

 Supplementary files are available for this work. For more information about accessing these files, follow the link from the Table of Contents to "Reading the Supplementary Files".

Long Term Consequences of Genetically Modified Crops in Agriculture

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KEYWORDS

GM (genetically modified) Crops, GC (genetically contaminated) weeds, gene jump, insect mutation, agricultural modeling, ecosystem dynamics

ABSTRACT

There is evidence in published reports and scientific literature that GM crops can contaminate natural crops of the same family in the field or even weeds that are their distant relatives. We are considering the problem from an evolutionary point of view. Will GM crops exhibit a controllable dynamics, will they be dominated by or will they dominate the ecosystem? Will GM crops lead to new species? How will these new species affect the agriculture? These are the types of questions that we try to answer in this paper. The scenario that we model is a situation where a “gene jump” occurs from some experimental genetically modified plot into a natural crop field. By a series of simulation experiments, we investigate the possible long term consequences of this gene jump. Our results indicate that in most situations, either GC crop or GC weed would dominate the field in the long term, which is an alarming result, justifying further research.

INTRODUCTION

GM Crops are produced such that they have the important properties of resistance to herbicides, insects and diseases. Herbicides are chemicals that are used to destroy weeds but they give harm to the crops too. Herbicide resistant GM crops are more resistant to herbicides than natural crops. On the other hand, insect resistant GM Crops contain special proteins which prevent them from being eaten by insects. Some GM crops possess both of the herbicide resistance and insect resistance properties (Please see websites of producers: <http://www.monsanto.com> and <http://www.mycogen.com>).

Over 95% of the GM crops grown in the US fall into one of these two categories (True Food Network, website). Since herbicide resistance and insect resistance are the most widespread properties of GM crops, they are the two traits that will be considered in this paper. Other traits (virus resistance, bacterial disease resistance etc.) are out of the scope of this paper; hence they will not be employed in the model.

There are two groups arguing about the benefits and risks of GM crops. One group claims that the genetic modification of crops can increase the amount and quality of food on a global scale, decrease global starvation and contribute to the human health which are the fundamental goals of genetic modification. The opponents claim that these crops may go out of control, dominate the ecosystem and reduce agricultural biodiversity. Some of the possible problems of biotechnology that will be considered in this research are as follows:

Genes may jump from one plant to another:

Genes that lead to the herbicide resistance or insect resistance properties of GM crops may "flow" to their relatives (Teitel and Wilson 1999, 37). According to a recent article in *Nature* (Dalton 2001, 337), I. H. Chapela and David Quist found growing GC corn (maize) in Oaxaca-Mexico. Since this is the place where corn was first cultivated in the world, this finding initiated concern among scientists and environmentalists. According to an editorial in the *New York Times* (2 October 2001) Oaxaca is a remote area where scientists do not expect to find genetic contamination. This result reveals that the GM crop genes may flow to distant fields faster than scientists had estimated. Because these foreign genes may be highly advantageous, plants to which these genes have flowed could begin to dominate the ecosystem. As the plants that do not carry these advantageous genes decline, genetic diversity will be lost.

GM crops may lead to herbicide and insect resistant weeds:

Any gene of a crop or plant may flow to its wild relatives, as well. If a transgene improves the resistance of a wild relative (weed) against herbicides, insects, bacteria or diseases, it will be more difficult to fight against this weed (Teitel and Wilson 1999, 37). In such situations, weeds may dramatically change the balance in the ecosystem.

Resistant genes may not serve their function for very long:

It is known that in some cases insects have adapted to insecticides and insect resistant crops. If any insect adapts to the insect resistant crops in a field, it begins to feed on these crops; hence the crops lose their advantage with respect to the insects and the other plant types in the ecosystem. This adaptation may occur even in a period of one or two years. Planting more and more insect resistant crops (such as corn, cotton, and rice) over large fields increases the probability of insect adaptation (Kendall et al. 1997, 23).

The other problems mentioned in literature are development of new viruses from virus-containing transgenic crops, gene transfer to bacteria, poisoning people or farm

animals etc. These problems are out of the scope of this paper; therefore they are not included in the model.

MODEL

The model represents a part of the real system related to the problems mentioned above and variables used in the model are defined accordingly. Then, relations between variables are determined and described in a causal loop diagram (See Figure 1). The major feedback loops involved in this structure will be described below, when discussing the dynamic behavior of the model.

