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Do Refuge Requirements for Biotechnology Crops Promote Economic Efficiency? Some Evidence for Bt Cotton

Michael J. Livingston, Nicholas P. Storer, John W. Van Duyn, and George G. Kennedy

We examine producer behavior, resistance evolution, and returns under alternative refuge requirements in an eastern North Carolina region with multiple corn, cotton, and soybean fields infested by a mobile pest. Returns are highest, pyrethroid sprays occur least frequently, and pyrethroid resistance evolution is delayed most effectively with no refuge requirement. Complying with the current 20% refuge requirement costs the producer $8.67 per cotton acre, or $34.21 per non-transgenic insecticidal (Bt) cotton acre. Returns are highest under each refuge requirement when one-toxin Bt cotton is not phased out; however, removal of the technology at the earliest phase-out date minimizes regional pyrethroid sprays.

Key Words: bollworm, Bt cotton, pyrethroids, resistance, structured refuge, unstructured refuge

JEL Classifications: Q16, Q56, Q57, Q58, R34, R38

The bollworm (*Helicoverpa zea*) is an important pest of cotton in the Southeast and mid-South United States and, during 2000–2004, was associated with $341 million per year in producer losses.[1] The bollworm is also a pest of corn, soybean, and many other cultivated and wild plants. Cotton and soybean producers use foliar insecticides (e.g., pyrethroids) for control and, since 1996, corn and cotton producers have adopted transgenic insecticidal (Bt) crops. Because bollworms are highly mobile (Gould et al., Kennedy and Storer) and because there is no direct pecuniary cost for killing them, a regional population's susceptibility to a control toxin is an open-

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Michael J. Livingston is agricultural economist, Economic Research Service, U.S. Department of Agriculture. Nicholas P. Storer is entomologist, Dow Agrosciences, LLC. John W. Van Duyn and George G. Kennedy are, respectively, Philip Morris Professor and William Neal Reynolds Professor of Agriculture, Department of Entomology, North Carolina State University.

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[1] We use the 2005 price floor (Table 1) and mean state-level control costs and yield losses attributed to the bollworm-budworm complex and mean U.S.-level fractions of the bollworm-budworm complex composed of bollworms (Williams) to estimate producer loss. We report all pecuniary values in 2005 US dollars using the implicit price deflator for real gross domestic product (U.S. Department of Commerce).

Table 1. Model Parameters, Values, and Sources

Parameter	Value	Source
Day first-generation flight begins (June 28)	25	Storer, Storer et al. (2003a, 2003b)
Day cornfields start to silk (July 6)	33	
Day corn preference starts decline (July 14)	41	
Day second-generation flight begins (July 23)	50	
Day early soybean preference starts decline (July 24)	51	
Day corn preference reaches minimum (July 24)	51	
Earliest pupal diapause day (July 30)	57	
Day early soybean preference reaches minimum (August 3)	61	
Day late soybean preference starts to increase (August 6)	64	
Day early soybean starts to deteriorate (August 10)	68	
Day late soybean preference reaches maximum (August 11)	69	
Day cotton starts to deteriorate (August 20)	78	
Day late soybean starts to deteriorate (August 20)	78	
Mean pupal diapause day (August 27)	85	
Last day of the year (October 5)	124	
Acres per field	10	
Initial population of adults in each field	10,000	
Corn ears per cornfield	220,000	
Egg spray threshold for non-Bt cotton field	600,000	
Larval spray threshold for cotton field	65,000	
Larval spray threshold for soybean field	185,000	
Overwinter survival rate for diapaused pupae	0.0340	
Initial preference for corn (relative to cotton)	10.0000	
Initial early soybean preference (relative to cotton)	1.4000	
Initial late soybean preference (relative to cotton)	0.0400	
Adult daily survival rate	0.8500	
Eggs per adult female when day < 25	1.7662	
Eggs per adult female when $25 \leq$ day < 50	15.4543	
Eggs per adult female when day ≥ 50	2.6493	
Initial proportion of adults migrating between fields	0.1000	
Maximum number of fields adults can fly (d^{max})	8.6603	
Variance of bivariate normal distance kernel ($\sigma^2 = d^{max}/2$)	4.3301	
Cry1A resistance gene frequency beginning of 2000	4.3×10^{-4}	Burd et al.
Cry2A resistance gene frequency beginning of 2000	3.9×10^{-4}	
Degree of dominance Cry1A resistance gene	0.5000	Kurtz, Gould, and Bradley (2004, 2005)
Degree of dominance Cry2A resistance trait	0.5000	
Susceptible genotype survival on Cry1A corn (*s1ab*)	0.1140	
Susceptible genotype survival on Cry1A cotton (*s1ac*)	0.0720	
Susceptible genotype survival vs. Cry2A cotton (*s2ab*)	0.0570	
Susceptible genotype survival vs. two-toxin cotton (*sdual*)	0.0130	
Heterozygote survival Cry1A Bt corn (*rs1ab*)	0.5570	
Heterozygote survival Cry1A Bt cotton (*rs1ac*)	0.5360	
Heterozygote survival Cry2A Bt cotton (*rs2ab*)	0.5285	
Fitness cost of Cry1A and Cry2A resistance gene	0.0250	

Table 1. (Continued)

