Corn Hybrid and *Bt* Transgene Performance in Yield and Protection from Pre-harvest Losses Caused by Lepidopteran Feeding

Luke Pruter[1], Michael Brewer[1], Mac Young[1], Julio Bernal [2]

[1] Texas A&M AgriLife Research, Department of Entomology,
Corpus Christi, TX
2 Texas A&M University, Department of Entomology,
College Station, TX

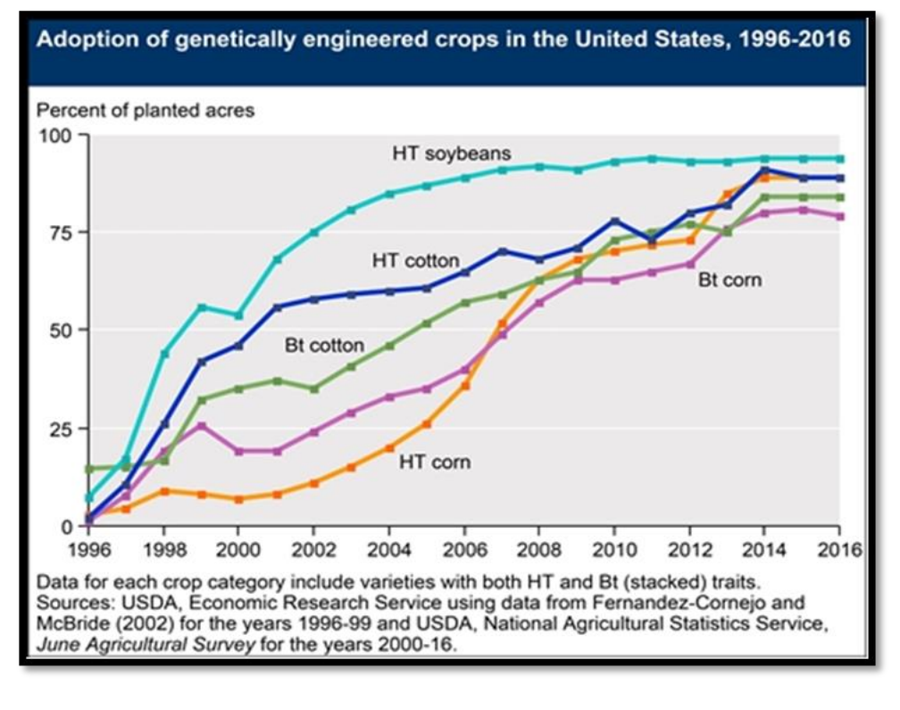
INTRODUCTION

One of the most common problems facing Texas corn farmers is the injury brought on by corn feeding lepidopteran pests [1]. The fall armyworm and corn earworm are continuous residents of Texas that are known to reduce health and value of corn [2, 3]. Insect injury can reduce yield although the relationship is variable across hybrids [4]. Advancing technologies in the farming industry have offered a solution to this problem that doesn't involve increasing pesticide use. Corn growers have the option to combat insect injury on their corn with the use of genetically modified seed, however there is added cost to the seed. This poster compares the effects of hybrid background and their commercial *Bt* transgenes in their ability to reduce pre-harvest losses due to insect feeding.

BACILLUS THURINGIENSIS OR *Bt*

Bacillus thuringiensis (or *Bt*) is a bacterium commonly used as a biological pesticide. When *Bt* toxin is ingested by a lepidopterous insect it begins to crystalize in the gut, and destroys the digestive tract of the caterpillar feeding on it [6]. Since the release of transgenic *Bt* maize in 1996, many different types of *Bt* traits have been developed for sale. *Bt* corn has become increasingly popular over the last 15 years and has grew from about 8 percent of U.S. corn acreage in 1997, to 79 percent in 2016 [8]. There is a wide range of Lepidoptera control in corn with commercially available *Bt* transgenes [5]. This poster reviews the effectiveness of several Bt transgenes and hybrid families in their ability to reduce insect feeding, and preserve yield.

