *H. zea* in the U.S.

1. New definition of resistance for 'non-high dose' Lep



All non-high dose Lep are
assumed to be at
heightened risk of resistance

Old definition:

- Bt resistance must be confirmed in lengthy lab assays of insects collected from a field



New definition:

- unexpected injury in field is 'practical resistance' which prompts immediate action



2. Short-term phase out single
trait hybrids (3-year)
(for real, this time)



3. Longer-term phase out 'non-functional' pyramids
hybrids (5-year)

CryAb + Cry1F

Optimum Intrasect, Xtra, Xtreme, & Trisect
Optimum Acremax, Xtra, Xtreme, & Trisect
Qrome

Agrisure 3122 & 3122 EZ, 3120 and Duracade 5122 hybrids

Cry1A015/Cry2Ab2

Genuity VT Double Pro & Triple Pro

Cry1A015/Cry2Ab2 + Cry1F

SmartStax & Powercore

= all hybrids that do
not have VIP Bt

DiFonzo's Handy Bt Trait Table, Feb 2020

Currently-available Bt trait packages

Trait packages in alphabetical order (acronym that may be used)	Bt protein(s) in the trait package	Marketed for control of:											Resistance confirmed to the combination of Bts in package (check local situation)	Herbicide trait			Non-Bt Refuge % (cornbelt)
		B	C	E	F	S	S	T	W	C	R			G	L	E	
AcreMax (AM)	Cry1Ab Cry1F	x	x	x	x	x	x	x					CEW FAW WBC	x	x		5% in bag
AcreMax CRW (AMRW)	Cry34/35Ab1											x	NCR WCR	x	x		10% in bag
AcreMax1 (AM1)	Cry1F Cry34/35Ab1	x	x	x	x	x	x	x				x	ECB FAW SWB WBC NCR WCR	x	x		10% in bag 20% ECB
AcreMax Leptra (AML)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x	x		5% in bag
AcreMax TRisect (AMT)	Cry1Ab Cry1F mCry3A	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x	x		10% in bag
AcreMax Xtra (AMX)	Cry1Ab Cry1F Cry34/35Ab1	x	x	x	x	x	x	x				x	CEW FAW WBC NCR WCR	x	x		10% in bag
AcreMax Xtreme (AMXT)	Cry1Ab Cry1F mCry3A Cry34/35Ab1	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x	x		5% in bag
Agrisure 3010 (BR)	Cry1Ab	x	x										CEW	x	x		20%
Agrisure 3000GT & 3011A	Cry1Ab mCry3A	x	x									x	CEW WCR	x	x		20%
Agrisure Viptera 3110 (VR)	Cry1Ab Vip3A	x	x	x	x	x	x	x	x	x				x	x		20%
Agrisure Viptera 3111 (A4)	Cry1Ab Vip3A mCry3A	x	x	x	x	x	x	x	x	x			WCR	x	x		20%
Agrisure 3120 E-Z Refuge (BZ)	Cry1Ab Cry1F	x	x	x	x	x	x	x					CEW FAW WBC	x			5% in bag
Agrisure 3122 E-Z Refuge	Cry1Ab Cry1F mCry3A Cry34/35Ab1	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x			5% in bag
Agrisure Viptera 3220 E-Z (VZ)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x			5% in bag
Agrisure Viptera 3330 E-Z	Cry1Ab Vip3A Cry1A.105/Cry2Ab2	x	x	x	x	x	x	x	x	x				x			5% in bag
Agrisure Duracade 5122 E-Z (D1)	Cry1Ab Cry1F mCry3A eCry3.1Ab	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x			5% in bag
Agrisure Duracade 5222 E-Z (D2)	Cry1Ab Cry1F Vip3A mCry3A eCry3.1Ab	x	x	x	x	x	x	x	x	x			WCR	x			5% in bag
Herculex I (HXI)	Cry1F	x	x	x	x	x	x						ECB FAW SWB WBC	x	x		20%
Herculex RW (HXRW)	Cry34/35Ab1											x	NCR WCR	x	x		20%
Herculex XTRA (HXX)	Cry1F Cry34/35Ab1	x	x	x	x	x	x					x	ECB FAW SWB WBC NCR WCR	x	x		20%
Intrasect (YHR)	Cry1Ab Cry1F	x	x	x	x	x	x	x					CEW FAW WBC	x	x		5%
Intrasect TRisect (CYHR)	Cry1Ab Cry1F mCry3A	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x	x		20%
Intrasect Xtra (YXR)	Cry1Ab Cry1F Cry34/35Ab1	x	x	x	x	x	x	x				x	CEW FAW WBC NCR WCR	x	x		20%
Intrasect Xtreme (CYXR)	Cry1Ab Cry1F mCry3A Cry34/35Ab1	x	x	x	x	x	x	x				x	CEW FAW WBC WCR	x	x		5%
Leptra (VYHR)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x	x		5%
Powercore ^a (PW)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x						CEW WBC	x	x		^a 5%
PW Refuge Advanced ^b (PWRA)	Cry1F																5% in bag
Powercore Enlist (PWE)	Same as Powercore	x	x	x	x	x	x						Same as Powercore	x	x	x	5% in bag
QROME (Q)	Cry1Ab Cry1F mCry3A Cry34/35Ab1	x	x	x	x	x	x					x	CEW FAW WBC WCR	x	x		5% in bag
SmartStax ^a (SX, STX or SS)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x					x	CEW WBC	x	x		^a 5%
STX Refuge Advanced ^b (SXRA)	Cry1F Cry3Bb1												NCR WCR				^b 5% in bag
STX RIB Complete ^b (STXRIB)	Cry34/35Ab1																
SmartStax Enlist (SXE)	Same as SmartStax	x	x	x	x	x	x					x	Same as SmartStax	x	x	x	5% in bag
Trecepta ^a (TRE)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x	x	x					x			^a 5%
Trecepta RIB Complete ^b (TRERIB)	Vip3A																^b 5% in bag
TRisect (CHR)	Cry1F mCry3A	x	x	x	x	x	x					x	ECB FAW SWB WBC WCR	x	x		20%
VT DoublePRO ^a (VT2P)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x						CEW	x			^a 5%
VT2P RIB Complete ^b (VT2PRIB)																	^b 5% in bag
VT TriplePRO ^a (VT3P)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x					x	CEW	x			^a 20%
VT3P RIB Complete ^b (VT3PRIB)	Cry3Bb1												NCR WCR				^b 10% in bag
Yieldgard Corn Borer (YGC)	Cry1Ab	x	x										CEW	x			20%
Yieldgard Rootworm (YGRW)	Cry3Bb1											x	NCR WCR	x			20%
Yieldgard VT Triple (VT3)	Cry1Ab Cry3Bb1	x	x									x	CEW NCR WCR	x			20%

Bt Trait Table after proposed EPA changes

Eliminates singles & 'nonfunctional' pyramids

Trait packages in alphabetical order (acronym that may be used)	Bt protein(s) in the trait package	Marketed for control of:											Resistance confirmed to the combination of Bts in package (check local situation)	Herbicide trait			Non-Bt Refuge % (cornbelt)
		B	C	E	F	S	S	T	W	C	R			G	L	E	
AcreMax Leptra (AML)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x	x		10% in bag
Agrisure Viptera 3110 (VR)	Cry1Ab Vip3A	x	x	x	x	x	x	x	x	x				x	x		20%
Agrisure Viptera 3111 (A4)	Cry1Ab Vip3A mCry3A	x	x	x	x	x	x	x	x	x			WCR	x	x		20%
Agrisure Viptera 3220 E-Z (VZ)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x			10% in bag
Agrisure Viptera 3330 E-Z	Cry1Ab Vip3A Cry1A.105/Cry2Ab2	x	x	x	x	x	x	x	x	x				x			10% in bag
Agrisure Duracade 5222 E-Z (D2)	Cry1Ab Cry1F Vip3A mCry3A eCry3.1Ab	x	x	x	x	x	x	x	x	x			WCR	x			10% in bag
Leptra (VYHR)	Cry1Ab Cry1F Vip3A	x	x	x	x	x	x	x	x	x				x	x		5%
Trecepta ^a (TRE)	Cry1A.105/Cry2Ab2	x	x	x	x	x	x							x			^a 5%
Trecepta RIB Complete ^b (TRERIB)	Vip3A																^b 10% in bag

What would be left?