Parameter	Value	Source
Pyrethroid resistance gene frequency beginning of 2000	0.2000	Livingston, Carlson, and Fackler (2002)
Resistant survival vs. pyrethroid (*rr*)	0.8500	
Heterozygote survival vs. pyrethroid (*rs*)	0.1300	
Susceptible survival vs. pyrethroid (*ss*)	0.0300	
Survival rate multiplier for neonates and young larvae vs. pyrethroid in soybean	0.1333	Storer
Survival rate multiplier for adults vs. pyrethroid in cotton	0.8000	
Survival rate multiplier for neonates and larvae vs. pyrethroid in soybean	0.2667	
Survival rate multiplier for adults vs. pyrethroid in soybean	0.5164	
Annual discount rate $(1 - \rho)/\rho$	0.0534	Lence
Exponential cdf damage function parameter (δ)	−0.0270	Williams
Pyrethroid spray cost per field	$82.00	
Pest-free yield per Bt cotton field (pounds)	7,237	
Pest-free yield per non-Bt cotton field (pounds)	7,196	
Fixed cost per non-Bt cotton field	$4,748.40	Williams, USDA (1997, 2001a), Monsanto
Fixed cost per one-toxin Bt cotton field	$5,099.80	
Fixed cost per two-toxin Bt cotton field	$5,179.80	
Cotton lint price/pound (FSRIA 2002, price floor)	$0.742	2005 price floor, Farm Security and Rural Investment Act (FSRIA), 2002
Cotton seed price per ton	$110.09	USDA (2000, 2001b, 2002–2003, 2004a, 2005)
Proportion of corn planted to one-toxin Bt	0.2700	USDA-ERS (2005)

access resource. Profit maximizers might not consider the effects of bollworm control decisions on resistance, and as a result, resistance could evolve at an inefficient rate (Hueth and Regev).[2] One-toxin Bt cotton and Bt corn plants, which express the Cry1Ac toxin (Cry1), are only moderately effective against the bollworm. In addition, because selection pressure occurs continuously (Tabashnik et al.), the risk of Cry1 resistance evolving can be high, especially where corn and cotton are grown nearby (Storer). Because Bt resistance might increase producer costs, increase the use of environmentally harmful insecticides, and reduce the effectiveness of foliar Bt products, scientists, developers, and marketers of the Bt technology and regulatory officials have promoted regulations to conserve susceptibility in target pests (Matten and Reynolds).

The U.S. Environmental Protection Agency (EPA) requires Bt technology developers to design and enforce structured refuge requirements (refugia) to obtain temporary U.S. marketing rights. Refuges delay resistance by increasing the average rate susceptible insects survive and reproduce relative to resistant insects.[3] A structured refuge for a given Bt crop is an area of non-Bt fields planted to the same crop, whereas non-Bt varieties of different nearby cultivated or wild host plants are known as unstructured refuges. Cotton pro-

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[2] Bt toxins do not harm animals and beneficial insect predators and parasites (Mendelsohn et al.).

[3] We use the word "refugia" to refer to the structured refuge requirement(s) and the words "refuge" or "refuges" to refer to the actual physical structure(s) (e.g., non-Bt cotton fields).

ducers in the Southeast and mid-South have four refugia options, including the subject of this study, the external sprayable refugia, wherein a minimum 20% refuge is planted that can be treated with non-Bt foliar insecticides.

The appropriate size for this refugia, however, is uncertain. First, no change in Cry1 susceptibility in bollworms collected from 14 states had been detected as of 2003 (Blanco et al.), although resistance was predicted to evolve quickly (Gould and Tabashnik). Second, pest mobility is a principle justification for public intervention (Miranowski and Carlson); however, efficient cotton refugia have not been examined using a spatial model with pest mobility. Secchi and Babcock examine the effects of pest mobility, market penetration, conventional insecticide use, and refugia on resistance and corn producer returns. Focusing on one-toxin Bt corn, Hurley, Babcock, and Hellmich (2001) and Hurley et al. (2002) were the first to study efficient static refugia, and they evaluated efficient dynamic refugia under foliar insecticide use; however, those models and Livingston, Carlson, and Fackler's (2004) models of efficient static and dynamic refugia do not incorporate pest mobility. Third, Bt cotton varieties that express one (Cry1) and two toxins (the same Cry1 plus Cry2) are currently available, and even though the latter is over 80% more lethal to susceptible bollworms than the former (Kurtz, Gould, and Bradley 2004, 2005) and costs over $15 more per acre (Monsanto), the same refugia applies to both varieties. Fourth, the bollworm infests corn, cotton, and soybean in the Southeast; as a result, the availability of unstructured refuges is likely to have important effects on efficient refugia (Jackson, Bradley, and Van Duyn). Fifth, pyrethroids are used to kill bollworms in Bt cotton, non-Bt cotton, and soybean, and might affect rates of Bt and pyrethroid resistance evolution (Livingston, Carlson, and Fackler 2002, 2004); however, such effects are generally ignored. Sixth, Monsanto has petitioned the EPA to eliminate refugia for its two-toxin technology. Finally, the EPA has asked the scientific community to examine the implications of continued producer access to the one-toxin technology because one- and two-toxin cottonseeds share a common toxin, and some have argued that the former should be phased out to prevent Cry2 resistance from evolving too rapidly.

The first objective of this study is to examine one- and two-toxin Bt cotton adoption and pyrethroid use by a representative eastern North Carolina cotton producer, Bt and pyrethroid resistance evolution, and returns under five external sprayable refugia: 0%, 5%, 10%, 15%, and 20%.[4] Livingston, Carlson, and Fackler (2004) examine the effects of refugia on the annual percentage of a single cotton acre planted to one-toxin Bt cotton, resistance evolution, and returns received per acre, but space and insect population dynamics are not explicitly modeled. We extend their analysis by modeling space, bollworm population dynamics, and the availability of two Bt cotton technologies. Annual numbers of cotton fields planted to one- and two-toxin Bt cotton are simulated in a region with multiple corn, cotton, and soybean fields that are infested by a population of mobile bollworms. As a result, our model characterizes actual field conditions faced by cotton farmers in diverse production environments with a high degree of realism. In addition, our model allows examination of interactions between bollworm control decisions on nearby cotton, soybean, and corn farms. The second objective of this study is to examine the effects of spatial crop distributions to determine how distance between cotton, corn, and soybean fields could affect behavior, resistance, and returns under alternative refugia. The final objective is to examine the implications of phasing out the one-toxin technology.