Adoption of genetically engineered crops in the United States, 1996-2016

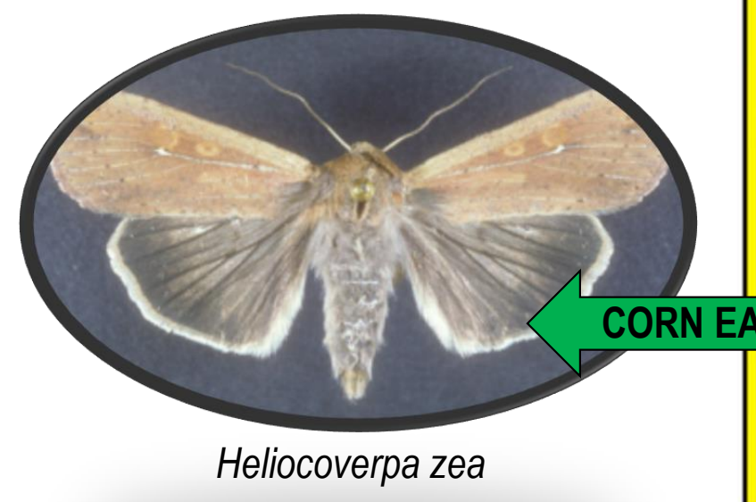


Data for each crop category include varieties with both HT and Bt (stacked) traits. Sources: USDA, Economic Research Service using data from Fernandez-Cornejo and McBride (2002) for the years 1996-99 and USDA, National Agricultural Statistics Service, *June Agricultural Survey* for the years 2000-16.

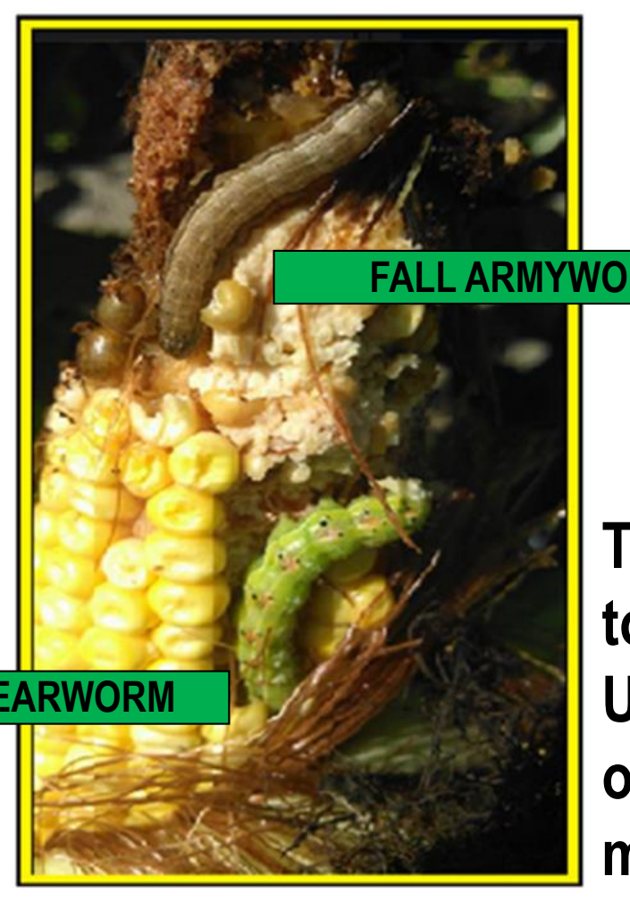
TARGET PESTS

CORN EARWORM

Heliocoverpa zea or the Corn earworm is an active resident of south Texas throughout the year [7].



Heliocoverpa zea



FALL ARMYWORM

Spodoptera frugiperda

The fall armyworm is native to southern regions of the United States, but it can only overwinter in the southern most regions of Texas [6].