- Agrisure Viptera
- Leptra
- Trecepta

3. Longer-term phase out 'non-functional' cotton varieties (5-year)

CryAc + Cry2Ab

Bollgard 2

= all non-VIP cotton

Cry1Ab + Cry2Ae

TwinLink

All in on VIP corn and cotton = increased selection pressure for evolution of VIP resistance

4. Increase refuge in seed blends from 5% to 10%

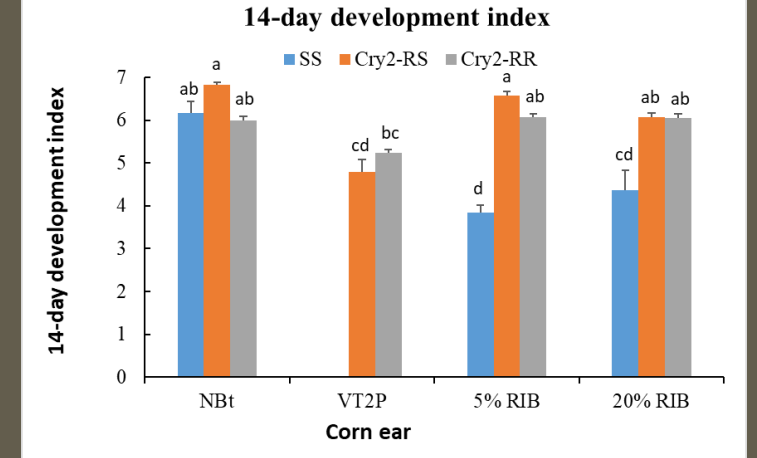
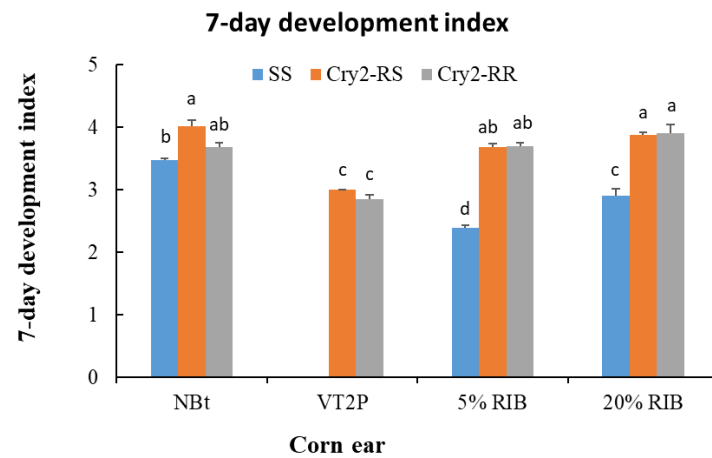
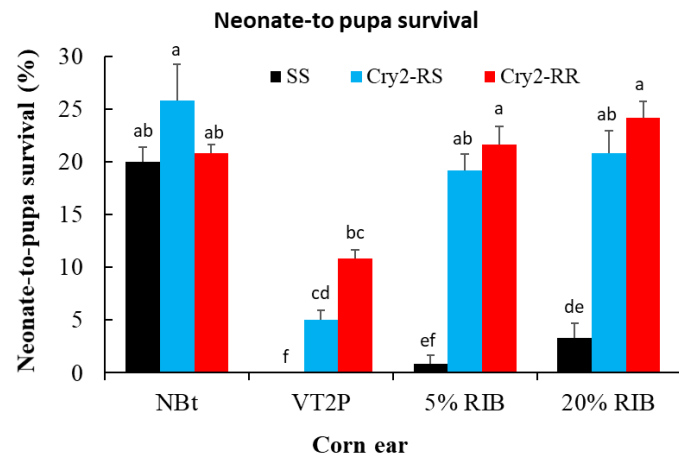


Cotton states will still be required to plant a 20% block refuge

What the entomologists told the EPA:

Increasing the % of non-Bt plants in the Vip seed blend may accelerate resistance to Vip

RIB CORN STUDY

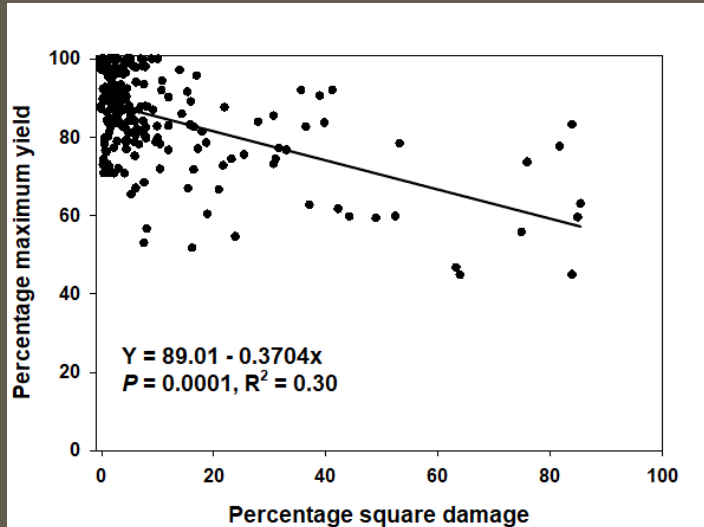


BT COTTON THRESHOLD

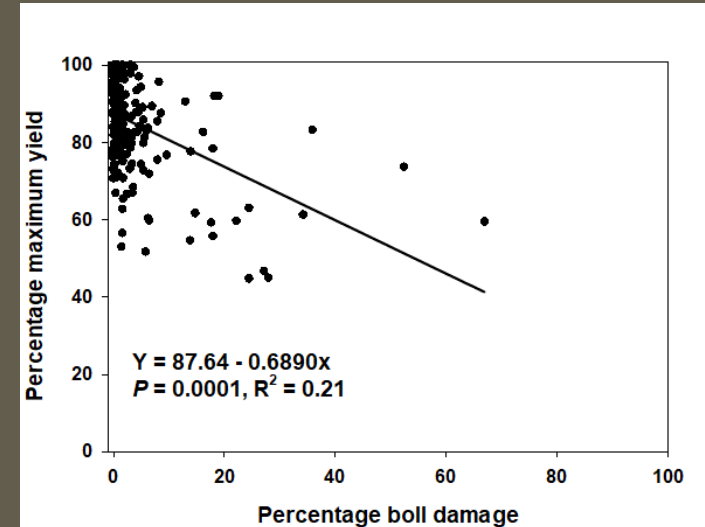


DEVELOPING A BOLLWORM ECONOMIC THRESHOLD

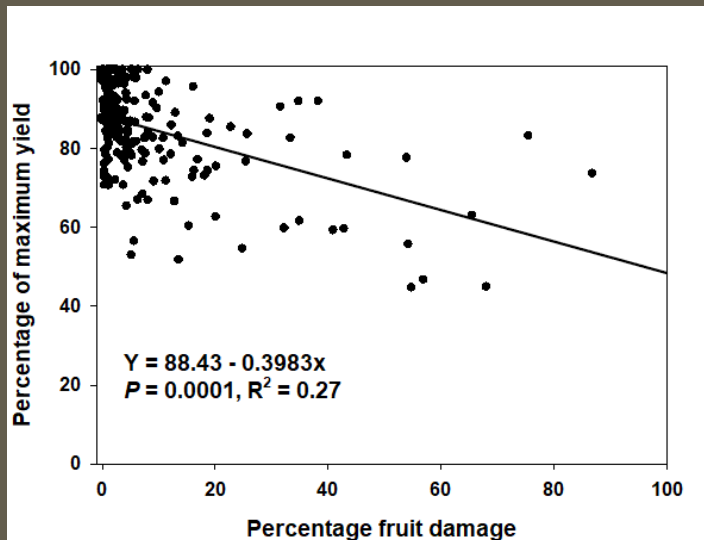
1% square damage =
0.37% yield reduction



