

US EPA ARCHIVE DOCUMENT

SIMULATION MODELING OF THE PINK BOLLWORM ERADICATION PROGRAM IN ARIZONA

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Information prepared by Bruce Tabashnik
Simulations run by Mark Sisterson

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SUMMARY

SIMULATION MODELING OF THE PINK BOLLWORM ERADICATION PROGRAM IN ARIZONA as of July 28, 2006

Methods

We used a computer model to simulate potential effects of the Arizona pink bollworm eradication program on resistance to Bt cotton and population suppression. Details of our objectives, approach, scenarios, time horizon, and criteria were emailed to Sharlene Matten on June 23, 2006 (see attached). Briefly, we used a model of pink bollworm in Arizona that has been described in detail in a research publication (Sisterson et al. 2004, attached), with minor modifications including the release of sterile moths.

We began by simulating the eradication program with the best estimates available for all parameters, based as much as possible on published data (Table 1). These values are referred to as “default values,” because they are used unless noted otherwise. We systematically examined alternatives to the default values that were more pessimistic, i.e., more likely to result in resistance. A region with 4096 cotton fields was modeled for 4 years. In preliminary results to date, we have examined 12 sets of assumptions, each of them simulated 5-16 times, for a total of 128 simulation runs.

Results

In 11 of 12 sets of assumptions examined so far, the simulated eradication program eliminated the pink bollworm from the 4096 fields modeled in two years or less without causing a resistance problem (Table 2). The only set of assumptions examined that did not yield loss of pink bollworm from the region included no release of sterile moths in Bt cotton fields. After 4 years in this exceptional case, population density declined by 98% and the resistance allele frequency increased from 0.01 to 0.02. Note that in all simulations, sterile moths were released in non-Bt cotton fields at the default rate of 500 moths per ha in each release with one release per three days.

The 12 sets of simulations include the default values (best estimates for all parameters) and 11 other sets in which assumptions were purposely more pessimistic to increase the chances of resistance evolution. In particular, the default assumption was an initial resistance allele frequency (r) of 0.001 based on extensive bioassays (Tabashnik et al. 2005, attached) and DNA screening (Tabashnik et al., unpublished data). In the 11 sets with more pessimistic assumptions, r was 0.01, ten times higher.

The additional pessimistic assumptions that resulted in loss of pink bollworm from the region in 2 years included dominant (rather than recessive) inheritance of resistance, 90% Bt cotton and 10% non-Bt cotton refuges (rather than 100% Bt cotton), no fitness cost of resistance (rather than a 10% fitness cost in homozygous resistant insects), and release rates of 1, 2, 3, 4, 5, 10, or 15 sterile moths per ha in Bt cotton fields (rather than 75 sterile moths per ha).

With no steriles released in Bt cotton fields, 90% Bt cotton, and $r = 0.01$, pink bollworm persisted in the region for the 4 years of the eradication program in all 5 replicate simulations. From the 5 replicate simulations, the means were 0.02 for the final value of r , and 460 larvae per field surviving overwintering. The final resistance allele frequency represents a doubling over 4 years from the initial value, but is well below the 0.50 value typically used as a criterion for a resistance problem. With recessive resistance (as seen in pink bollworm) and $r = 0.02$, the frequency of phenotypically resistant individuals (rr) capable of survival on Bt cotton would be 4 in 10,000 (0.0004). The mean final population density of 460 overwintering larvae per field is less than 2% of the starting population density in the simulations (29,000 overwintering larvae per field). In sum, with no steriles released in Bt cotton fields, 98% population suppression occurred without a major resistance problem.

Discussion

Preliminary results from simulations suggest that it is likely that the eradication program in Arizona will suppress pink bollworm without creating a problem with resistance to Bt cotton. The preliminary simulation results suggest that best estimates for parameters and some more pessimistic assumptions do not yield rapid evolution of resistance under the conditions of the pink bollworm eradication program in Arizona. We plan to analyze results in greater detail to test their robustness. We will also explore additional pessimistic assumptions to determine which conditions might cause severe resistance problems. The simulation results suggest that release of sterile moths in Bt cotton is important for driving pink bollworm population densities to extremely low levels.

References Cited

- Sisterson, M. S. L. Antilla, Y. Carrière, C. Ellers-Kirk and B. E. Tabashnik. 2004. Effects of insect population size on evolution of resistance to transgenic crops. *J. Econ. Entomol.* 97: 1413-1424.
- Tabashnik, B. E., T. J. Dennehy, and Y. Carrière. 2005. Delayed resistance to transgenic cotton in pink bollworm. *Proc. Nat'l. Acad. Sci. U.S.A.* 102: 15389-15393.

Table 1. Parameter values for eradication model (revised from Sisterson et al. 2004). Default values, which are used unless noted otherwise for parameters with more than one value, are indicated by an asterisk.

Parameter	Values
Adults	
Mean % of adults that leave their natal field	10, 55*, 75
Number of eggs per female per day in Bt cotton fields	10
Number of eggs per female per day in non-Bt cotton fields	10
Mean % of adults that die each day	10
Egg-pupae	
Mutation rate (from S to R per allele)	5×10^{-5}
Mean % of SS and RS killed in non-Bt cotton fields	79.2
Mean % of RR killed in non-Bt cotton fields	79.2, 81.3*(10% fitness cost)
Mean % of SS and RS killed in Bt cotton fields	99.8 ^a , 100*
Mean % of RR killed in Bt cotton fields	79.2, 83.2*(incomplete R=0.9)
Development time (degree days)	433
Mean % of larvae that die during overwintering	95
Region	
Initial R allele frequency	0.0001, 0.001* , 0.01
Number of fields	4096 (64 X 64 square)
Size of fields	15 hectares
Percentage of Bt fields	80, 85, 90, 95, 100*
Percentage of Bt plants in Bt fields	99 ^a , 100*
Distribution of fields	Random
Carrying capacity per field	4,200,000
Initial overwintering larvae per field	2900, 29,000* , 290,000