Next, accumulations and their flows are determined. Finally, relations between variables are converted to mathematical and graphical functions. Starting point of the model is the finding of Chapela and Quist, which is explained above. In the model, we are considering a farmer who has a field in which “Natural Corn” (not GM corn) is planted. Somehow, a gene jump has occurred as it happened at Oaxaca, Mexico and there is some “GC Corn” (genetically contaminated) in his field (Quist and Chapela 2001, 541-542). The farmer is not aware of this situation. At the end of each year he collects a portion of the yield in order to use them as the seeds of next year. Therefore, the genetic materials of the crops in the field are transferred to the next year's yield.

GC corn mentioned in our model has two main advantages when compared with the natural corn: The herbicide resistance and insect resistance genes have jumped to it, thus it is herbicide and insect resistant. Herbicide resistance does not mean 100% resistance, but GC Corn is more resistant to herbicides than a natural corn. GC corns also contain a special protein that prevents them from being eaten by insects. There is also, of course, a “Natural Weed” population in the field and the farmer uses herbicides to fight against weeds. However, herbicides have a harmful effect on the corns, too. In the long run, the situation may get more complicated and herbicide and insect resistance genes may jump to the weeds in the field. As a result, “GC Weeds” may emerge which are resistant to herbicides and insects.

In the field there are also insects around corns and weeds. “Natural Corn Insects” (Corn Borer) feed on the natural corn while the nutrition source of “Natural Weed Insects” is natural weed. GC corns are insect resistant thus natural corn insects can not eat them. Despite this situation, GC corns may face future risks. As explained above, insects have the ability to adapt to crop varieties which have resistance genes. According to this fact, we may expect to have adapted insects which will feed on GC Corn (we assumed that natural insects will adopt this trait via mutation). These insects are called “GC insects”. Natural weed insects can not eat GC weeds; they can only eat Natural Weeds. However, in the future a new species, which has the capability to feed on GC weeds, may emerge as a result of mutation. These insects are called “GC weed insects” in the model.

Total area of the farmer's field is 1000 m^2 (= 20m x 50m) in this model and the regeneration of all the plants (Natural Weed, GC Weed, Natural Corn and GC Corn) is

density dependent. Their regeneration fractions depend on "crowding" which is defined as "total plant area/total field area". We assumed that natural weeds and GC weeds have higher birth (or regeneration) fractions than natural corns and GC corns because their need for water and minerals is much less than that of natural corns and GC corns. When it comes to death fractions, we assumed that the difference between death fractions stem from herbicide resistance and insect resistance (for all plant types). In the model natural weeds are the ones that are most affected from herbicides (for more information please see <http://dragon.zoo.utoronto.ca/~jlm-gmf/T0501A/herbicide.html>). Then come GC weeds, natural corns and GC corns, respectively. We assume that, since weeds are targeted by herbicides, even if the weeds contain herbicide resistant genes, they will be more vulnerable to the harm of herbicides than natural corns and GC corns.

While modeling the emergence of GC weeds, the approach that will be used in the model is a delay structure. We assume that the GC weeds emerge as a result of cross pollination between natural weeds and GC crops, which will take a very long time.

Stock-Flow diagram

Stock-flow diagram of the model (See Figure 2) is a mathematical representation of the problem. In our model, there are eleven stocks. Eight of the stocks, i.e. Natural Corn Area, GC Corn Area, Natural Weed Area, GC Weed Area, Natural Corn Insect, Natural Weed Insect, GC insect and GC Weed Insect are very important in the problem. Three of the stocks are used for the third order smoothing, i.e. Gene Jump 1-2 and Gene Jump.

Natural Corn Area, GC Corn Area, Natural Weed Area and GC Weed Area are measured in m^2 . They represent the area of the related plant type. Their values are summed up to find the total plant area which is used to define the dimensionless variable crowding ($crowding = \text{total plant area} / \text{total field}$). In our model, total field is constant and is $1000 m^2$. Crowding affects the regeneration fractions of all the plant types in a negative way. As crowding gets bigger, regeneration fractions get smaller. We assigned the same regeneration fractions to natural corns and GC corns since their difference stems from the resistance of GC corns to herbicides and insects. Resistance affects death fraction, not the regeneration fraction. Likely, natural weeds and GC weeds both have the same regeneration fraction. The difference between them stems from their different resistance properties against herbicides. As explained before, regeneration fraction of natural weeds and GC weeds is greater than that of natural corns and GC corns because weeds are not domesticated and they do not need as much resources (water, minerals) as the domesticated crops to reproduce (See Figure 3 for regeneration fraction graphical functions of natural corns, GC corns, natural weeds and GC weeds).