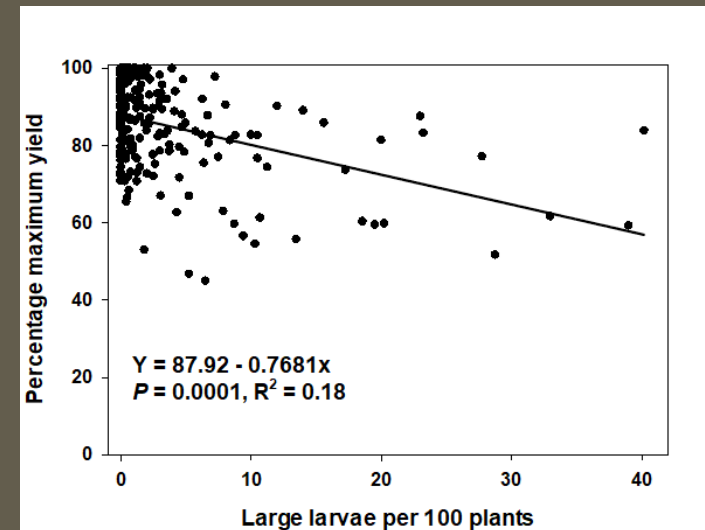
1% boll damage =
0.69% yield reduction



1% fruit damage =
0.40% yield reduction
(1 boll = 1.86 squares)



1% large larvae =
0.78% yield reduction



ECONOMIC THRESHOLD (70% EIL)

Yield potential (lbs-lint/ac)	Market value (\$/lbs)	% square damage	% boll damage	% fruit damage	% large larvae
1200	0.50	9	5	8	4
	0.60	8	4	7	4
	0.70	6	3	6	3
	0.80	6	3	5	3
1400	0.50	8	4	7	4
	0.60	6	3	6	3
	0.70	6	3	5	3
	0.80	5	3	5	2

Cost of control = \$22.97 [\$16.37 (insecticide) + \$6.60 (application)]

