9-14-06 TABASHNIK ANSWERS TO MATTEN MODELING QUESTIONS

Date: Thu, 14 Sep 2006 13:45:11 -0400
From: Matten.Sharlene@epamail.epa.gov
Bruce -- I have some modeling analysis questions (Vol. 5 of the submission). Please send answers to me ASAP. I am trying to finish everything up today, if possible, but at the latest tomorrow afternoon. Thank you for your help.
Sincerely, Sharlene

1. Resistance allele frequency, genetics of resistance, likely inheritance pattern is based on Cry1Ac resistance only? Yes or No?
Yes. **Do you have the data on the acreage in Arizona of Cry1Ac cotton vs. Cry1Ac + Cry2Ab cotton?**

How are these parameters addressed for Cry2Ab resistance?
We are not considering Cry2Ab resistance in the modeling.

There could be two different resistance mechanisms and two different inheritance patters?
Yes.

How should I use the model to address resistance to both toxins?
If some or all of Arizona's Bt cotton had two toxins, Cry1Ac + Cry2Ab, evolution of resistance would be much less likely than it is with only Cry1Ac. If you want, I can summarize the reasoning for that conclusion. By modeling resistance to cotton that produces only Cry1Ac, we are choosing a more pessimistic scenario than one that includes cotton with Cry1Ac + Cry2Ab. So, in this aspect, all of the modeling predictions are conservative, i.e., they tend to overestimate resistance risk.

2. What values/parameters would be changed based on the 2006 field data?
We will use data from the field to test the model's predictions about the ratios of sterile:native moths and resistance allele frequency. If the model's predictions are wrong, incorrect assumptions will be changed to improve the accuracy of the model.

Are additional simulations planned to used these data?
Yes. We are also conducting additional simulations now. We have modified some of the assumptions and run another set of scenarios using sensitivity analysis varying emigration (10, 55, or 75%), dominance (recessive or dominant), number of fields in the region (400 or 4096), percentage of Bt fields (80, 95, 100), carrying capacity per field (2,885, 28,885, 288,850), and numbers of steriles per ha per release in Bt and non-Bt cotton fields (0,0; 2,10; 100, 500; and 200, 1000). Again, with one exception, all scenarios yielded regional loss in 2 years. The only case in which loss did not occur was with no steriles released in Bt or non-Bt cotton (0, 0). The lowest non-zero release rate tested was 2 per ha per release in Bt cotton and 10 per ha per release in non-Bt cotton (2,10). This low release rate scenario yielded regional loss in 2 years.

3. The modeling output is represented in a qualitative way. Do you have another table that summarizes each of the twelve scenarios? I think this would be clearer.
If you let me know more specifically what additional information you seek, we can probably provide it. Regional loss means zero PBW in the region. So, we could put zeroes in the table instead of "regional loss." R allele frequency is not relevant when regional loss occurs.

4. Do I understand that for 11/12 scenarios, resistance did not evolve and no PBW were present after the 4 year eradication program.
Correct. In 11/12 scenarios, no PBW were present after 4 years.

One scenario had a 98% population suppression with a r frequency of 0.02 (below resistance threshold of 0.50). The r frequency in question is Cry1Ac only?
Yes.

5. Sterile release rates in the model. The sampling/trapping protocol description in vol. 1 indicates that steriles were released at a rate of 20 steriles/acre/day (3X per week) in Bt fields and 100 steriles (or more)/acre/day (3X per week) in non-Bt fields. I converted these to hectacres and so the sterile rate in Bt fields = 8 steriles/ha/day and in non-Bt fields = 40 steriles/ha/day. However, in the model, I see that the default values are much higher than what was actually done in 2006, i.e., 75 steriles/ha/day in Bt cotton fields and 500 steriles/ha/per release in non-Bt cotton fields. How do you explain this difference? How does this difference affect the model outcome?
Your conversions are off by ca. 6.25X (too low) because the conversion requires multiplying X 2.47 (not dividing by 2.5). Also, the model assumptions are stated in steriles per release (not per day). The sensitivity analysis results submitted to EPA at the beginning of August included 1, 2, 3, 4, 5, 10, and 15 steriles per ha per release in Bt cotton. These lower levels also yielded regional loss (i.e., no pink bollworm) in 2 years. More recent simulations show regional loss with 2 per ha per release in Bt cotton and 10 per ha per release in non-Bt cotton.