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[4] We examine eastern North Carolina because the biological model we use was developed for this region, within which unstructured refuges are prevalent. We examine efficient sprayable but not unsprayable refugia, because the bollworm is the primary target pest in this region, and, as a result, profit is generally much higher under the former option.

The Model

Storer and Storer et al. (2003a, 2003b) examine bollworm populations in a 24 by 24 matrix with each cell representing a 10-acre corn, cotton, or soybean field.[5] We extend their models, as described in the Appendix, but examine the deterministic case. Model parameters and their sources are reported in Table 1, and the simulation model is available from Livingston on request. We note at the outset that, because bollworms can fly from farm to farm, the control decisions made by one producer could, over time, affect production possibilities available to the former and neighboring producers. In this analysis, we use a representative producer model, assuming that interseasonal effects are not considered in the producer's contemporaneous control decisions. As a result, we do not examine external effects on other cotton producers, which we leave to future studies. However, because we do simulate one-toxin Bt corn use and pyrethroid sprays in soybean fields, which are triggered by population threshold rules, we are able to examine interactions between pest control decisions on neighboring crop fields.[6]

Economic Model

Total annual production costs (c) for each non-, one-toxin, or two-toxin Bt cotton acre in a given 10-acre cotton field are, respectively,

$$\text{(1)}\qquad \begin{aligned} c_t^n &\equiv \$498.73 + \$8.09s_t^n, \\ c_t^{b1} &\equiv \$521.35 + \$8.09s_t^{b1}, \\ c_t^{b2} &\equiv \$536.53 + \$8.09s_t^{b2}, \end{aligned}$$

where superscripts *n*, *b1*, and *b2* index, respectively, non-, one-toxin, and two-toxin Bt cotton fields and s_t denotes the number of pyrethroid sprays for year t. The cost of one spray, $8.09, is the mean of real North Carolina insecticide costs attributed to the bollworm-budworm complex during 2000–2005 (Williams). Mean fixed production cost, $525.17 (USDA 1997), is modified to reflect non-, one-toxin, and two-toxin Bt cotton seed costs, with mean spray costs during 2000–2005 deducted. Because a very high proportion of all cotton grown in eastern North Carolina is genetically modified to tolerate glyphosate applications, we assume that non-Bt cotton fields are planted with Roundup Ready® cottonseed, at $29.00 per acre. Because good-quality one-toxin Bt–only cotton seed varieties are not available for eastern North Carolina, we assume that one-toxin Bt cotton fields are planted with Bollgard® with Roundup Ready seed, at $41.07 per acre. Because good-quality two-toxin Bt–only cotton seed varieties are not available for eastern North Carolina, we assume two-toxin Bt cotton fields are planted with Bollgard II® with Roundup Ready Flex® seed, at $56.25 per acre (Monsanto). We assume 250,000 seeds per bag, which plants five acres.

Pounds of harvested lint for each non-, one-toxin, and two-toxin Bt cotton acre in the respective fields are

$$\text{(2)}\qquad \begin{aligned} y_t^n &\equiv 725.81\exp\left(\hat{\delta}s_t^n\right), \\ y_t^{b1} &\equiv 714.16\exp\left(\hat{\delta}s_t^{b1}\right), \\ y_t^{b2} &\equiv 714.16\exp\left(\hat{\delta}s_t^{b2}\right), \end{aligned}$$

where 725.81 and 714.16 are estimates of mean bollworm-budworm–free yield for non-Bt and one-toxin Bt cotton fields in North Carolina during 2000–2005; $\exp(\hat{\delta}s_t)$ maps sprays into the proportion of pest-free yield harvested; and $\hat{\delta}$ is a coefficient estimate (Tables 1 and 3).

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[5] Simulation output varies little with region sizes above 12 by 12 (Storer).

[6] Because pyrethroid use in corn is rare, it is not simulated, and neither are economic returns to representative corn or soybean producers. Therefore, we do not simulate the effects of cotton producer decisions on corn or soybean producer decisions. The percentage of corn planted to one-toxin Bt corn is exogenous and fixed throughout the analysis, however, effects of higher Bt corn percentages could easily be examined. Pyrethroid sprays in individual soybean fields occur when population thresholds are reached; therefore, although the model does not simulate profit-maximizing soybean producer control decisions, it can be used to examine likely interactions between control decisions on cotton and soybean fields.

To calculate pest-free yields, reported yields are inflated by attributed annual yield losses during 2000–2005. Similar equations are used to simulate tons of cottonseed harvested per non-, one-toxin, and two-toxin Bt cotton acre in the respective cotton fields,

$$(3)\qquad \begin{aligned} z_t^{\pi} &\equiv 0.502\exp\left(\hat{\delta}s_t^{\pi}\right),\\ z_t^{b1} &\equiv 0.493\exp\left(\hat{\delta}s_t^{b1}\right),\\ z_t^{b2} &\equiv 0.493\exp\left(\hat{\delta}s_t^{b2}\right). \end{aligned}$$

Average seed yields for North Carolina during 2000–2005 (USDA 2000, 2001b, 2002–2003, 2004b, 2005), the proportion of North Carolina cotton acres planted to one-toxin Bt, and the ratio of non-Bt to one-toxin Bt pest-free lint yield are used to estimate the mean pest-free seed yields in Equation (3).