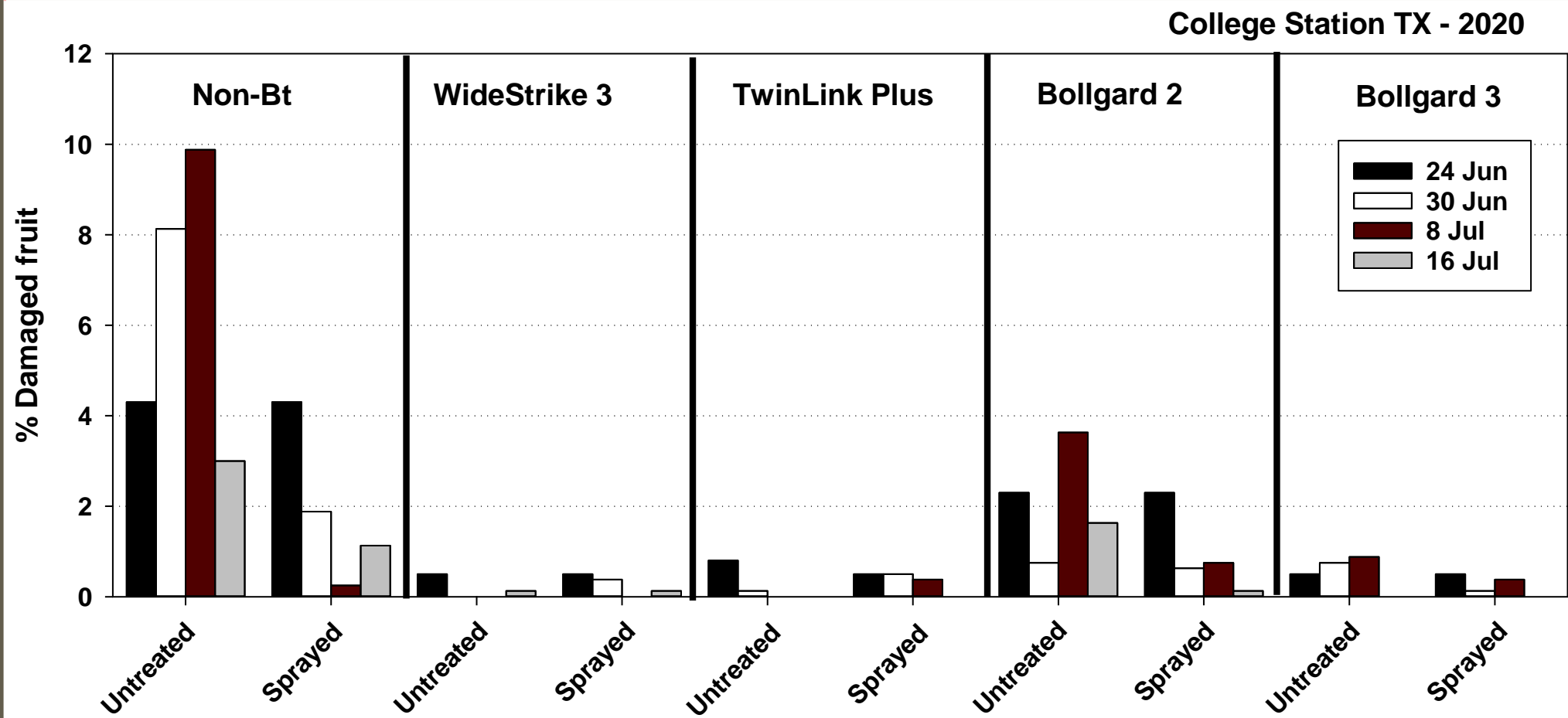


FIELD PERFORMANCE

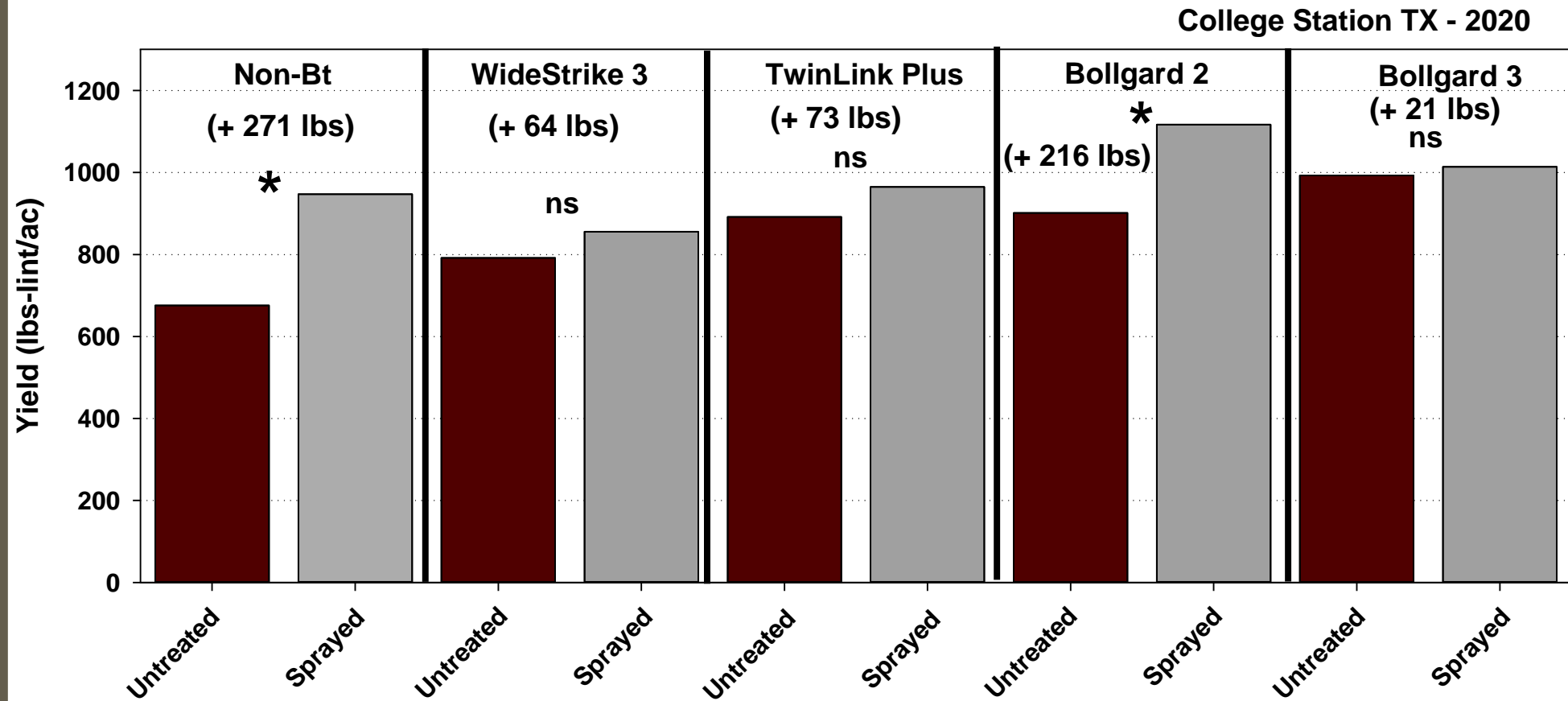
EFFICACY OF BT COTTON TECHNOLOGIES AND
VALUE OF TREATING WITH INSECTICIDE



Bt TRAITS (UNTREATED VS TREATED)



Bt TRAITS (UNTREATED VS TREATED)



NEW BOLLWORM INSECTICIDE CHOICES



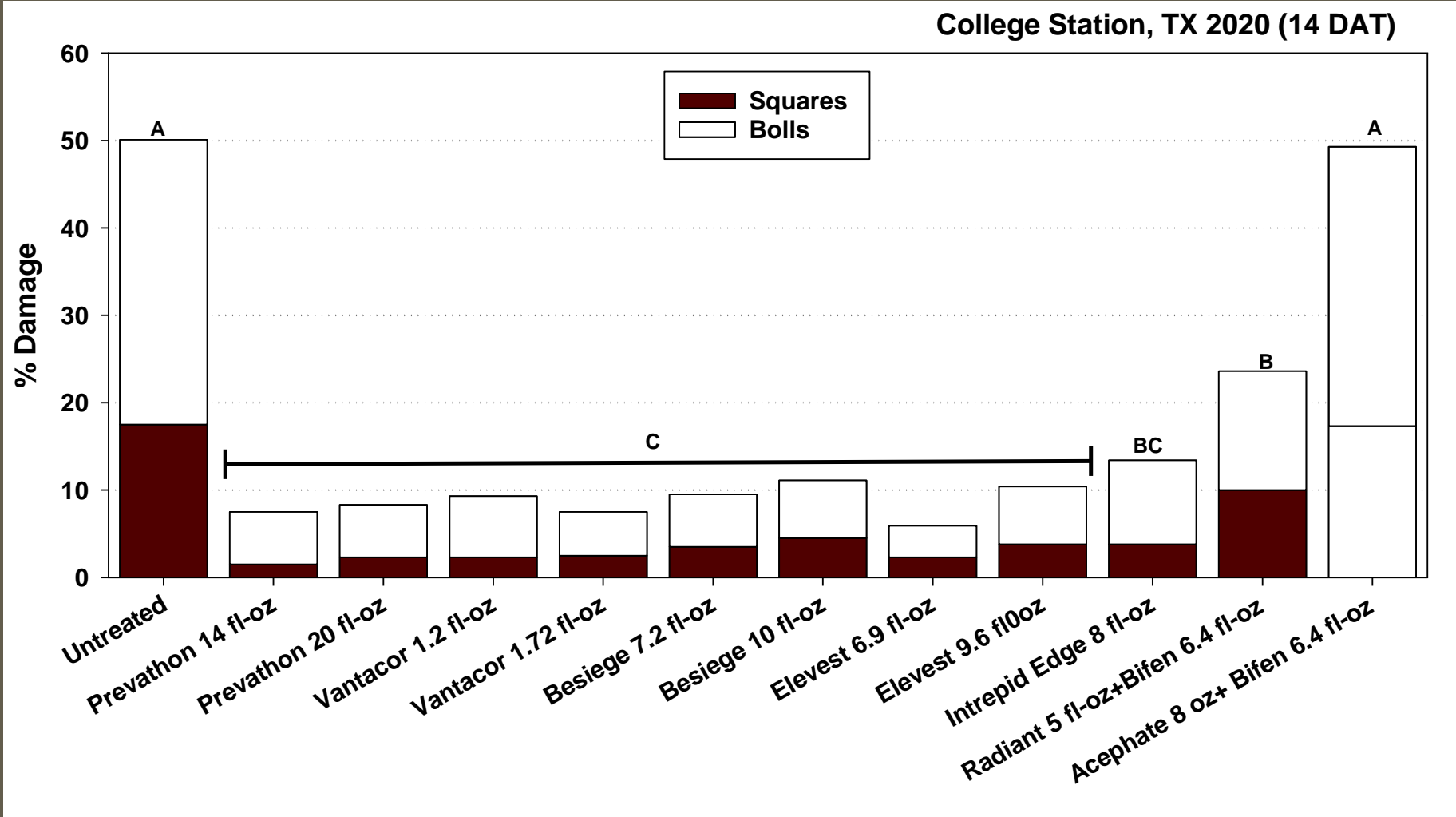
- Mixture of Chlorantraniliprole and Bifenthrin
- Rate range in cotton is 5.6-9.6 fl-oz/ac
- Prevathon at 14 fl-oz = 6.8 fl-oz Elevest (+ 4.5 fl-oz Bifenthrin 2EC)
- Prevathon at 20 fl-oz = 9.6 fl-oz Elevest (+ 6.4 fl-oz Bifenthrin 2EC)
- Thus, low rate (5.6 fl-oz) of Elevest = Prevathon 11.6 fl-oz