While considering the death fraction of natural corns, we assumed that there is a normal death fraction of them. This normal death fraction is not related to the effect of herbicides and insects. It may be due to diseases or another source which is out of the scope of this model. Natural corn death fraction is the sum of natural corn normal death fraction, effect of herbicide on natural corn death fraction and effect of natural insects on natural corn death fraction. As mentioned above, herbicide usage affects the death fraction of natural corns. Herbicide usage methods and amounts used vary considerably.

There are many different methods and chemicals used. The amount changes according to the percentage of weed in the field and according to the type of chemical used. According to Mr. Tuna Dogan (Associate Professor, Agricultural Engineering), 10 grams of herbicide may be a reasonable amount for a 1000 m² field, 10% of which is covered with weeds. For the field in the model, reference herbicide usage is found by (herbicide usage for 1000 m² field covered with 10% weed*(total field area/reference field area)). Reference Field area is 1000 m². Then we multiply (reference herbicide usage) with (effect of weed percentage on herbicide used) and find (amount of herbicide used). Effect of weed percentage on herbicide used is formulated by a graphical function. It takes (percentage of weeds/reference percentage of weeds) as input. Reference percentage of weeds is 10%. As the percentage of weeds gets bigger, amount of herbicide used gets bigger, too. However, herbicides are extremely poisonous chemicals which have side effects on crops, soil, underground water sources and thus on human health. For this reason, they are used in very small amounts. We set the upper limit of the graphical function to 2 (corresponds to the herbicide usage of 20 grams for a 1000 m² field -please see Figure 4 for the graphical function of effect of weed percentage on herbicide usage).

After finding the amount of herbicide used, effect of herbicide on natural corn death fraction is computed. It is represented by a graphical function. Input of the function is (Amount of Herbicide Used/ Reference Herbicide Usage for the Field). The whole structure is established such that one can change the total field area for having different runs for different agricultural fields and modify the model easily. In other words, this approach increases the portability of the model.

Similar function definitions and formulations are done for GC corn, natural weed and GC weed. The key point is that natural weeds are the ones that are affected by the herbicides most. Then come GC weeds, natural corns and GC corns (Please see Figure 5 for effect of herbicide used on natural corn df, GC corn df, natural weed df, GC weed df)

Insects also affect death fraction of natural corns. Natural Corn Insect (Corn Borer) per Natural Corn influences the death fraction of natural corns. In this formulation, number of natural corn cobs is used instead of the area of natural corns. According to Mr. Tuna Dogan, corns are raised in straight rows. The distance between two rows is 70 cm and the distance between two corn cobs in a row is 15 cm. A simple calculation reveals that, in a field of 20 m x 50 m, approximately 9000 corn cobs exist. Corn per m² is thus assumed to have a constant value of 9 and weed per m² is given the value 15 (A point that should be mentioned with the insect per corn (or weed insect per weed) formulation is, we cannot assign the initial value of 0 to corns since the formulation will yield an indefinite value. In order to be able to perform that assignment, we inserted an IF statement to the formulation. If the amount of corns is 0, then insects per corn will be 999,999 which represent infinity in our model).

If number of natural insect per number of natural corn is equal to 1, the corn loss will be 5% (Willson 1989). Effect of natural insects on natural corn death fraction is formulated with a graphical function. Input is natural insect per natural corn. (See

Figure 6 for the graphical function). Same formulation is also done for GC insects-GC corns, Natural Weed Insects-Natural Weeds, GC Weed Insects-GC Weeds.