Generally, yield loss and insecticide use increase with pest pressure and resistance; therefore, we estimate a relationship between the proportion of pest-free lint yield harvested and insecticide use, $E[\ln(1.0 - d_t)|\hat{s}_t] = \delta\hat{s}_t$; where d_t and $\hat{s}_t$ denote, respectively, mean annual yield loss and the first-stage estimate of bollworm-budworm sprays in non-Bt and one-toxin Bt cotton in North Carolina during 2000–2005. ($E[\,|\,]$ denotes conditional expectations with respect to a zero-mean, constant-variance error.) First- and second-stage estimates are statistically different from zero, and $\hat{\delta}_t$ indicates that losses increased with insecticide use (Table 2).

Profit received by the representative cotton producer at the end of year t is

$$(4)\qquad \begin{aligned} \pi(b1_t, b2_t|r) = &\sum_{\pi=1}^{f-b1_t-b2_t}\left(p^l y_t^{\pi} + p^s z_t^{\pi} - c_t^{\pi}\right)\\ &+ \sum_{b1=1}^{b1_t}\left(p^l y_t^{b1} + p^s z_t^{b1} - c_t^{b1}\right)\\ &+ \sum_{b2=1}^{b2_t}\left(p^l y_t^{b2} + p^s z_t^{b2} - c_t^{b2}\right) \end{aligned}$$

where f is the total number of cotton fields, $b1_t$ and $b2_t$ are numbers of one-toxin Bt and two-toxin Bt cotton fields, p^l and p^s are fixed prices per pound and ton of lint and seed, respectively, and r is the maximum number of Bt cotton fields that can be planted. Because of the open-access nature of susceptibility, we assume the producer's annual planting choices are made without considering the effects on resistance in subsequent years. Profit maximization, therefore, is subject to Tables 1–3, Equations (1)–(4), the biological model (see the Appendix), $b1_t \geq 0$ and $b2_t \geq 0$, and $0 \leq b1_t + b2_t \leq r$.

Less than 6% of corn was planted to Bt in North Carolina during 2001 (USDA 2001a), which is apparently the only published estimate available; however, USDA–Economic Research Service (USDA-ERS 2005) reports that 27% of corn acres planted in "Other States," which includes North Carolina, was planted to Bt during 2005. We therefore assume 27% of the region's cornfields are planted to one-toxin Bt corn. During 2002, 0.70, 0.92, and 1.32 million acres were planted to corn (24%), cotton (31%), and soybean (45%), respectively, in North Carolina (USDA 2004c); therefore, we partition the region accordingly. Starting with the field in the northwest corner of the region and continuing south, until all fields in a column are assigned a crop type and then moving east to the top of the next column, the first 128 fields in the region are planted to early-blooming soybean, the next 140 fields are planted to corn, the next 180 fields are planted to cotton, and the remaining 128 fields are planted to late-blooming soybean. We refer to this crop distribution as "soybean-soybean." We also examine a distribution wherein the region is bordered on the west by corn and on the east by early- and late-blooming soybean, which we denote "corn-soybean." Early-blooming soybean is farther from corn but closer to cotton, and late-blooming soybean is farther from corn and cotton under corn-soybean relative to soybean-soybean; therefore, unstructured refuge fields conserve Bt and pyrethroid susceptibility less effectively under the former distribution.

Because pest densities tend to be higher initially in fields planted to non-Bt cotton the previous year, Bt varieties are generally more useful when planted to last year's non-Bt

Table 2. Gamete and Genotype Frequencies and Survival Rates

Gametes	Frequencies
abc	$g1 = q_1q_2q_3$
abC	$g2 = q_1q_2(1 - q_3)$
aBc	$g3 = q_1(1 - q_2)q_3$
aBC	$g4 = q_1(1 - q_2)(1 - q_3)$
Abc	$g5 = (1 - q_1)q_2q_3$
AbC	$g6 = (1 - q_1)q_2(1 - q_3)$
ABc	$g7 = (1 - q_1)(1 - q_2)q_3$
ABC	$g8 = (1 - q_1)(1 - q_2)(1 - q_3)$