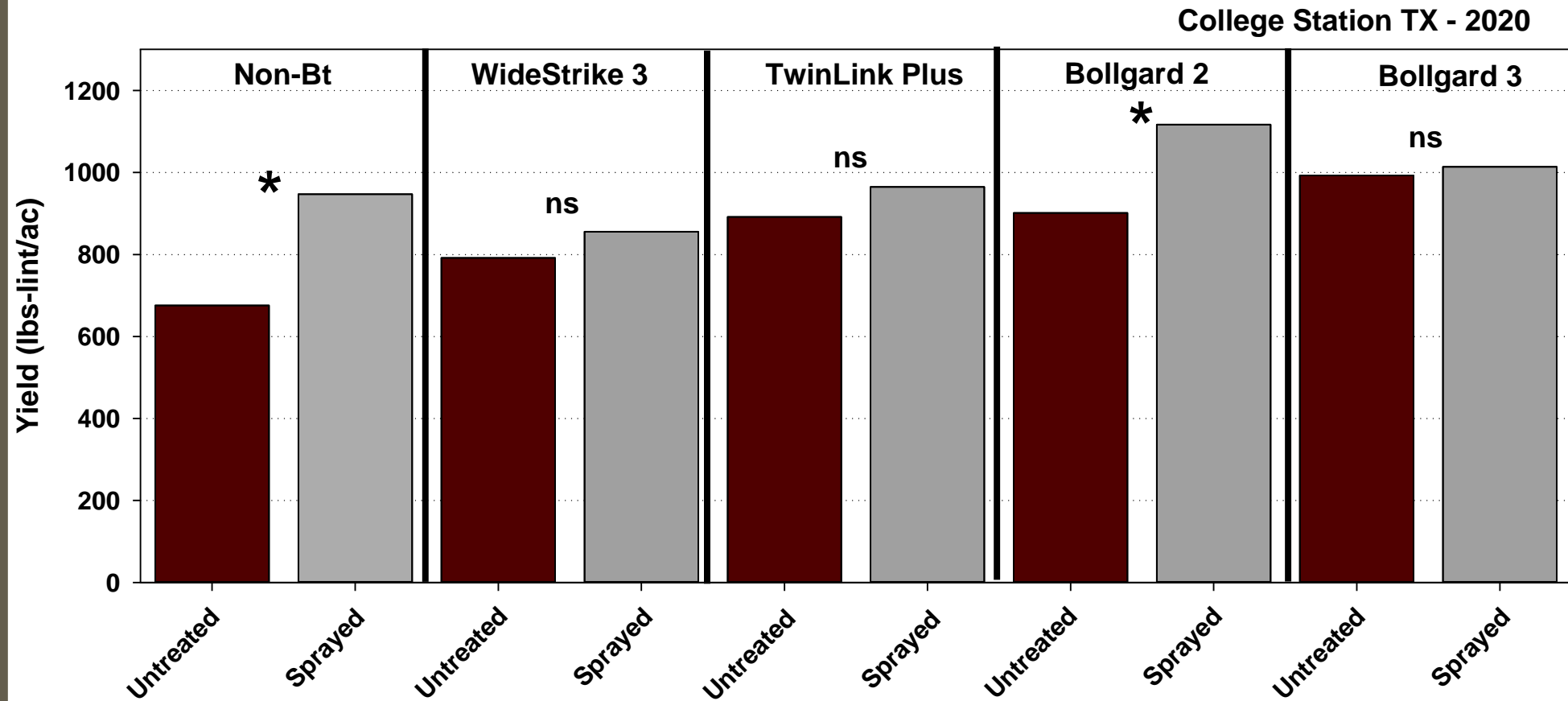
- More concentrated formulation of Chlorantraniliprole
 - 5 lbs-ai/gal
- Rate range in cotton is 1.2-2.5 fl-oz/ac
- Prevathon at 14 fl-oz = Vantacor at 1.2 fl-oz
- Prevathon at 20 fl-oz = Vantacor at 1.7 fl-oz

The logo for FMC, consisting of the letters "FMC" in a bold, red, sans-serif font.

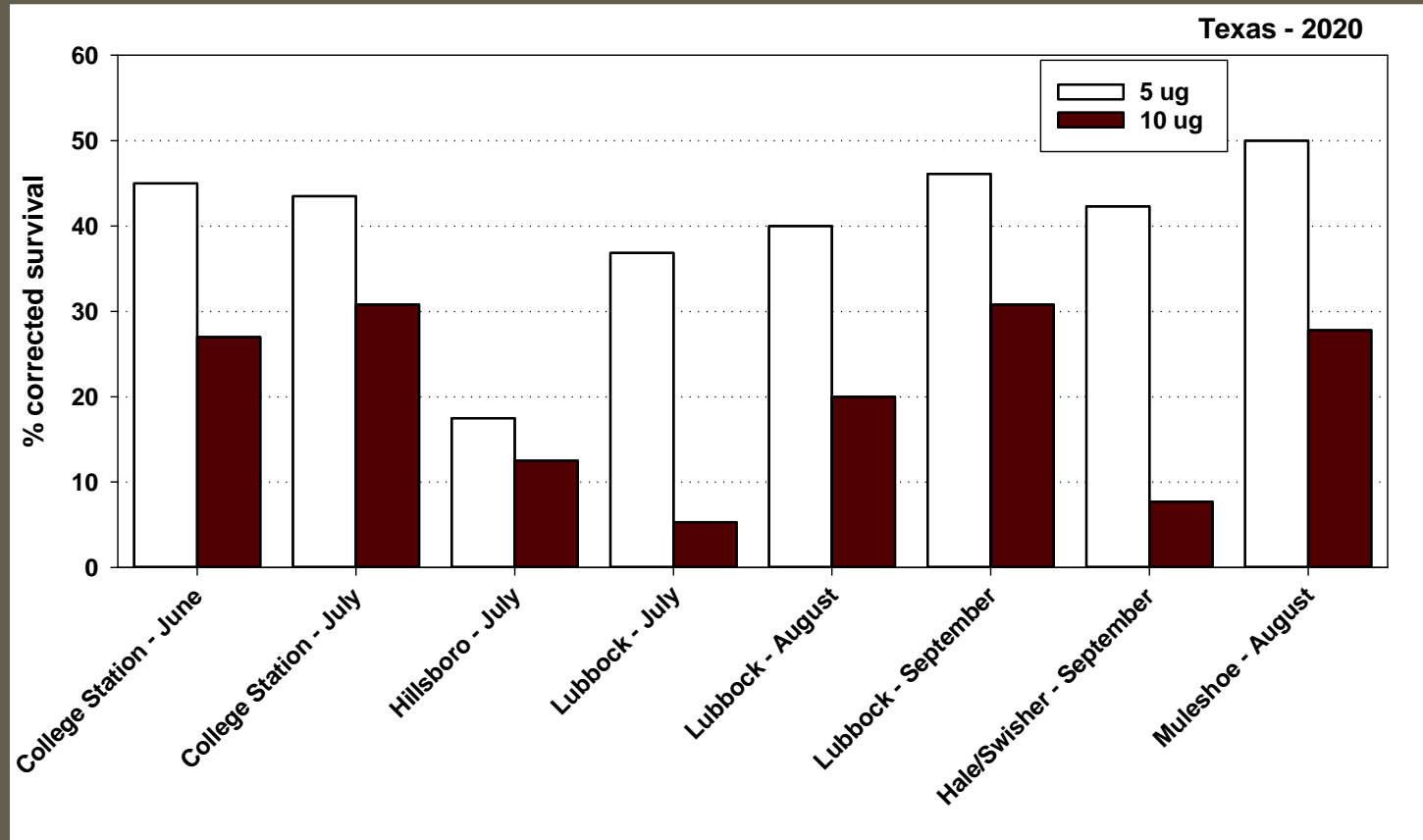
FOLIAR BOLLWORM CONTROL



Bt TRAITS (UNTREATED VS TREATED)