OBJECTIVES

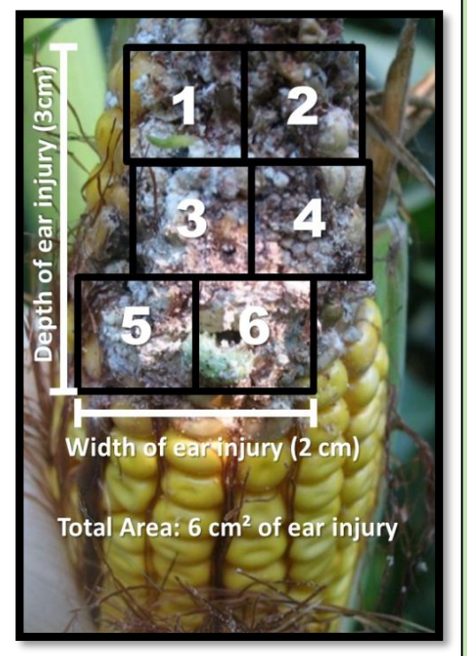
Objective 1: Evaluate yield and ear injury caused by insects of selected commercial hybrid families with and without *Bt* transgenes.

Objective 2: Evaluate the relative contribution of the hybrid families and the *Bt* transgenes in yield protection and ear injury.

Objective 3: Review financial indicators and compare hybrid family performance based on cumulative 10-year cash flow/per acre predictions including input costs.

METHODOLOGY

Random split block design trials were planted in Corpus Christi April 1, 2016. Plots were composed of 4 rows (38 in. x 20 ft.) There were 14 plots per rep. with a total of 5 reps. Ear injury measurements included total area of insect feeding injury (cm²), and the deepest point of insect injury measuring from the tip of the ear (cm). Yield measurements included harvest weight (lbs/bushel) and (moisture %) and were used to calculate the yield adjusted to (bushels/acre) used in objectives 1, 2, & 3.



Bt Transgene Protection/Abbreviation Guide

Bt Transgene Trade Name	Transgene Abbreviation	Corn Earworm Protection	Fall Armyworm Protection
No Bt Transgene	RR/RR2	No	No
Genuity® Smart Stax™	SS	Yes	Yes
Genuity®DroughtGard™	DG	No	No
Genuity® VT Double Pro™	VT2P	Yes	Yes
Genuity® VT Triple Pro™	VT3P	Yes	Yes
YieldGard™ + Herculex™	YHR	Yes	Yes
Agrisure® Viptera 3111™	V	Yes	Yes

OBJECTIVE 1: HYBRID FAMILY 1

HYBRID 1 GENETICS + SS

HYBRID FAMILY 1			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.82 ± 0.25	*Bt* proteins expressed	Cry1A.105, Cry2Ab2Cry1F, Cry3Bb1, Cry34Ab1/Cry35Ab1
Ear length (cm)	19.52 ± 0.34	Area of ear injury cm²	3.14 ± 0.88
Bushels per acre	106.67 ± 9.01	Depth of ear injury cm	2.78 ± 0.59

HYBRID 1 GENETICS + DGVT2P

HYBRID FAMILY 1			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.44 ± 0.04	*Bt* proteins expressed	Cry1A.105, Cry2Ab2
Ear length (cm)	19.44 ± 0.34	Area of ear injury cm²	2.96 ± 0.83
Bushels per acre	107.33 ± 6.14	Depth of ear injury cm	2.68 ± 0.50

OBJECTIVE 1: HYBRID FAMILY 2

HYBRID 2 GENETICS + VT2P

HYBRID FAMILY 2			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	15.3 ± 0.17	*Bt* proteins expressed	Cry1A.105, Cry2Ab2
Ear length (cm)	20.12 ± 0.14	Area of ear injury cm²	1.98 ± 0.58
Bushels per acre	138.29 ± 3.28	Depth of ear injury cm	2.1 ± 0.82

HYBRID 2 GENETICS + NO *Bt* (RR2)

HYBRID FAMILY 2			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	15.26 ± 0.19	*Bt* proteins expressed	No *Bt* proteins
Ear length (cm)	19.92 ± 0.25	Area of ear injury cm²	3.9 ± 0.37
Bushels per acre	135.71 ± 3.47	Depth of ear injury cm	2.86 ± 0.32