		Survival Rates			
Genotypes	Frequencies	One-Toxin Bt Corn	One-Toxin Bt Cotton	Two-Toxin Bt Cotton	Pyrethroids
abc/abc	g_1^2	1.0	1.0	1.0	*rr*
abc/aBc	$2g_1g_3$	1.0	1.0	*rs2ab*	*rr*
aBc/aBc	g_3^2	1.0	1.0	*s2ab*	*rr*
abc/Abc	$2g_1g_5$	*rs1ab*	*rs1ac*	*rs1ac*	*rr*
abc/ABc and aBc/Abc	$2(g_1g_7 + g_3g_5)$	*rs1ab*	*rs1ac*	*rs1ac*rs2ab*	*rr*
aBc/ABc	$2g_3g_7$	*rs1ab*	*rs1ac*	*rs1ac*s2ab*	*rr*
Abc/Abc	g_5^2	*s1ab*	*s1ac*	*s1ac*	*rr*
Abc/ABc	$2g_5g_7$	*s1ab*	*s1ac*	*s1ac*rs2ab*	*rr*
ABc/ABc	g_7^2	*s1ab*	*s1ac*	*sdual*	*rr*
abc/abC	$2g_1g_2$	1.0	1.0	1.0	*rs*
abc/aBC	$2g_1g_4$	1.0	1.0	*rs2ab*	*rs*
aBc/aBC	$2g_3g_4$	1.0	1.0	*s2ab*	*rs*
abc/AbC	$2g_1g_6$	*rs1ab*	*rs1ac*	*rs1ac*	*rs*
abc/ABC and aBc/AbC	$2(g_1g_8 + g_3g_6)$	*rs1ab*	*rs1ac*	*rs1ac*rs2ab*	*rs*
aBc/ABC	$2g_3g_8$	*rs1ab*	*rs1ac*	*rs1ac*s2ab*	*rs*
Abc/AbC	$2g_5g_6$	*s1ab*	*s1ac*	*s1ac*	*rs*
Abc/ABC	$2g_5g_8$	*s1ab*	*s1ac*	*s1ac*rs2ab*	*rs*
ABc/ABC	$2g_7g_8$	*s1ab*	*s1ac*	*sdual*	*rs*
abC/abC	g_2^2	1.0	1.0	1.0	*ss*
abC/aBC	$2g_2g_4$	1.0	1.0	*rs2ab*	*ss*
aBC/aBC	g_4^2	1.0	1.0	*s2ab*	*ss*
abC/AbC	$2g_2g_6$	*rs1ab*	*rs1ac*	*rs1ac*	*ss*
abC/ABC and aBC/AbC	$2(g_2g_8 + g_4g_6)$	*rs1ab*	*rs1ac*	*rs1ac*rs2ab*	*ss*
aBC/ABC	$2g_4g_8$	*rs1ab*	*rs1ac*	*rs1ac*s2ab*	*ss*
AbC/AbC	g_6^2	*s1ab*	*s1ac*	*s1ac*	*ss*
AbC/ABC	$2g_6g_8$	*s1ab*	*s1ac*	*s1ac*rs2ab*	*ss*
ABC/ABC	g_8^2	*s1ab*	*s1ac*	*sdual*	*ss*

Notes: Cry1, Cry2, and pyrethroid resistance gene frequencies for the adults in the field are q_1, q_2, and q_3, respectively. See *Biological Model* section and Table 1 for symbols and base model values.

cotton fields. Therefore, we assume that the producer plants Bt cotton and Bt corn to the cotton and corn fields, respectively, with relatively high numbers of diapaused pupae. Bt resistance evolves more rapidly relative to, assuming the producer plants roughly the same fields to non-Bt and Bt plants year after year (Storer).

Let int(x) map x into the nearest integer, and let $b1_i(r)$ and $b2_i(r)$ denote numbers of one- and two-toxin Bt cotton fields that maximize profit (5) during t when the refuge constraint is r. The $b1_t(r)$ and $b2_t(r)$ are restricted to the set $\{0, \text{int}(0.05r), \text{int}(0.10r), \ldots, \text{int}(0.95r), r\}$, and the number of non-Bt cotton fields is $f - b1_t(r) - b2_t(r)$.

Initially, for each r, we found the $b1_t(r)$ and $b2_t(r)$ that maximized profit (4) by assessing each possible combination; however, because this is time intensive and because the base model results were identical, we use a shortcut to generate the reported results. At the beginning of each t, the three-corner solutions are evaluated—C^1: $b1_t(r) = r$, $b2_t(r) = 0$; C^2: $b1_t(r) = 0$, $b2_t(r) = r$; and C^3: $b1_t(r) = b2_t(r) = 0$. If profit is highest under C^1, $b1_t(r)$ is reduced $\varepsilon = \text{int}(0.05f)$ fields, and the model is rerun. With $b1_t(r)$ at this value, $b2_t(r)$ is increased ε fields, the model is rerun, and both steps are repeated until a local maximum is bracketed. Similarly, if profit is highest under C^2, $b2_t(r)$ is reduced ε fields, the model is rerun, and, with $b2_t(r)$ at this value, $b1_t(r)$ is increased ε fields, with both steps repeated until a local maximum is bracketed. If profit is highest under C^3, $b1_t(r)$ is increased ε fields, the model is rerun, and, with $b1_t(r)$ at this value, $b2_t(r)$ is increased ε fields, with both steps repeated until a local maximum is bracketed.

When $b1_t(r)$ and $b2_t(r)$ are found, the model is rerun and numbers of diapaused pupae of each genotype in each field are stored as the new baseline, from which $b1_{t+1}(r)$ and $b2_{t+1}(r)$ are subsequently found. For each scenario examined, the regional distribution of diapaused pupae at the beginning of the first model year is the same and is based on model output at the end of year 2005. Starting in year 2000, Cry1, Cry2, and the pyrethroid resistance gene frequencies are based on published estimates (Table 1). With these frequencies the biological model is used to estimate the distribution of diapaused pupae at the beginning of year 2006 assuming 53%, 57%, 66%, 71%, 82%, and 89% of cotton fields (Williams) and 11%, 12%, 16%, 19%, 25%, and 27% of cornfields (USDA-ERS 2005) are planted to one-toxin Bt cotton and one-toxin Bt corn during 2000–2005, respectively. Because two-toxin Bt cotton adoption data for North Carolina are not available, it was not possible to specify how much was planted in eastern North Carolina during 2004 and 2005. As a result, with the use of the initial Cry2 resistance gene frequency for North Carolina in 2000 (3.9×10^{-4}), the Cry2 resistance gene frequency goes extinct. Therefore, we scale the estimate of Burd et al. so that the initial Cry2 resistance gene frequency at the beginning of 2006 is approximately 3.9×10^{-4}. With this procedure, mean Cry1, Cry2, and pyrethroid resistance gene frequencies in diapaused pupae at the beginning of year 2006 are 2.7×10^{-3}, 3.9×10^{-4}, and 0.287.