BEWARE OF PYRETHROID RESISTANCE



TEXAS TREATMENT RECOMMENDATIONS

- Areas with history of Bt failures or where reports of failures are occurring
 - Dual-gene cotton (VWS, TL, BG2)
 - Treat based on a 20% egg lay
 - 20% of plants found with at least 1 egg
 - Vip cotton (VWS3, TL+, BG3)
 - Treat based on 6% damaged squares and/or bolls with larvae present
 - If unacceptable injury is noted and facing a large egg lay consider spraying eggs
- Areas where Bt failures have not manifest
 - Treat based on 6% damaged squares and/or bolls with larvae present
- Use pyrethroids with caution
 - Resistance was detected throughout much of the state in 2018
 - Ramifications of flaring aphids and/or mites
- Prevathon and Besiege
 - Where residual control is needed
 - Rule of thumb each ounce of Prevathon or one-half ounce of Besiege will provide that length of control in days
 - Use Prevathon 18-20 fl-oz, Besiege at 9-10 fl-oz
 - Where residual control is not needed
 - Can get by with Prevathon 14 fl-oz, Besiege at 7-8 fl-oz
 - Timing is more important than rate

COTTON FLEAHOPPER RESEARCH



COTTON FLEAHOPPER INFESTATION – YIELD RESPONSE

- Tests conducting in 2019 & 2020
- Used linear regression to determine the relationship with yield
- For every 1% increase in CFH infestation there is reduction of 2.65 lbs-lint/ac
- Calculating the EIL with cotton valued at \$0.70/lb-lint and a single insecticide application at \$10/ac

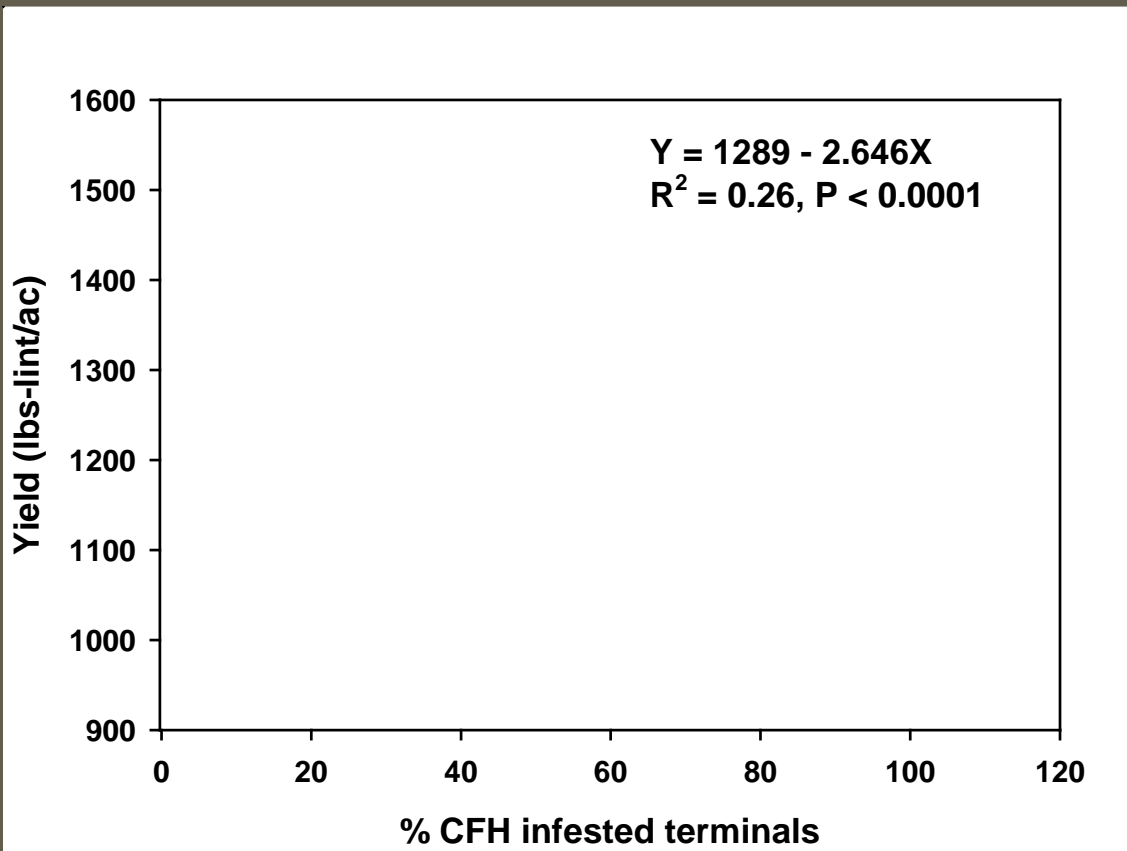


Table 2. Calculated economic injury level and threshold for CFH.

No. of insecticide applications	% CFH infested cotton terminals	
	Economic Injury Level (EIL)	Economic Threshold (ET=70% of EIL)
1	5.40	4.42
2	10.80	8.64
3	16.20	12.96

Based on \$0.70/lbs-lint cotton and \$10.00/ac per insecticide application.



COMPENSATION

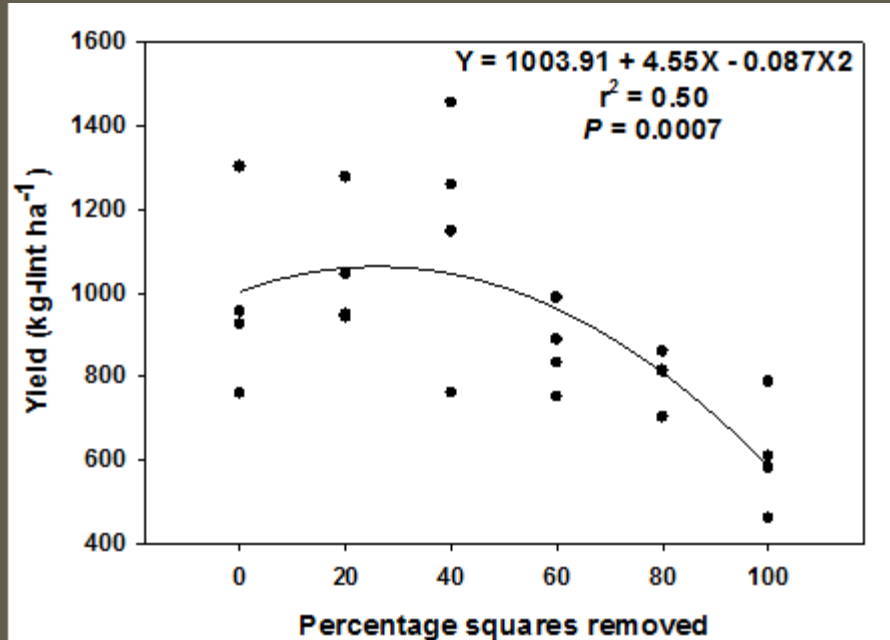


Figure 4. Curvilinear relationship by plot between pre-bloom square removal and mean lint yield in full-season cotton, 2011.