^a 99.8% mortality of RS and SS simulates 100% Bt fields that have 99% Bt cotton plants and 1% non-Bt cotton plants (contaminants); 100% die on the Bt plants, 79.2% die on the non-Bt plants (0.99 X 100% + 0.01 X 79.2% = 99.8%)

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Steriles

Release period	May 1-Oct 15 (1st bloom to defoliation)
Frequency of releases in each field	1 per 3 days per field
Sex ratio of steriles	1 female: 1 male
Steriles per ha per release in Bt cotton fields	0, 1, 2, 3, 4, 5, 10, 15, 75* 0, 100, 500* , 1000
Steriles per ha per release in non-Bt cotton fields	

Pheromone ropes only in non-Bt cotton fields

All non-Bt fields treated once early in season	May 17-June 20 (6-leaf stage)
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Daily % reduction in fecundity caused by pheromone ropes 20, **40***, 60 for 30 days

Insecticide & pheromone sprays only in non-Bt cotton fields

Spray threshold	≥60 no spray
(check sterile male:native male ratio weekly)	30-59 spray pheromone
	0-29 spray pheromone + insecticide

Daily reduction in fecundity caused by pheromone sprays	20, 40*, 60 for 14 days
Mean % of adults killed daily by insecticide	37 per day for 5 days
Larvae are not killed by sprays	95 per day for 5 days

Table 2. Simulation outcomes: effects of pessimistic assumptions on simulated outcomes of the pink bollworm eradication program in Arizona. In all cases except the default case, the initial resistance allele frequency (r) was 0.01, which is ten times higher than the default value of 0.001. In all cases, 500 sterile moths per ha were released in non-Bt cotton fields, with one release per three days.

Parameter values different from default values	Outcome*
None (all parameters at default values)	Loss in 1 year
Initial resistance allele frequency (r) = 0.01	Loss in 2 years
No fitness cost, r = 0.01	Loss in 2 years
Dominant resistance to Bt cotton, r = 0.01	Loss in 2 years
90% Bt cotton, r = 0.01, Loss in 2 years Steriles released in Bt cotton fields at 1, 2, 3, 4, 5, 10, or 15 steriles per ha	
90% Bt cotton, r = 0.01 No steriles released in Bt cotton fields	averages after 4 years r = 0.02 460 larvae per field (overwintering survivors)

*loss means that no pink bollworm were present in any of the 4096 cotton fields modeled

June 23, 2006

Dear Sharlene,

We are in the early stages with modeling. We'd like to optimize the contribution of the modeling to EPA's evaluation of the proposed pink bollworm (PBW) eradication program in AZ. So, this is a good time to begin discussing with you the objectives, approach and scenarios to be modeled.

A draft of parameter values is attached. As this is research in progress, we ask you to protect its confidentiality as much as possible. We understand that the results of the simulations will be provided to EPA for analysis and public comment as part of the SAP process.

Your input is welcome.

Best wishes,

Bruce

Objectives

- 1) Simulate scenarios to aid EPA evaluation of resistance risk vs. population suppression associated with the proposed pink bollworm (PBW) eradication program in AZ
- 2) Produce a manuscript suitable for publication that describes the results of simulations and their relevance to the PBW eradication program.

Approach

We will use as our core model the PBW model described in detail by Sisterson et al. (2004) (attached). We will make relatively minor modifications to the core model to simulate various scenarios relevant to the AZ PBW eradication program.

This approach has several advantages. By using an established model, we can produce results in a timely fashion. We know the model works. It has been tested thoroughly and scrutinized by the peer review process. Its assumptions are published. The model contains sufficient spatial and temporal detail to realistically address key issues of population suppression and resistance risk for PBW in AZ.

The simulations will examine population suppression (number of pink bollworm per ha) and risk of resistance to Bt cotton (rate of increase of resistance allele frequency). We will use realistic assumptions that incorporate the best and most recent data available for pink bollworm on the genetic basis of resistance to Bt cotton, the frequency of resistance alleles in field populations, population sizes, population dynamics, and movement. As much as possible, we will rely on published data for parameter estimates.

We will describe qualitative patterns and quantitative effects of various parameters on population size and resistance allele frequency. Because the model is stochastic, we will

replicate runs to determine variation among runs and record the proportion of runs with various outcomes.

Scenarios

We will analyze a variety of scenarios, including those based on the best estimates for all parameters, as well as more optimistic and more pessimistic scenarios. We will accomplish this by using sensitivity analyses that systematically vary parameters that are naturally variable (e.g., movement) or for which there is uncertainty (e.g., resistance allele frequency). The modeling will also explore the impact on population suppression and resistance risk of alternative management options (e.g., variable refuge size and release rates of sterile moths).

Time Horizon and Criteria

Simulations will be run for 4 years to match the statutory limit for the AZ program, with overwintering larvae from the 4th year checked to assess the following criteria:

Resistance will occur if the resistance allele frequency exceeds 0.50.

Population recovery will occur if the final population size is equal to or greater than the initial population size (29,000 overwintering larvae per field is the default value).

Population suppression will occur if the mean PBW density in the region is equal to or less than 0.1 overwintering larvae per 15 ha field (= 0.0067 larvae per ha).

Regional loss will occur if all fields in the region modeled have 0 PBW.

Reference

Sisterson, M. S. L. Antilla, Y. Carrière, C. Ellers-Kirk and B. E. Tabashnik. 2004. Effects of insect population size on evolution of resistance to transgenic crops. *J. Econ. Entomol.* 97: 1413-1424.