We assume a 15-year planning horizon because it has been used by EPA in previous policy deliberations. To simulate the effect of the EPA's emergency action plan regarding Cry1 resistance, if the mean resistance gene frequency in diapaused pupae exceeds 0.5 at the end of any year, one-toxin Bt corn and one-toxin Bt cotton cannot be planted the following year.

Results

The annualized present value of profit per cotton acre (return) declines monotonically with the refugia (Table 4), and mean profit per cotton acre, which is not reported, is statistically different at the 5% level under the 0% and 20% refugia. Therefore, the cost of complying with the current 20% refugia varies between $6.99 and $8.67 per cotton acre, or $19.43 and $34.21 per structured refuge acre, under corn-soybean and soybean-soybean, respectively. Bt adoption and pyrethroid use, pest pressure, pyrethroid sprays, Cry1 and pyrethroid resistance evolution, and the return depend on the crop distribution.

Mean one-toxin Bt cotton adoption is higher under soybean-soybean than corn-soybean, and statistically different for the 0%, 5%, and 10% refugia; however, mean two-toxin Bt cotton adoption is higher under corn-soybean and is not statistically different for any refugia. Pest pressure is higher under corn-soybean than soybean-soybean, which helps explain why mean sprays are always statistically higher under the former distribu-

Table 3. Two-Stage Least-Squares Estimates for the Yield Damage Function

Dependent Variable	Insecticide Applications Attributed to the Bollworm-Budworm Complex			
First-Stage Least-Squares Regression Results				
R^2	0.87			
Standard error of estimate	0.34			
F-statistic	68			
F-value	9×10^{-6}			
Observations	12			
Parameter	Estimate	SE	t-statistic	p-value
Intercept	2.345	0.138	17.051	1×10^{-8}
Bt cotton dummy	−1.598	0.194	−8.216	9×10^{-6}
Second-Stage Least-Squares Regression Results				
	ln(1.0 − proportionate yield loss attributed to the bollworm-budworm complex)			
R^2	0.86			
Standard error of estimate	0.02			
F-statistic	68			
F-value	9×10^{-6}			
Observations	12			
Parameter	Estimate	SE	t-statistic	p-value
Estimated bollworm-budworm complex insecticide applications from the first stage	−0.027	0.003	−8.265	5×10^{-6}

Notes: Proportionate yield losses and conventional insecticide sprays attributed to the bollworm-budworm complex in North Carolina during 2000–2005 are from Williams. The Bt cotton dummy is 0 and 1 for observations from non-Bt and Bt cotton, respectively.

tion. Mean sprays in cotton are not statistically different; however, mean sprays in soybean are 45% higher under corn-soybean than soybean-soybean, and statistically different for each refugia. This occurs because late-blooming soybean fields are farther from cotton fields under corn-soybean, and because bollworm levels are highest when cotton and late-blooming soybean are the preferred hosts. Increasing the distance between cotton and late-blooming soybean increases the proportion of bollworms developing in soybean that also lay their eggs in soybean. This increases sprays in soybean directly because larval and adult thresholds are exceeded more frequently, and indirectly, because fewer offspring of bollworms developing in soybean are ultimately subjected to Bt toxins.

Because sprays occur more frequently under corn-soybean than soybean-soybean, end-horizon mean pyrethroid resistance gene frequencies are statistically higher under the former distribution. This occurs not only because sprays occur more frequently, but also because soybean fields are farther from cornfields under corn-soybean. Corn is a source of refuge for bollworms susceptible to pyrethroids, because pyrethroids are not used; therefore, increasing the distance between soybean and corn reduces the efficacy of the latter in delaying resistance. In addition, one-toxin Bt and two-toxin Bt cotton fields serve as pyrethroid refuges, because sprays are much lower on these fields than on non-Bt cotton and soybean fields. Because total Bt adoption (the sum of mean one-toxin Bt and two-toxin Bt cotton adoption) is lower under corn-soybean than under soybean-soybean, the availability of pyrethroid refuge is further reduced under the former distribution.

Pest pressure increases monotonically with the refugia because total Bt cotton adoption generally declines monotonically with the refugia. As a result, cotton and soybean sprays follow suit and, although increased Bt adoption can, in some modeling environments, lead to the negative externality of an increased rate of Bt resistance evolution, increased Bt adoption in our region leads to a positive external effect of statistically significant reductions in cotton sprays and minor reductions in soybean sprays as the refugia is reduced.

Mean end-horizon Cry2 resistance gene frequencies are not reported in Table 4 because the gene invariably goes extinct by the end of model year 4. This occurs for three reasons. First, two-toxin Bt cotton adoption is low under each crop distribution. Second, 69% of the region is planted to corn and soybean, which serve as unstructured Cry2 refuges. Third, one-toxin Bt cotton fields also serve as an important source of unstructured Cry2 refuge. Cry1 resistance evolves; however, mean end-horizon resistance gene frequencies are low, and statistically lower under soybean-soybean than under corn-soybean. Mean end-horizon Cry1 resistance gene frequencies are low because 62% of the region is planted to unstructured non-Bt corn and soybean refuge; and Cry1 resistance evolves more rapidly under corn-soybean than under soybean-soybean, even though one-toxin Bt cotton adoption is higher under the latter distribution because late-blooming soybean is farther from cotton under corn-soybean, which reduces their efficacy as an unstructured Cry1 refuge.