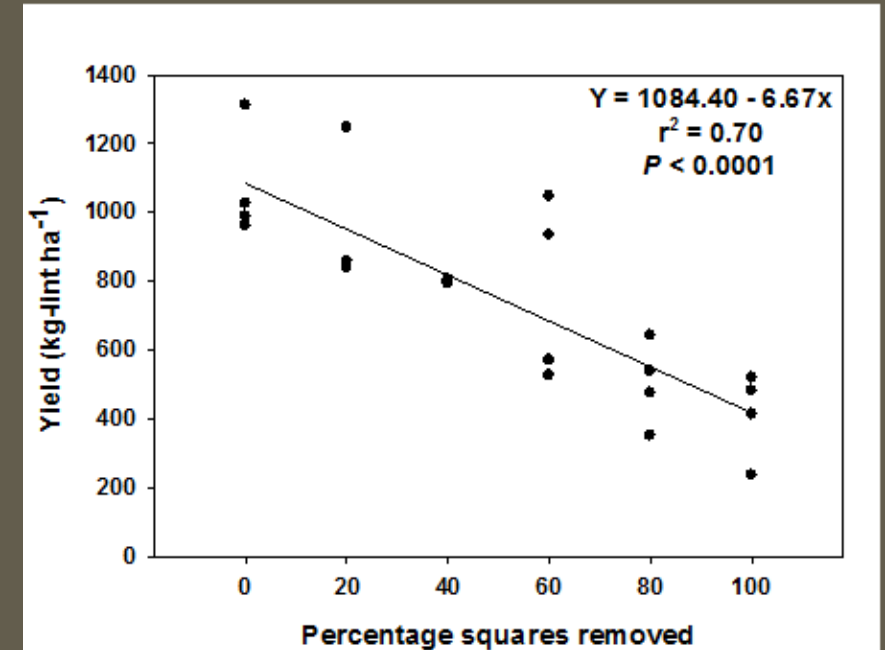


Figure 3. Linear relationship by plot between pre-bloom square removal and mean lint yield in early-terminated cotton, 2011.

IMPACT ON MICRONAIRE

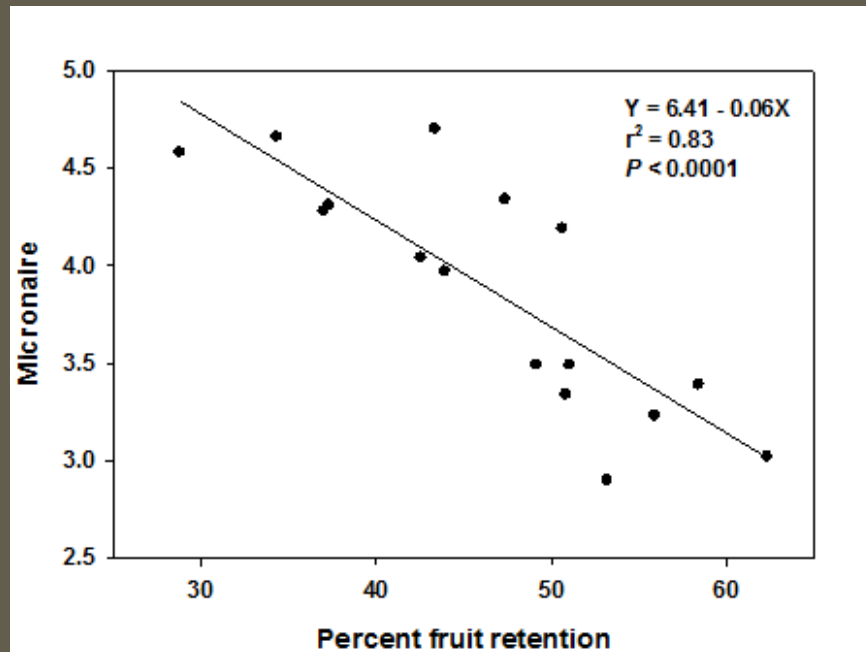


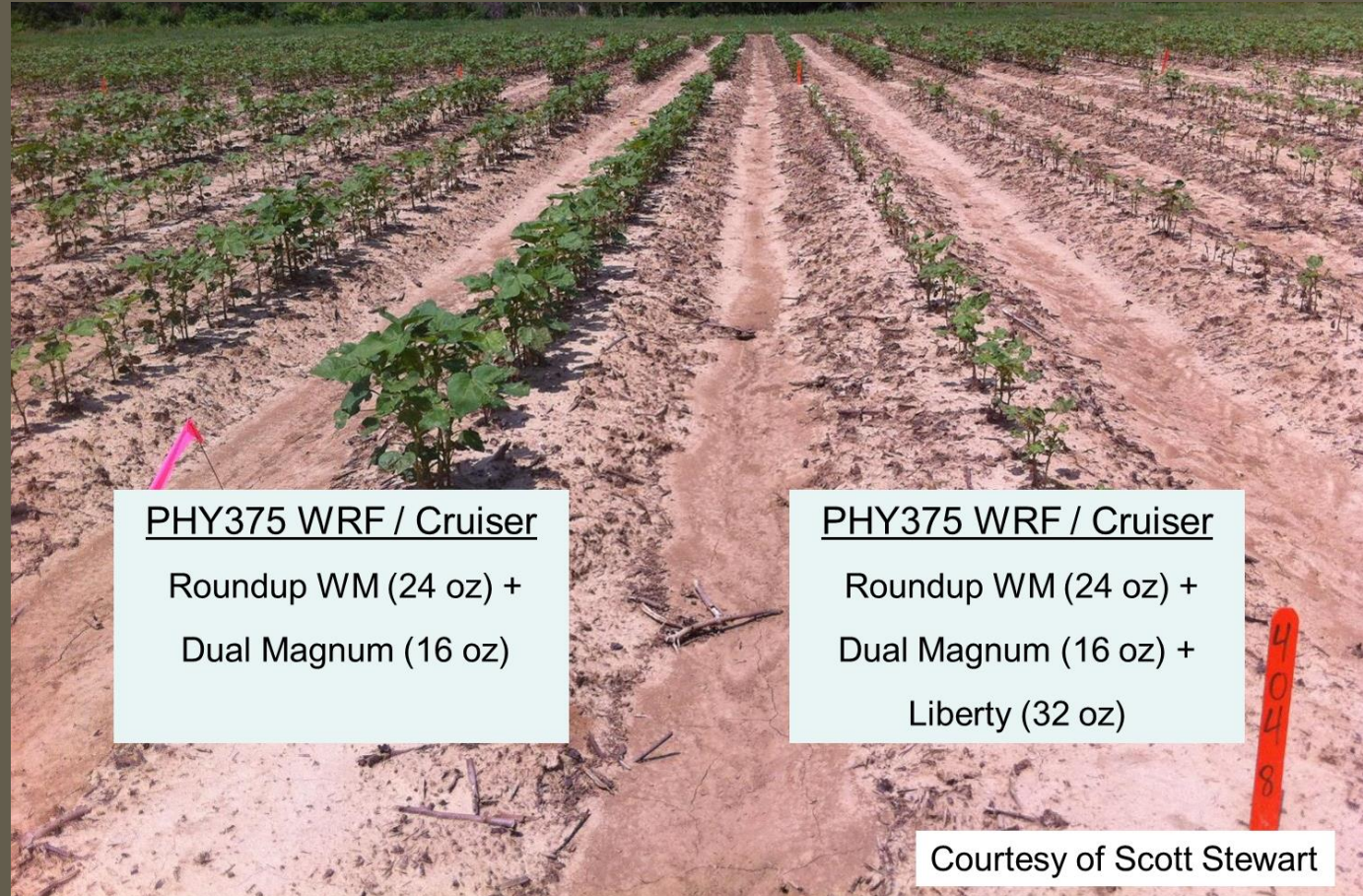
Figure 1. Linear relationship by plot between percent fruit retention and fiber micronaire, 2009.



