A Binary Logit Analysis of Factors Impacting Adoption of Genetically Modified Cotton

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Abstract

Agricultural Resource Management Survey (ARMS) data for 2003 were used to estimate two binary logit models for two definitions of genetically modified (GM) cottonseed adoption. Results indicate conservation tillage did not positively affect adoption of GM cotton with either of these definitions, while adoption of GM cotton in the previous year did. Refuge cotton also did not affect these adoption decisions for the study year.

Key Words: Agricultural Resource Management Survey (ARMS), binary logit model, conservation tillage, cotton, genetically modified seed, herbicide-resistant cotton, jackknife procedure, refuge cotton, stacked-gene cotton, technology adoption.

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Introduction

The U.S. Environmental Protection Agency has mandated an Insect Resistance Management (IRM) program that attempts to preserve the benefits and insect protection of *Bacillus thuringiensis* (Bt) cotton. According to that mandate, growers planting Bt cotton are required to follow the IRM practices designed to keep some lepidopteran populations from being exposed to the Bt protein. Thus, a refuge of non-Bt cotton must be planted. Other than Bt (insect-resistant) cotton, genetically modified (GM) types of cotton include herbicide-resistant (HR) cotton and stacked-gene (SG) cotton, the latter combining the traits of insect resistance with herbicide resistance.

Conservation tillage in general and no-till practices in particular have increased over the past few years (Figures 1 and 2). Conservation tillage (either no-till or reduced tillage practice) is reported to reduce soil erosion by preventing reduction in crop residue on the soil surface (Harper). Yet, despite the apparent advantages of conservation tillage in reducing soil erosion, soil degradation, runoff, and in improving soil quality (Edwards; Sandretto), some farmers adopt no-till or minimum-till while others do not.
With the use of HR or SG seed technology, it indirectly reduces the use of residual herbicides and increases profit potential of the farmer (Marra, Pardey, and Alston). The use of conservation-tillage (CT) practices may be even more important in cotton production than in other row crop production because of the minimal amount of residue left on the soil surface. Crop residues after planting averages 3% for cotton compared with 29% for corn (U.S. Department of Agriculture).

Past studies have attempted to show the relationship between adoption of GM (specifically HR) seed and adoption of conservation tillage, and determine the causal effects between them. For example, Fernandez-Cornejo and McBride's cross-sectional study for 1997 using USDA's ARMS data investigated a potential simultaneous relationship between HR soybean seed and CT practices using two simultaneously estimated binomial probit models, and compared those results with two single-equation probit models. Their study suggested that accounting for simultaneity was important for the no-till decision but not for the seed-use decision. In a more recent study with time-series data for 1992-2004, Roberts et al. used Bayesian theorem and a two-equation simultaneous logit analysis to find that the introduction of the HR cottonseed in Tennessee increased the probability that farmers would adopt conservation tillage and farmers who had previously adopted CT practices were more likely to adopt HR cottonseed. They concluded that the simultaneous adoption of conservation tillage and HR cottonseed reduced soil erosion and residual herbicide use, and increased profit. However, with ARMS data for 2003, Banerjee et al. found no evidence of a simultaneous relationship between these two adoption decisions.

The overall objective of this study was to identify factors that led to the adoption of GM cotton in the United States. Specifically, the study sought to identify farm and farmer characteristics driving the production of GM cotton in the United States in general. In particular, the impact (or otherwise) of conservation tillage (i.e., no-till and reduced till: ridge-till, strip-till, and mulch-till) and conventional cotton used as refuge on the adoption of GM cottonseed across the United States and within selected regions was studied.

Data and Methods

This study used two definitions of genetic modification of cottonseed adoption: *Bacillus thuringiensis* (Bt) cotton or HR cotton (denoted as BH); and Bt, HR, or SG cotton (denoted as BHS). The survey respondents

were classified as adopters of a particular type of GM cotton according to these definitions. The "yes" responses received for these definitions as percentages of the sample used in the regressions were 65% and 86%, respectively. Two single-equation binary logit models (Maddala) were estimated using the same set of independent variables, except for the relevant adoption variable of the previous year that uses the definition specific to the relevant adopter classification.