The mean end-horizon Cry1 resistance gene frequency displays a nonmonotonic relationship with the refugia. This occurs for four reasons. First, the producer adopts two-toxin Bt cotton as Cry1 resistance evolves. Second, the threshold mean Cry1 resistance gene frequency at which the switch occurs is low. Third, the mean Cry1 resistance gene frequency declines with the level of two-toxin Bt cotton planted because Cry1-resistant bollworms emerge at a much higher rate from one-toxin Bt cotton than from two-toxin Bt cotton fields. Fourth, because we assume a 0.025 fitness cost of carrying the Cry1 resistance gene or the Cry2 resistance gene, fitness costs are low and justified by available empirical evidence. Bollworm susceptibility to Cry1, therefore, is renewable. This explains why the mean end-horizon Cry1 resistance gene frequencies under soybean-soybean and the 5% and 10% refugia are statistically higher than the mean end-horizon Cry1 resistance gene frequency for the 0% refugia and why the mean end-horizon Cry1 resistance gene frequencies under corn-soybean and the 5%, 10%, 15%, and 20% refugia are statistically higher than for the 0% refugia.

Phasing Out One-Toxin Bt Cotton

Between 71% (USDA-ERS 2005) and 89% (Williams) of North Carolina cotton was planted to one-toxin Bt cotton during 2005. Because simulated one-toxin Bt cotton adoption for the 20% refugia is interior to this range under soybean-soybean, but not under corn-soybean, we examine the effects of phasing one-toxin Bt cotton out under the former distribution. Specifically, we examine the effects of removing one-toxin Bt cotton from the market at the end of 2008, perhaps the earliest date the technology may be removed; the end of 2010, after which one-toxin Bt cotton will have been available for 15 years; and at the end of 2015 for comparison purposes. For brevity, we discuss but do not present the complete set of numerical results.

The producer's return increases with the phase-out date. Although returns are not statistically different for the 2008, 2010, and 2015 phase-out dates, under any refugia, returns are statistically lower under the 2008 phase-out date than under the base case for each refugia. Although one-toxin Bt cotton adoption increases and two-toxin Bt cotton adoption declines with the phase-out date, total adoption does not depend on the phase-out date and is, therefore, the same as in the base case. Pest pressure declines, but total sprays increase monotonically with the phase-out date under each refugia. Cotton sprays increase monotonically with the phase-out date because one-toxin Bt cotton is used more and two-toxin Bt cotton less as the phase-out date increases, sprays occur more in one-toxin Bt cotton than in two-toxin Bt cotton, and soybean sprays increase but then decline with the phase-out date, with the declines in soybean sprays lower than the increases in cotton sprays. Because the Cry2 resistance gene invariably goes extinct by the end of model year 4, the mean end-horizon Cry2 resistance frequency does not depend on the phase-out date. As expected, the mean end-horizon Cry1 resistance gene frequency increases with the phase-out date; however, even though the means are statistically different under the 2008 and 2015 phase-out dates for the 0%, 5%, and 10% refugia, the magnitudes of the differences are small. The mean end-horizon pyrethroid resistance gene frequency declines with the phase-out date; however, the differences are not statistically significant for any refugia under the 2008 and 2015 phase-out dates. As in the base model, the return declines with the refugia under each phase-out date, and the return under the 0% refugia is always statistically higher than the return under the 20% refugia.

Conclusions

We examine representative producer behavior, resistance evolution, and returns under alternative refuge requirements (refugia) in an eastern North Carolina region with multiple corn, cotton, and soybean fields infested by a mobile pest. Returns are highest, pyrethroid sprays occur least frequently, and pyrethroid resistance evolution is delayed most effectively with no refugia, results that support not only the recent petition to eliminate a refuge requirement for two-toxin Bt cotton, but also elimination of a refuge requirement for the one-toxin technology for this region because corn and soybean provide sufficient unstructured refuge to manage Bt resistance efficiently, even in the absence of a structured refuge requirement. Complying with the current 20% refugia costs the producer $8.67 per cotton acre, or $34.21 per non-Bt cotton acre. In addition, producer returns are highest under each refugia when one-toxin Bt cotton is not phased out; however, removal of the technology at the earliest phase-out date minimizes regional pyrethroid sprays under each refugia examined and, across refugia, are lowest when the refuge requirement is eliminated.

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APPENDIX: THE BIOLOGICAL MODEL

The egg stage and 40 larval and seven adult age classes are simulated. At the beginning of each 125-day growing season, bollworm adults emerge from diapaused pupae in mid-May. During each day in each field, the model simulates adult egg production; natural mortality; time-varying pyrethroid spray residue neonate mortality in cotton and soybean; neonate mortality from Bt exposure; pyrethroid mortality of all age classes resulting from intraseasonal sprays triggered by egg (cotton) and larval (cotton and soybean) population thresholds (Bacheler); larval mortality in one-toxin Bt corn ears caused by exposure to Cry1 and cannibalism; time-varying neonate mortality because of corn, cotton, and soybean plant deterioration; and the aging of all individuals, the recruitment of new adults, pupal diapause, and winter mortality.

Indices that characterize the relative attractiveness of corn, cotton, and soybean plants are updated daily to mimic the dynamics of adult host preference and crop phenology for eastern North Carolina, and the proportions of adults potentially migrating between fields are updated daily to reflect these preference changes (Storer et al. 2003a,b). The proportion of potentially migrating moths in each three by three block of fields centered at field (i, j), which are relocated to field (k, l), with $h_{i,j} = [(k - i)^2 + (l - j)^2]^{0.5} \leq d^{max}$, is $m(i, j, k, l) = \exp(-h_{i,j}/2\sigma^2)(2\pi\sigma^2)^{-0.5}$; where σ^2 is the bivariate normal kernel's variance. Migration is simulated for each distinct three by three block of fields, as opposed to each field, because the time it takes to run the model is reduced considerably and the results are not appreciably affected. Although bollworm moths can fly many miles in search of suitable hosts, during the growing season, such hosts are plentiful in the region; we therefore impose a maximum flight distance, d^{max}. For each field (k, l) $F_{i,j} \equiv \{(k, l): h_{i,j} \leq d^{max}\}$, $m(i, j, k, l)$ is weighted by the field's host preference index and then scaled to sum to one, $\Sigma_{F_{i,j}}\, m(i, j, k, l) = 1.0$.