Natural corn insect birth fraction depends on natural corn insect per natural corn. As natural insect per natural corn increases, birth fraction decreases. Same formulation is valid for GC insects-GC corns, Natural Weed Insects-Natural Weeds, GC Weed Insects-GC Weeds, too (See Figure 7). There is one important point that should be noted here: Initially there are no GC insects. We have mentioned that insects can adapt to insect resistant crops. According to this, if we have GC corns in the field, we may have GC insects after a time period. GC insect variable has two inflows, GC insect births and insect mutation; and one outflow, GC insect deaths. The underlying idea behind the structure of mutation in the model is as follows: As GC corn ratio increases, probability of GC insect mutation increases. The logic behind this is generating a random variable between 0 and 1 and comparing it with the probability given as input. If the random variable is smaller than the input, the computer returns the value 1, otherwise it returns 0 (See Figure 8 for probability of GC insect mutation and GC weed insect mutation). If there are enough Natural Corn insects in the field and no GC insects, a mutation may occur in the model and the new GC insect species may emerge. However, this is a probability and it is not certain that mutant insects will actually emerge. Same probabilistic formulation (as a function of GC weed ratio) is employed for GC weed insect mutation.

The flow of modified genes and emergence of GC weeds is modeled with a delay structure. As the GC Corn Ratio (GC Corn Area/Total Plant Area) increases, gene jump fraction increases too. We multiply the area of natural weeds and gene jump fraction, thus we find the possible gene jumps. We assume that this GC weed emergence process will take considerable time to occur. Thus, a third order exponential smoothing is used for modeling the GC weed produced by gene jump. (See Figure 9 for the graphical function of gene jump fraction)

SIMULATION RESULTS

We ran the model with initial values of 890 m² for natural corns, 10 m² for GC corns, 100 m² for natural weeds, 0 m² for GC weeds, 9000 for natural corn insects, 10000 for natural weed insects, 0 for GC insects and GC weed insects (See Appendix 1 for the equations of the model and the initial values). The probabilistic functions in MUTATEORNOT and MUTATEORNOT2 variables were assigned seeds of 1500 and 50 in this main run. We did not use any seeds in the other runs. The simulation results of this main run may be found in Figure 10. According to these results, in the long run, natural corns and GC corns display a boom then decline behavior and natural weeds display a continuous decay behavior. On the other hand, GC weeds follow an S-shaped growth and they dominate the field in the long run.

GC corns are superior to natural corns and GC weeds are superior to natural weeds; thus the competition for dominating the field will take place between GC corns and GC weeds. Thanks to their greater regeneration fractions, GC weeds are advantageous against GC corns in the long run. As the area of a certain plant increases, the number of insects that feed on this plant is positively affected. On the other hand, as the number of

insects gets bigger, area of the plant they feed on decreases. Herbicide usage is another factor that harms all four plant types and decreases crowding. Decreasing crowding increases the regeneration fraction of GC weeds and GC corns. As GC weeds have higher regeneration fractions they will reproduce faster than GC corns in a field where crowding gets smaller. These loops and a few other important ones are chosen and illustrated in Figure 11.

When the behaviors of total corn area and weeds are investigated, the results are striking. For the first 40 years, after a very slight decrease at the beginning, total corn area continuously increases. During this time period, area of natural weeds decline dramatically. These are very positive indicators in the short run. However, in the long run GC weeds begin to increase and they dominate the area.

As mentioned earlier, emergence of GC corn insects and GC weed insects is both random and a function of GC corn and GC weed areas and they may never emerge at all in the time horizon of the model. In the main run, all four insect types emerge and GC weeds dominate the field, due to the higher regeneration fraction as explained above. When GC weed insects do not emerge but GC corn insects emerge, GC weeds dominate the field again as expected (See Figure 12). But if GC corn insects do not emerge and GC weed insects emerge then GC corns this time dominate the field (See Figure 13). Finally, in the case of no GC corn insect and no GC weed insect emergence, GC corns dominate the field (See Figure 14). These results reflect the fact that differing conditions change the dominant plant type in the field, depending on the relative strength of loops shown in Figure 11.