Administered by USDA-ERS, data from the 2003 ARMS, which is a random sample of cotton farms across the United States, were used to estimate the two binary logit models with two definitions of genetic modification. The dependent variable for each equation indicated the adoption of GM cotton (with the relevant GM definition) vis-à-vis its non-adoption (i.e., adoption of conventional cotton). The explanatory variables for each equation included the following:
1) demographic information of the survey respondents/farmers: age, if college graduate, gross annual farm income, length of tenure in cotton farming;
2) farm characteristics: farm size, farm labor expense, refuge size in field surveyed, percentage of farm acres in cotton, if they grew genetically engineered cotton (using the relevant definition) in the previous year (2002), if any part of their surveyed field was declared highly erodible land (HEL) by the Natural Resources Conservation Service (NRCS), if they no-tilled in 2002, cotton acres harvested, percentage of cotton acres harvested using one or more CT equipment; and
3) region-specific dummy variables: one for each cotton-producing region, the 17 cotton-producing states being divided into five regions.

The logit equation is written as (Greene):

$$(1) \qquad \Pr(Y = 1) = \frac{e^{\beta'x}}{1 + e^{\beta'x}},$$

with the cumulative distribution function given by:

$$(2) \qquad F(\beta'x) = \frac{1}{1 + e^{\beta'x}},$$

where β' represents the vector of parameters associated with the factors x.

Assuming the probability that farmer n will choose to produce cotton using a particular technology (BH or BHS seed) is equal to the proportion of cotton farmers using that technology, the individual empirical models to be estimated may be specified as:

$$BH = \beta_0 + \beta_1 CONSTILL + \beta_2 BH02 + \beta_3 LABEXP + \beta_4 CTA + \beta_5 CTP + \beta_6 HEL + \beta_7 REFUGE$$
$$(3) \quad + \beta_8 YIELD + \beta_9 PNT + \beta_{10} AGE + \beta_{11} EDU + \beta_{12} TEN + \beta_{13} GFI + \sum_{\substack{i=14 \\ j}}^{17} \beta_i REGION_j + \varepsilon_T,$$

$$BHS = \gamma_0 + \gamma_1 CONSTILL + \gamma_2 BHS02 + \gamma_3 LABEXP + \gamma_4 CTA + \gamma_5 CTP + \gamma_6 HEL + \gamma_7 REFUGE$$
$$(4) \quad + \gamma_8 YIELD + \gamma_9 PNT + \gamma_{10} AGE + \gamma_{11} EDU + + \gamma_{12} TEN + \gamma_{13} GFI + \sum_{\substack{i=14 \\ j}}^{17} \gamma_i REGION_j + \varepsilon_G,$$

where
CONSTILL is a dummy variable indicating whether or not CT practices were adopted;
BH02 is a dummy variable indicating if Bt or HR cotton was grown in the prior year, 2002;
BHS02 is a dummy variable indicating if Bt, HR, or SG cotton was grown in the prior year, 2002;
LABEXP is the total labor expense on the farm ($100,000);
CTA denotes the total harvested cotton acres (dryland and irrigated) on the farm (100 acres);
CTP is the percentage of cotton acres on the farm;

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HEL is a dummy variable indicating if NRCS classified any part of the field surveyed as HEL;

the *REFUGE* dummy indicates if refuge cotton was used in the survey year;

YIELD is lint yield in pounds per acre harvested or expected in 2003;

PNT is a dummy variable indicating if no-till was used in the surveyed field in the year before the survey, 2002;

AGE is the age of the principal farm operator;

EDU is a dummy variable indicating the surveyed farm operator's education level (whether or not college graduate);

TEN is the length of tenure (in years) of the operator household for the surveyed field;

GFI is the gross farm income in 2003 ($100,000);

REGION is a set of four dummies:

REGION1 including Alabama, Florida, and Georgia;

REGION2 including North Carolina, South Carolina, and Virginia;

REGION4 including Texas, Oklahoma, and Kansas; and

REGION5 including Arizona, California, and New Mexico; with

REGION3 (Arkansas, Louisiana, Mississippi, Missouri, and Tennessee) excluded as the reference region to compare other regions with;

ε_T and ε_G are random error terms;

β's and γ's are parameters to be estimated; and

the subscript *n* for the nth farmer is suppressed for clarity.

Results

Results (as given by the maximum likelihood estimates from equations 3 and 4) indicate conservation tillage (*CONSTILL*) did not affect adoption of GM cotton with either definition for the study year (2003) at the 5% level, though it did seem to cause a reduction in the likelihood of BH adoption (equation 3) at the 10% level (Table 1). The latter counter-intuitive result brings to light one of the issues regarding the use of cross-sectional data. Instead of establishing causality, effects, determinants, or impacts, our regression results may be read as implying correlations, relationships, and associations. The "correlations" presented, however, assume *ceteris paribus* conditions. The weak negative correlation becomes weaker and no more significant even at the 10% level when stacked-gene cotton adopters are included in the mix, as apparent from the BHS adoption model (equation 4) estimation. It is plausible that farmers who had not adopted CT practices before BH seed was introduced might have first adopted BH seed and then decided that they could improve efficiency by adopting CT practices sometime during or before 2003. A similar study in a later year might make this variable positive and significant.