THRIPS MANAGEMENT



PRE-EMERGENT HERBICIDE AND THRIPS



PHY375 WRF / Cruiser

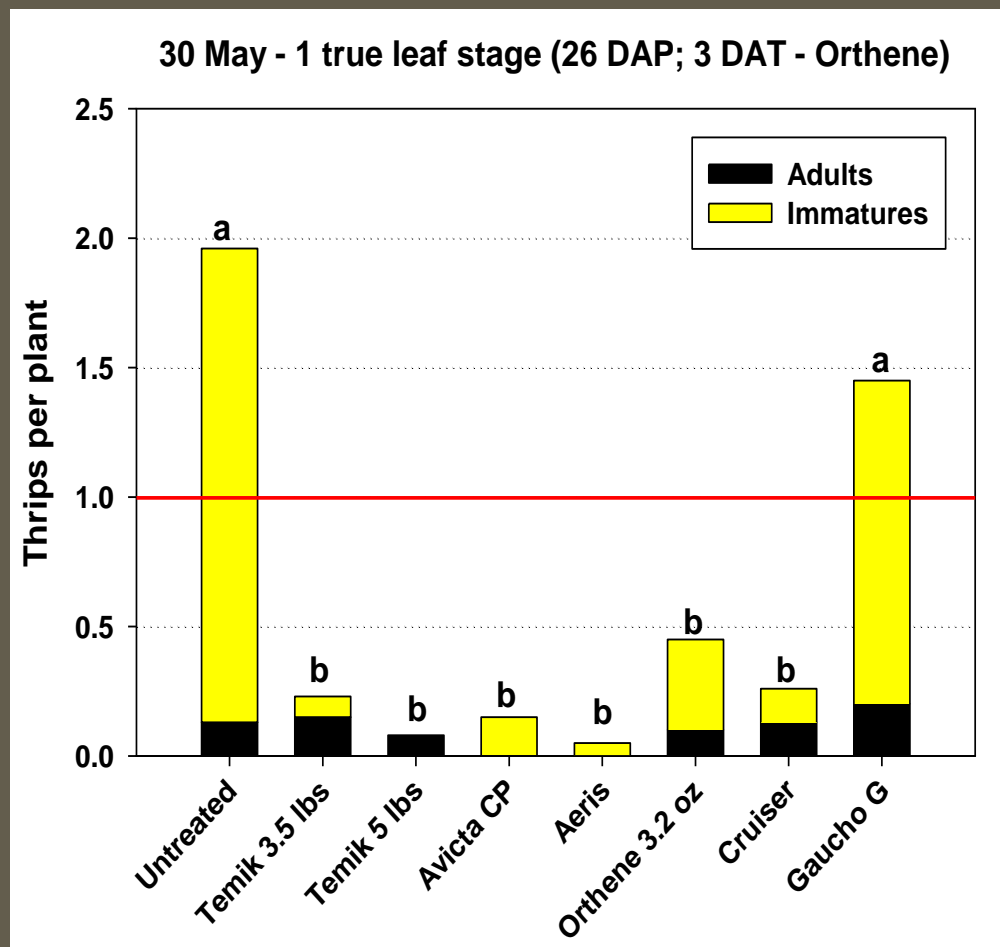
Roundup WM (24 oz) +
Dual Magnum (16 oz)

PHY375 WRF / Cruiser

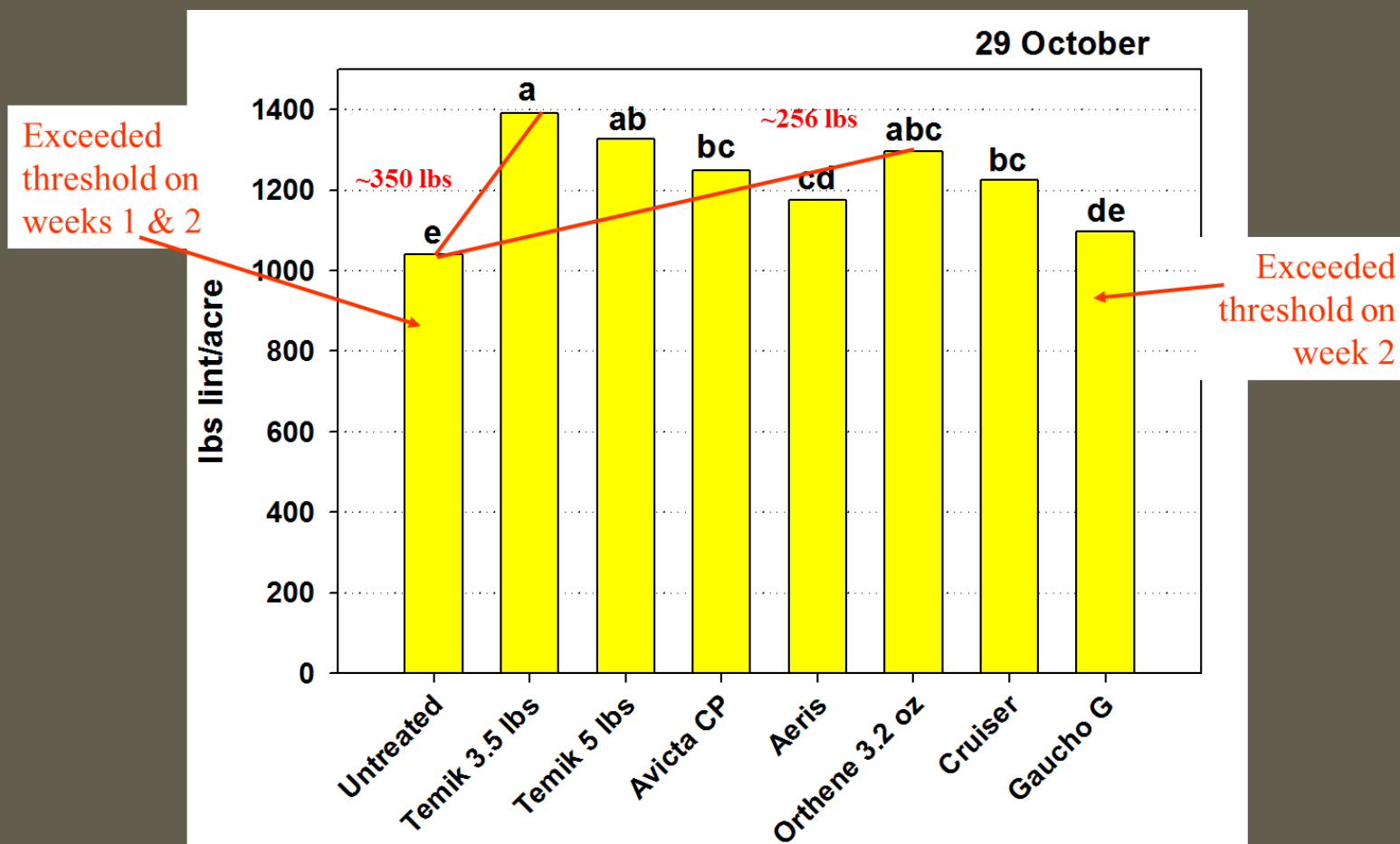
Roundup WM (24 oz) +
Dual Magnum (16 oz) +
Liberty (32 oz)

Courtesy of Scott Stewart

WESTERN FLOWER THRIPS



WESTERN FLOWER THRIPS



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TEXAS A&M
AGRILIFE
EXTENSION

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United States Department of Agriculture
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