OBJECTIVE 1: HYBRID FAMILY 3

HYBRID 3 GENETICS + VT3P

HYBRID FAMILY 3			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.4 ± 0.15	*Bt* proteins expressed	Cry1A.105, Cry2Ab2, Cry3Bb1
Ear length (cm)	19.08 ± 0.33	Area of ear injury cm²	1.76 ± 0.36
Bushels per acre	119.69 ± 3.43	Depth of ear injury cm	1.30 ± 0.18

HYBRID 3 GENETICS + NO *Bt* (RR2)

HYBRID FAMILY 3			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.68 ± 0.15	*Bt* proteins expressed	No *Bt* proteins
Ear length (cm)	18.72 ± 0.30	Area of ear injury cm²	4.00 ± 0.64
Bushels per acre	115.91 ± 4.26	Depth of ear injury cm	2.94 ± 0.52

OBJECTIVE 1: HYBRID FAMILY 4

HYBRID 4 GENETICS + NO *Bt* (RR)

HYBRID FAMILY 4			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.36 ± 0.10	*Bt* proteins expressed	No *Bt* proteins
Ear length (cm)	19.64 ± 0.46	Area of ear injury cm²	6.12 ± 0.68
Bushels per acre	101.16 ± 3.89	Depth of ear injury cm	3.64 ± 0.36

HYBRID 4 GENETICS + VYHR

HYBRID FAMILY 4			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	13.84 ± 0.14	*Bt* proteins expressed	Vip3Aa20
Ear length (cm)	20.34 ± 0.35	Area of ear injury cm²	0.15 ± 0.12
Bushels per acre	97.29 ± 5.25	Depth of ear injury cm	0.10 ± 0.08

HYBRID 4 GENETICS + YHR

HYBRID FAMILY 4			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	16.26 ± 2.31	*Bt* proteins expressed	Cry1Fa2, Cry1Ab
Ear length (cm)	20.26 ± 0.30	Area of ear injury cm²	3.72 ± 0.48
Bushels per acre	112.47 ± 4.5	Depth of ear injury cm	2.86 ± 0.38

OBJECTIVE 1: HYBRID FAMILY 5

HYBRID 5 GENETICS + VT2P

HYBRID FAMILY 5			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.27 ± 0.10	*Bt* proteins expressed	Cry1A.105, Cry2Ab2
Ear length (cm)	21.13 ± 0.29	Area of ear injury cm²	3.1 ± 0.36
Bushels per acre	109.34 ± 4.48	Depth of ear injury cm	2.28 ± 0.13

OBJECTIVE 1: HYBRID FAMILY 5 CONTINUED

HYBRID 5 GENETICS + VT3P

HYBRID FAMILY 5			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.06 ± 0.24	*Bt* proteins expressed	Cry1A.105, Cry2Ab2, Cry3Bb1
Ear length (cm)	20.2 ± 0.35	Area of ear injury cm²	3.48 ± 1.19
Bushels per acre	112.01 ± 3.01	Depth of ear injury cm	2.58 ± 0.83

OBJECTIVE 1: HYBRID FAMILY 6

HYBRID 6 GENETICS + NO *Bt* (RR)

HYBRID FAMILY 6			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.2 ± 0.13	*Bt* proteins expressed	No *Bt* proteins
Ear length (cm)	18.66 ± 0.3	Area of ear injury cm²	6.72 ± 0.55
Bushels per acre	81.78 ± 9.73	Depth of ear injury cm	3.76 ± 0.25

HYBRID 6 GENETICS + VT3P

HYBRID FAMILY 6			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.4± 0.21	*Bt* proteins expressed	Cry1A.105, Cry2Ab2, Cry3Bb1
Ear length (cm)	18.78 ± 0.45	Area of ear injury cm²	5.26 ± 0.65
Bushels per acre	101.86 ± 8.78	Depth of ear injury cm	2.92 ± 0.23