VALIDATION

a) Direct Structure Tests

- Dimensional Consistency Check:

The dimensions of all elements in the model may be found at Appendix 2. The results of dimensional consistency check may be found at Appendix 3. This chart represents the unit consistency of all formulations used in the model.

b) Indirect Structure Tests:

- Extreme Condition Tests:

a) Initial areas are: 1100 m² for Natural Corns, 90 m² for Natural Weeds, 10 m² for GC Corns and 0 m² for GC weeds. Thus, crowding is set to 1.2 initially. The total plant area falls below 1000 m² in one year and stays under 1000 m² after that time, which is logical. The simulation runs may be found in Figure 15.

b) Initial area of Natural corn, GC corn and Natural weed is 1 m². GC weed area is set to 0 m². At the beginning natural weed area and GC corn area increase very rapidly. Then, GC weeds begin to dominate the field. The simulation results may be found in Figure 16.

c) Natural weed area and GC weed area is 0 m^2 initially. Natural corn area is 990 m^2 and GC corn area is 10 m^2 . The simulation results may be found in Figure 17. The results are reasonable. Since there are no natural weeds initially no GC weeds emerge. Since there is no natural or GC weed, no herbicides are used.

d) GC corn area is initialized to 0. Natural corn area is 900 m^2 , natural weed area is 100 m^2 and GC weed area is 0 m^2 . The results may be found in Figure 18. The results are reasonable. Since there are no GC corns in the field, no GC weeds emerge. Similarly, neither any GC corn insect, nor any GC weed insect emerges.

e) Natural corn insects and natural weed insects are initialized to 0. Natural corn area is 900 m^2 , natural weed area is 90 m^2 and GC corn area is 10 m^2 . Results may be found in Figure 19. The results are reasonable. Since there are no natural corn insects and no natural weed insects, neither any GC corn insect, nor any GC weed insect emerged.

f) Initially, there are 80,000 natural corn insects and 15,000 natural weed insects. Natural corn area is 900 m^2 , natural weed area is 90 m^2 , GC corn area is 10 m^2 and GC weed area is 0 m^2 . The results may be found in Figure 20. Since the initial number of insects is very high, the number of insects declined dramatically at the beginning.

SENSITIVITY ANALYSIS

Since the effect of herbicide on four plant types in the model has a great influence on the previous results, we double the effect of herbicide on GC weeds to observe the system behavior. Another option is halving the effect of herbicides on GC corns.

- a) In this experiment, effect of herbicide on GC weed is doubled (See Figure 21). Initial values are 890 m^2 for natural corns, 10 m^2 for GC corns, 100 m^2 for natural weeds, 0 m^2 for GC weeds, 9000 for natural corn insects and 2000 for natural weed insects. Results may be found at Figure 22. According to these results, when the system reaches stability after approximately 250 years, GC corns dominate the system and GC weeds constitute a very small portion of the field. Due to the increasing effect of herbicide on the death fraction of GC weeds, the long term results change considerably.
- b) This time, with the same initial values, the effect of herbicide on GC corn is halved (See Figure 23). Results may be found in Figure 24. According to these results, when the system reaches stability after approximately 250 years, GC corns dominate the field.

These two results reflect a very serious fact. In the simulation results GC weeds have dominated the field. However, according to the sensitivity analysis results, we see that GC corns may dominate the field, too.

CONCLUSION

By a series of simulation experiments, we investigate the possible long term consequences of a gene jump from a GM crop to natural crops of the same family or to weeds that are their distant relatives. As shown in the results of simulation runs, GC crops may bring out very disastrous results because GC weeds dominate the field in most of the simulation runs. On the other hand, as the herbicide resistance parameters are changed, the runs show that GC crops may also dominate the field and productivity may increase. However, even in this desirable situation, there is a severe danger. While GC crops are dominating the field, natural crops become extinct and this situation leads to reduced biodiversity. Reduced biodiversity is a serious potential threat for the sustainability of global food sources.

Taking into account these observations and simulation results, it is clear that great effort should be spent to the investigation of the possible long term consequences of GC crops.