Cry1 endotoxins expressed by one-toxin Bt cotton and corn plants are similar in structure and mode of action, and cross-resistance has been documented in other moth pests; therefore, we assume that one-toxin Bt cotton and corn and two-toxin Bt cotton plants express the same Cry1 endotoxins. We use a three-locus, six-gene model to simulate resistance evolution. One- and two-locus genetic models have been shown empirically to simulate resistance evolution well (Croft and Dunley; Livingston, Carlson, and Fackler 2002, 2004). We assume (a) diploid females and males mate randomly, (b) genetic mutation and migration out of and into the region are insignificant relative to selection, (c) resistance to each toxin is conferred at one locus by one non–sex-linked gene (Groeters and Tabashnik), (d) the probability a gamete contains one gene is independent of its containing one of the other five genes, and (e) resistance to a toxin does not confer resistance to the other toxins. Regarding Assumption b, Gould et al. indicate that bollworms move from the corn belt into the mid-South annually. Similar movement might occur in eastern North Carolina and might affect the results of our analysis, in which we assume only local movement in a region with reflecting edges.

Let a and A denote genes that confer resistance and susceptibility, respectively, to Cry1 at locus 1, b and B confer resistance and susceptibility to Cry2 at locus 2, and c and C confer resistance and susceptibility to pyrethroids at locus 3. Let the frequencies of a, b, and c in a given field's adult population at the end of a given day be q_1, q_2, and q_3, respectively. Under Assumptions a–e, the population frequencies of the eight gametes and 27 genotypes in the field are as shown in Table 2.

Neonates and young larvae are the age classes most susceptible to pyrethroid sprays because they tend to be present on, or to come in contact with, directly sprayed plant parts. This is also true for old larvae in soybean; however, in cotton, old larvae tend to burrow into bolls or are deeper in the plant canopy and are therefore much less susceptible. Storer assumes that survival rates depend on age class and crop type, and we assume that survival rates also depend on genotype. Storer fixes the pyrethroid survival rates of neonates and young larvae, old larvae, and adults in cotton at 0.10, 0.75, and 0.60, respectively, and the survival rates of neonates and all larvae in soybean at 0.20. In our

Table 4. Base Model Results under Two-Crop Distribution

Refugia (%)	One-Toxin Bt Cotton Adoption (%)[a]	Two-Toxin Bt Cotton Adoption (%)[a]	Diapaused Pupae[b]	Cotton Sprays[c]	Soybean Sprays[c]	Cry1 R-Gene Frequency[d]	Pyrethroid R-Gene Frequency[d]	Annualized Present Value of Profit per Cotton Acre[e]	Compliance Cost[e]
Soybean-soybean									
5	95 F*	0 F	55,096 F	66	256 F*	0.1194*	0.6093 F*	$53.3 F	
10	90 FG*	0 F	55,374 F	95	258 F*	0.0900*	0.6086 F*	$51.0	$3.53
15	79 FGH	0 F	55,881 F	143 F	259 F*	0.0000 F*	0.6034 F*	$48.3	$6.19
20	75 FH	0 F	56,643 F	175 F	260 F*	0.0000 F*	0.6083 F*	$45.8	$8.67
Corn-soybean									
0	53 F	20 F	57,998 F	77 F	371 F	0.1343	0.9980 F	$56.4 F	
5	63 F	13 F	58,058 F	85 F	372 F	0.2355 F	0.9984 FG	$55.4 FG	
10	60 F	12 F	58,749 F	115 FG	374 F	0.1902	0.9984 FGH	$53.0	
15	62 F	6 F	60,079 F	143 FG	375 F	0.2982	0.9987 GHI	$51.5 FGHI	
20	59 F	5 F	61,074 F	170 G	376 F	0.2500 F	0.9988 I	$49.4 HI	$6.99

Notes There were 140 cornfields, 180 cotton fields, and 128 early- and 128 late-blooming soybean fields. Under soybean-soybean, the region is bordered on the west by early-blooming soybean, followed by corn, cotton, and late-blooming soybean. Under corn-soybean, the region is bordered on the west by corn, followed by cotton and early- and late-blooming soybean. For a given crop distribution, means in the same column with the same letter(s) are not statistically different at the 5% level.

[a] Mean annual percentage of cotton planted to one-toxin Bt cotton with Roundup Ready and two-toxin Bt cotton with Roundup Ready Flex.

[b] Mean annual diapaused pupae per field at the end of the year before winter mortality.

[c] Mean annual pyrethroid sprays occurring in the region.

[d] Resistance gene frequency per field in diapaused pupae before winter mortality after 15 years.

[e] Annualized present value (present value divided by the sum of the discount rates) of profit per cotton acre. Statistical differences refer to mean profit per cotton acre. Compliance cost for an x% refugia is given by the difference in the annualized present value of profit per cotton acre under the 0% and x% refugia. Only statistically significant compliance costs are reported.

* For a given refugia, the means under soybean-soybean and corn-soybean are statistically different at the 5% level.

model, Storer's survival rates are divided by 0.75 and used to scale Livingston, Carlson, and Fackler's (2002) genotype-specific survival rates. Adult survival in soybean is given by the square root of the survival rate of neonates and larvae in Storer; therefore, adult genotype survival rates in sprayed soybean are scaled by $0.52 = (0.20/0.75)^{0.5}$.