Whether or not GM cotton was used in the prior year (2002) positively affected the adoption of GM cotton in the study year using both definitions at the 1% level. Percentage of cotton acres on the farm (*CTP*) also positively affected both adoption decisions at the 1% level. The variable for Region 1 was significant at the 5% level and negative in the BH equation, with a marginal effect of -0.173, indicating that, estimated in isolation, this region (southeastern states of AL, FL, and GA) was 17.3% less likely to adopt BH relative to cotton farmers in Region 3 (AR, LA, MS, MO, TN).

Previous experience of no-till (*PNT*) in the BH equation and education level (*EDU*) in the BHS equation were significant only at the 10% level, with *EDU* having an unexpected negative sign.

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Labor expense, cotton acres on farm, HEL, refuge size, yield, tenure, gross farm income, and age were not significant factors in determining adoption of GM technologies in cotton production for the study year.

Conclusions

Recent studies involving adoption of conservation tillage and HR cotton have attempted to determine if the adoption of conservation tillage impacts the adoption of GM cottonseed and/or vice versa. If CT adoption impacts GM cottonseed adoption, then conservation tillage can indirectly affect residual herbicide use and farm profits. The current study using cross-sectional ARMS data does not provide strong evidence of such a correlation with either of the two definitions of genetic modification used. Refuge cotton also did not affect GM cottonseed adoption using any definition in this study. However, the limitations of a cross-sectional study using complex data such as from the ARMS are apparent.

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Table 1. Parameter Estimates and Marginal Effects from the Single-Equation Logit Models for Bt/Herbicide-Resistant (BH) and Bt/Herbicide-Resistant/Stacked-Gene (BHS) Cottonseed

	BH Cottonseed Equation			BHS Cottonseed Equation	
Explanatory Variable[a]	Parameter Estimate	Marginal Effect[b]	Explanatory Variable[a]	Parameter Estimate	Marginal Effect[b]
Constant**	-3.311 (1.648)[c]		Constant**	-4.717 (1.898)[c]	
CONSTILL*	-1.030 (0.550)	-0.116 (0.062)[d]	CONSTILL	-0.639 (0.952)	<-0.001 (<0.001)[d]
BH02***	4.615 (0.520)	0.519 (0.058)	BHS02***	7.906 (1.516)	0.002 (<0.001)
LABEXP	-0.022 (0.147)	-0.003 (0.017)	LABEXP	-0.718 (0.706)	<-0.001 (<0.001)
CTA	-0.068 (0.052)	-0.008 (0.006)	CTA	-0.054 (0.081)	<-0.001 (<0.001)
CTP***	2.486 (0.744)	0.280 (0.084)	CTP***	4.285 (1.090)	0.001 (<0.001)
HEL	-0.453 (0.812)	-0.051 (0.091)	HEL	-0.467 (1.490)	<-0.001 (<0.001)
REFUGE	-0.050 (0.042)	-0.006 (0.005)	REFUGE	0.618 (4.365)	<0.001 (0.001)
YIELD	<-0.001 (<0.001)	<-0.001 (<0.001)	YIELD	<-0.001 (0.002)	<-0.001 (<0.001)
PNT*	1.124 (0.631)	0.126 (0.071)	PNT	0.975 (1.300)	<0.001 (0.001)
AGE	0.021 (0.014)	0.002 (0.002)	AGE	0.040 (0.042)	<0.001 (0.001)
EDU	-0.264 (0.473)	0.030 (0.053)	EDU*	-1.340 (0.800)	<-0.001 (<0.001)
TEN	-0.019 (0.016)	-0.002 (0.002)	TEN	-0.042 (0.049)	<-0.001 (<0.001)

GFI	0.017	0.002		*GFI*	0.068	<0.001
	(0.059)	(0.007)			(0.134)	(0.001)
REGION1[e]**	-1.539	-0.173		*REGION1*[e]	-2.115	<-0.001
	(0.778)	(0.087)			(1.721)	(0.001)
REGION2	-1.139	-0.128		*REGION2*	3.089	<0.001
	(0.696)	(0.078)			(14.838)	(0.004)
REGION4	-0.309	-0.035		*REGION4*	-1.407	<-0.001
	(0.771)	(0.087)			(1.322)	(0.001)
REGION5	0.188	0.021		*REGION5*	-1.445	<-0.001
	(0.665)	(0.075)			(1.529)	(0.001)