FIGURES

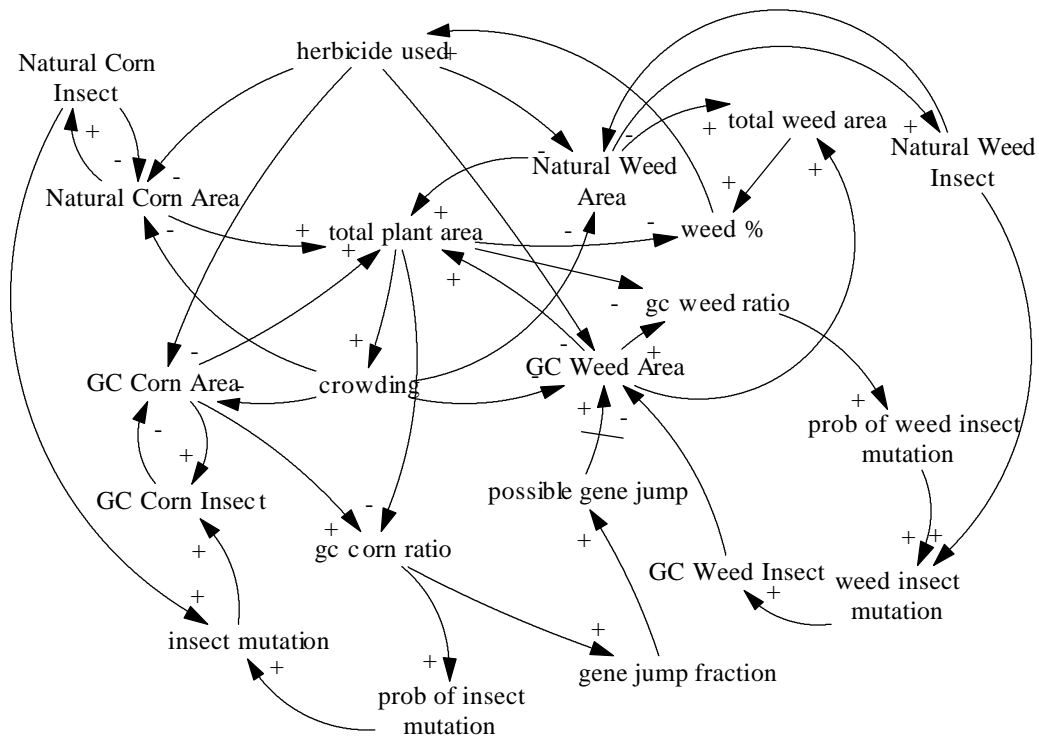


Figure 1: Overall Causal Loop Diagram of the Model

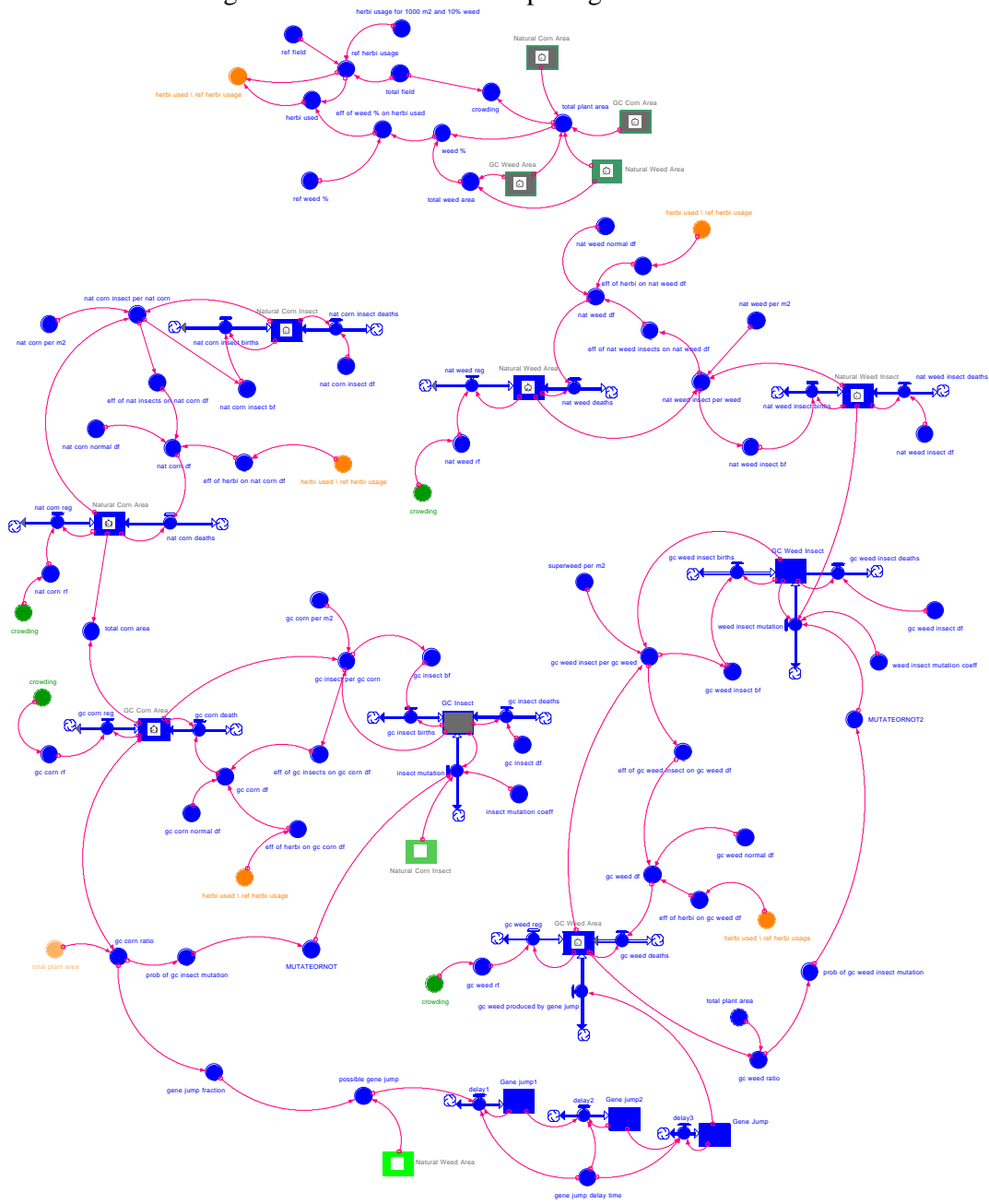


Figure 2: Stock Flow Diagram of the Model

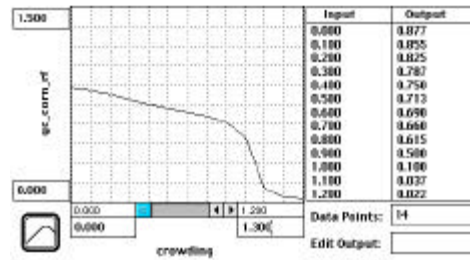
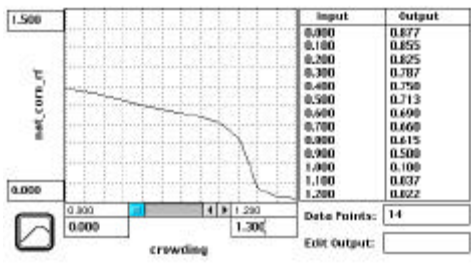


Figure 3-a) natural corn regeneration fraction Figure 3-b) gc corn regeneration fraction

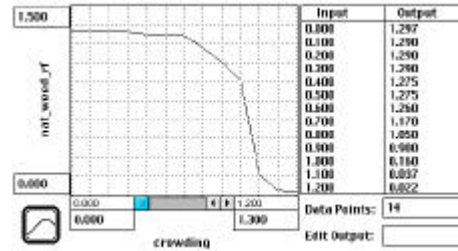
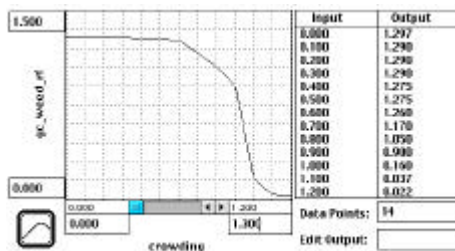


Figure 3-c) gc weed regeneration fraction Figure 3-d) natural weed regeneration fraction