HYBRID 6 GENETICS + SS

HYBRID FAMILY 6			
YIELD STATISTICS		INSECT DAMAGE	
Ear circumference (cm)	14.12 ± 0.52	*Bt* proteins expressed	Cry1A.105, Cry2Ab2Cry1F, Cry3Bb1, Cry34Ab1/Cry35Ab1
Ear length (cm)	18.04 ± 0.74	Area of ear injury cm²	2.76 ± 0.23
Bushels per acre	104.07 ± 3.68	Depth of ear injury cm	2.12 ± 0.22

OBJECTIVE 2: INSECT DAMAGE RESULTS

Hybrid Family	*Bt* Transgene	Means Separation	Mean Ear Injury (cm²)	Standard Error
6	RR	A	6.40	0.56
4	RR	A B	6.00	0.56
6	VT3P	B C	4.67	0.55
3	RR2	C D	3.94	0.56
2	RR2	C D E	3.87	0.56
4	YHR	C D E F	3.67	0.59
5	VT3P	C D E F	3.48	0.55
1	SS	C D E F	3.10	0.56
1	DGVT2P	D E F	3.00	0.59
5	VT2P	D E F	2.97	0.56
6	SS	D E F	2.85	0.56
3	VT3P	E F	2.33	0.55
2	VT2P	F	2.22	0.56
4	VYHR	G	0.39	0.59

Bt Transgene	Means Separation	Mean Ear Injury (cm²)	Standard Error
RR	A	5.75	0.70
RR2	A B	3.82	0.70
YHR	A B C	3.58	0.90
VT3P	B C	3.47	0.59
DGVT2P	B C	3.09	0.90
SS	B C	3.03	0.70
VT2P	B C	2.71	0.70
VYHR	C	1.18	0.90

Effect on Ear Injury (area cm²)	Contribution to Variation (%)
Hybrid Genetics [Not Including *Bt* transgene]	16.18
Bt transgene	43.95

Bt transgene is a significant factor relating to the amount of ear injury caused by insect feeding (P<.0001). The *Bt* transgenes accounted for 44% of the variation relating to insect injury. Hybrid family was also statistically significant (P=0.003), but played a much smaller role than *Bt* transgene accounting for 16% of the ear injury variation. This means that the *Bt* transgene is almost 3 times as important as hybrid family genetics when measuring insect derived ear injury. Looking at the transgene effect across the hybrids, hybrids containing no *Bt* transgenes (RR, and RR2) have significantly more insect ear injury, than hybrids with *Bt* transgenes (P=0.014). Also, the hybrid containing the Agrisure® Viptera™ *Bt* transgene (VYHR) had 5 times less injury than its closest competitor. These differences were seen even under the modest ear feeding pressure observed during 2016 (>12 cm² of ear injury has been previously seen in this location).

OBJECTIVE 2: YIELD RESULTS

Hybrid Family	*Bt* Transgene	Means Separation	Mean Bu/Acre	Standard Error
2	VT2P	A	133.61	5.19
2	RR2	A B	131.78	5.19
3	VT3P	B C	117.75	5.15
3	RR2	C	116.24	5.19
4	YHR	C D	112.10	5.25
5	VT3P	C D	111.72	5.15
5	VT2P	C D	110.88	5.19
1	DGVT2P	C D	107.7	5.25
1	SS	C D	106.9	5.19
6	SS	C D	104.86	5.19
6	VT3P	C D	103.74	5.15
4	RR	D	101.16	5.19
4	VYHR	D E	99.552	5.78
6	RR	E	85.95	5.19

Bt Transgene	Means Separation	Mean Bu/Acre	Standard Error
RR2	A	117.46	6.37
VT2P	A	116.52	6.37
YHR	A	110.74	7.45
VT3P	A	110.66	5.66
DGVT2P	A	109.14	7.45
SS	A	107.78	6.37
VYHR	A	106.17	7.52
RR	A	101.20	6.37

Effect on Yield (Bushels/Acre)	Contribution to Variation (%)
Hybrid Genetics [not including *Bt* transgene]	34.00
Bt transgene	19.48

OBJECTIVE 2: YIELD RESULTS CONTINUED

Hybrid family genetics accounted for 34% of the variation of yield and was significant (P<0.0001). The *Bt* transgenes accounted for only 19% of the variation in yield which is significant (P=0.032), but when it comes to yield the hybrid family is twice as important as *Bt* transgene. Although the *Bt* transgene effect influenced yield under our modest ear-feeding pressure, hybrid genetics played a much larger role.