Log Likelihood = -5,607.622
McFadden R^2 = 0.4527
Adjusted McFadden R^2 = 0.4513
Prediction Success:
  Concordant 85.3%
  Discordant 14.5%
  Tied   0.2%
Number of Observations = 537 in sample
≈ 9,128 farms in expanded full sample

Log Likelihood = -10,566.661
McFadden R^2 = 0.7835
Adjusted McFadden R^2 = 0.7823
Prediction Success:
  Concordant 96.3%
  Discordant   2.1%
  Tied   1.5%
Number of Observations = 898 in sample
≈ 12,126 farms in expanded full sample

Number of BH Adopters = 349 in sample
≈ 5,342 farms in expanded full sample

Number of BHS Seed Adopters = 769 in sample ≈ 9,163 farms in expanded full sample

Note: ***, **, and * indicate statistical significance at the 1%, 5%, and 10% levels, respectively.
[a] Explanatory variables are defined in Table 1.
[b] A marginal effect indicates the change in predicted probability of adopting the relevant technology for a unit change in an explanatory variable. Marginal effects of continuous variables were calculated at the means of the data. For dummy variables, a value of 0 was used if the mean was less than 0.5 and a value of 1 if the mean was greater than or equal to 0.5.
[c] Numbers in parentheses below parameter estimates are respective asymptotic delete-a-group jackknife standard errors of those estimates. Parameter estimates were obtained using the NASS "full-sample weight" variable.
[d] Numbers in parentheses below marginal effects are respective asymptotic delete-a-group jackknife standard errors of those effects. Marginal effects were obtained using the NASS "full-sample weight" variable.
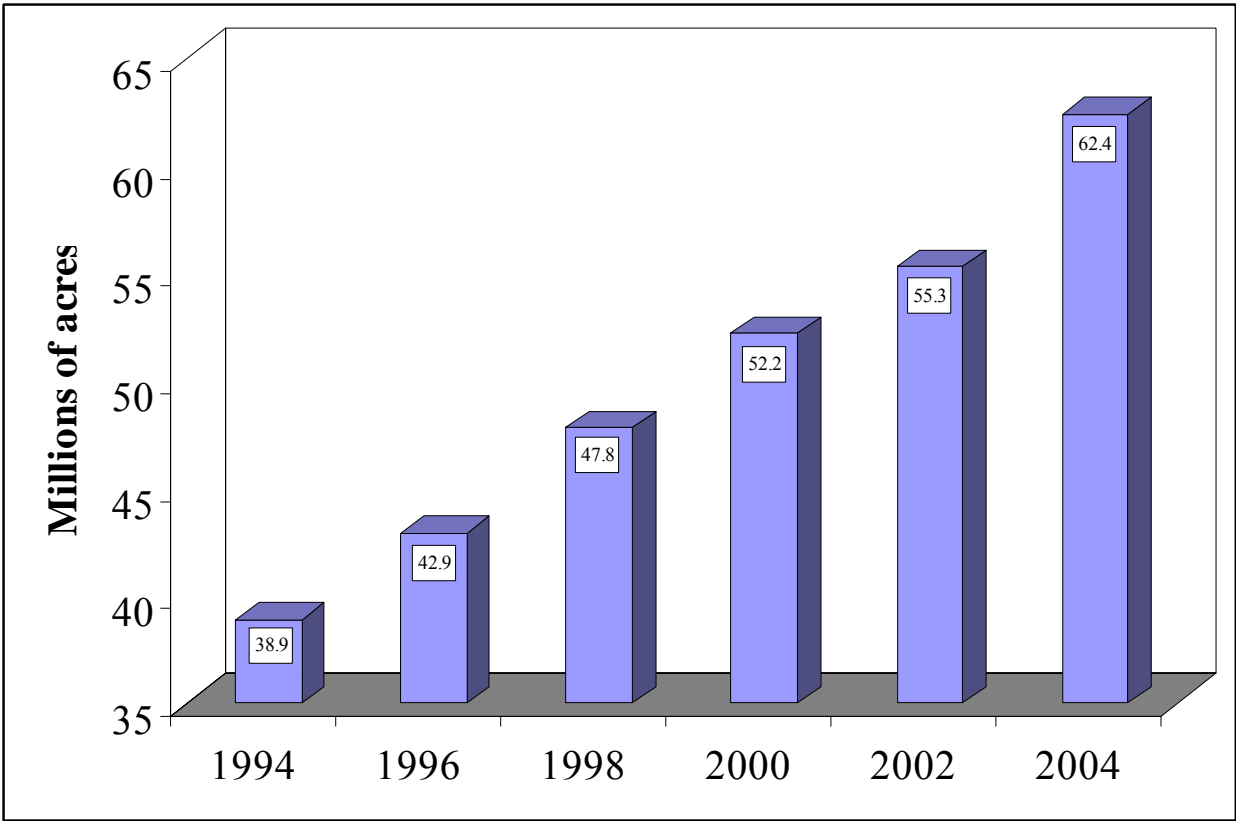[e] Regional dummy variables compare adoption relative to cotton farmers in Region 3 (AR, LA, MS, MO, TN).
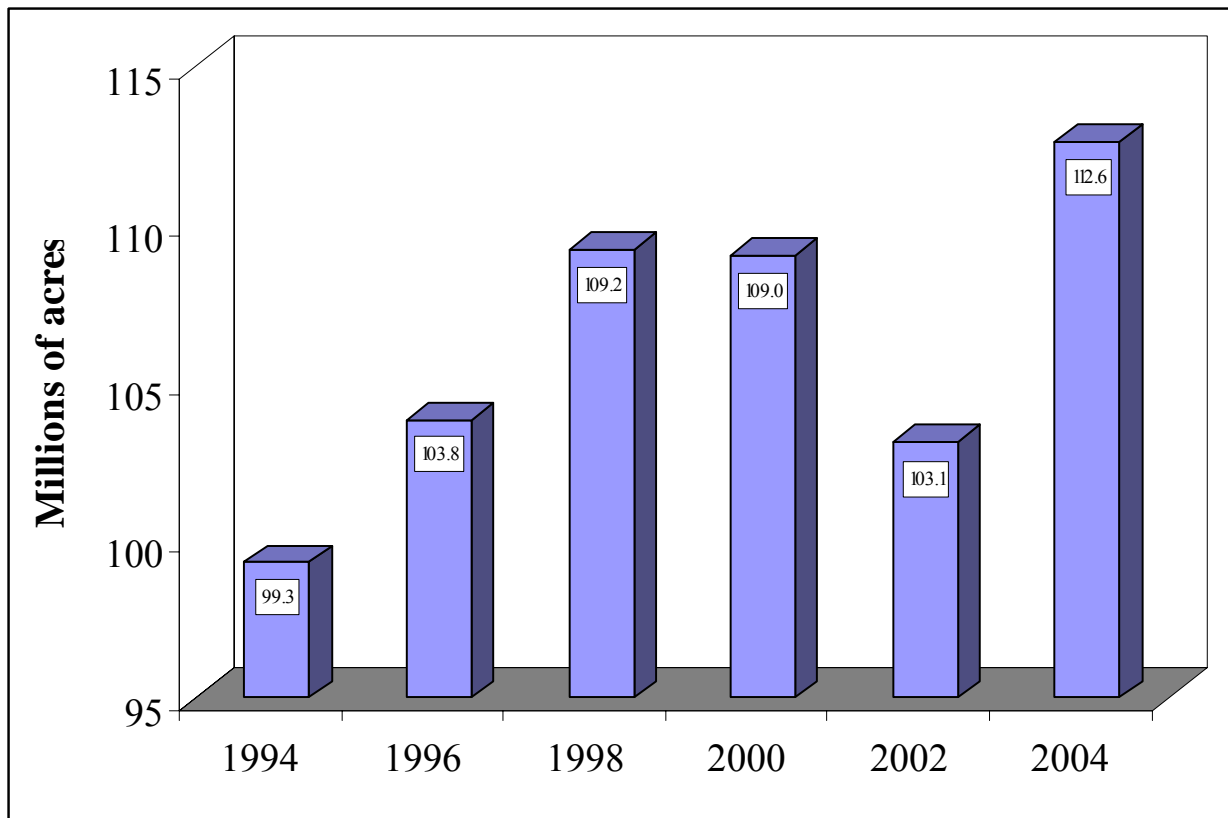
Source: Conservation Technology Information Center.

Figure 1. Conservation-tillage adoption in the United States, 1994-2004

Source: Conservation Technology Information Center.

Figure 2. No-till adoption in the United States, 1994-2004