OBJECTIVE 3: REVIEW FINANCIAL INDICATORS

10-Year Average Financial Indicators per Acre for 2016 *Bt* Transgene Test

Hybrid Family	*Bt* Transgene	Selected Input Costs			Yield/AC in Bushel/Acre	First Year Price/ Bu. (b)	10 Year Averages Per Acre			Cumulative 10-Yr Cash Flow/Acre x $1,000
		Seed Cost		Hauling			Total Cash Receipts	Total Cash Costs	Net Cash Farm Income	
		in $/Bag	in $/Ac.	in $/Ac			x $1,000	x $1,000	x $1,000	
6	SS	270	67.5	20.40	104.1	$3.25	0.37	0.48	-0.11	-1.05
6	VT2P	240	60	19.96	101.9	3.25	0.37	0.47	-0.10	-1.04
6	No *Bt* (RR)	180	45	16.03	81.8	3.25	0.30	0.47	-0.17	-1.71
1	DGVT2P	300	75	21.04	107.3	3.25	0.38	0.49	-0.10	-1.02
1	SS	300	75	20.91	106.7	3.25	0.38	0.49	-0.11	-1.05
5	VT3P	280	70	21.95	112.0	3.25	0.40	0.48	-0.08	-0.75
5	VT2P	250	62.5	21.43	109.3	3.25	0.39	0.47	-0.08	-0.75
2	VT2P	250	62.5	27.10	138.3	3.25	0.49	0.45	0.04	0.43
2	No *Bt* (RR2)	200	50	26.60	135.7	3.25	0.48	0.44	0.05	0.49
3	VT3P	280	70	23.46	119.7	3.25	0.43	0.47	-0.04	-0.42
3	No *Bt* (RR2)	200	50	22.72	115.9	3.25	0.41	0.45	-0.03	-0.30
4	VYHR	280	70	19.07	97.3	3.25	0.35	0.49	-0.14	-1.39
4	YHR	240	60	22.04	112.5	3.25	0.40	0.46	-0.06	-0.58
4	No *Bt* (RR)	200	50	19.83	101.2	3.25	0.35	0.46	-0.09	-0.92

The financial indicators listed above are rough estimates of the profitability of each hybrid when including inputs such as seed price and hauling costs under the modest ear-feeding pressure experienced in 2016. Members of hybrid family 1 performed similarly. Both members of hybrid family 2 (RR) had the highest cumulative 10-year cash flow projection (CFP). However hybrid family 2 (RR) ($490/acre) was more profitable than its (VT2P) counterpart ($430/acre). Hybrid family 3 (RR2) had a higher 10-year CFP over its (VT3P) counterpart. Hybrid family 4 saw its highest return with the (YHR) *Bt* transgene package followed by (No *Bt* (RR)) and following by VYHR due to the high input costs under this modest ear-feeding pressure. Hybrid family 5 (VT3P) slightly outperformed (VT2P) in yield, but the increased seed cost for (VT3P) made their 10-year CFP identical. Hybrid family 6 (SS) and (VT2P) both performed similarly beating out their (RR) counterpart in 10-year CFP even though the input costs were double. (Provided by Mac Young: based on experimental findings)

CONCLUSIONS

In Texas where insect injury is common, it's likely that corn farmers would see a significant reduction in ear injury caused by lepidopteran species if their hybrids incorporate *Bt* transgenes. Also, not all *Bt* transgenes are created equal. Hybrids containing Agrisure® Viptera™ transgenes will likely experience 5x less insect feeding injury to the ear when compared to all other *Bt* transgenes. However, the *Bt* transgenes only accounted for 19% of the variation in yield. This means that a *Bt* transgene will likely not make up for a poor hybrid selection. A farmer would be prudent to select a high yielding hybrid before selecting a *Bt* transgene package although both are important in Texas.

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