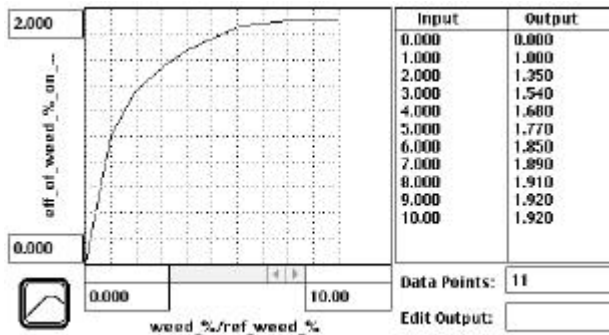


Figure 4: effect of weed percentage on herbicide used

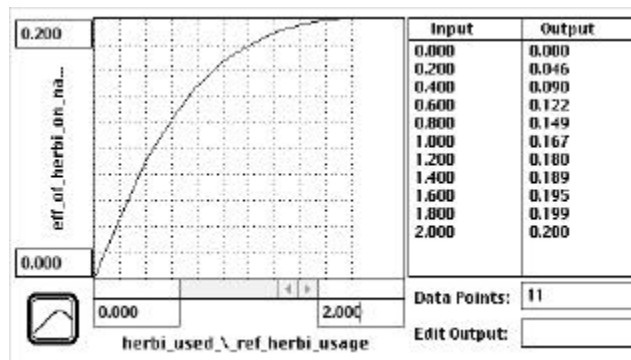


Figure 5-a) effect of herbicide on natural corn death fraction

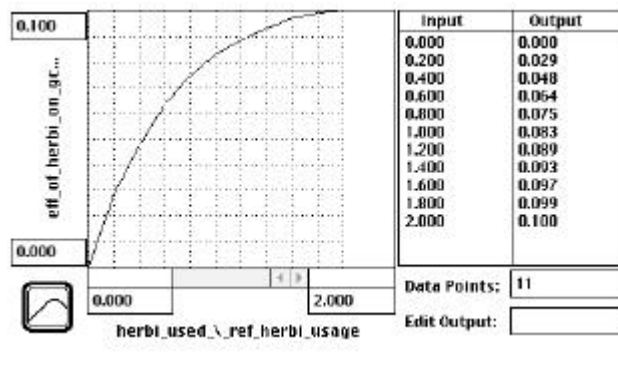


Figure 5-b) effect of herbicide on gc corn death fraction

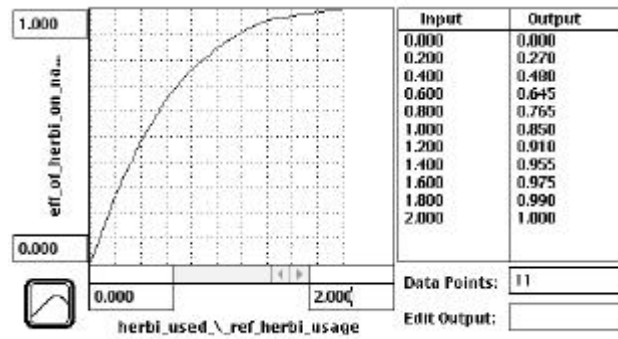


Figure 5-c) effect of herbicide on natural weed death fraction

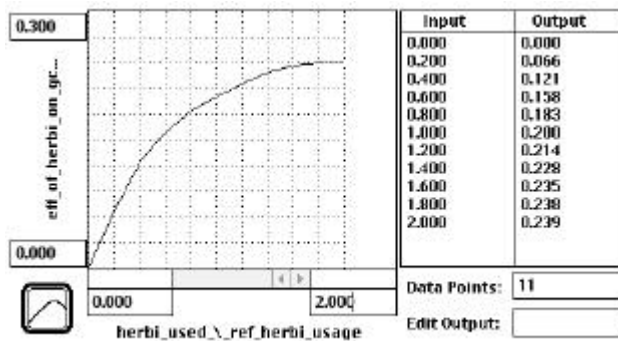


Figure 5-d) effect of herbicide on gc weed death fraction

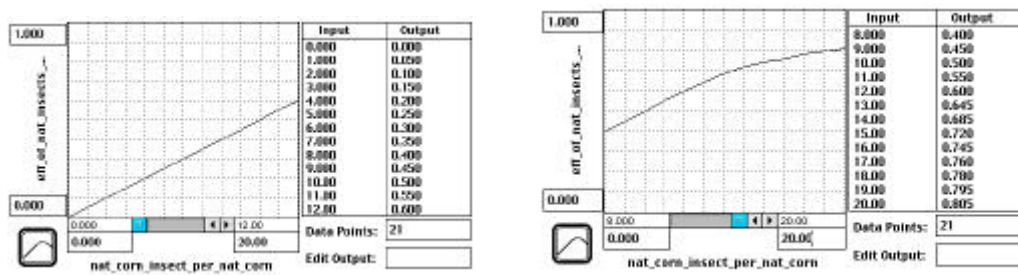


Figure 6-a) effect of natural insects on natural corn death fraction

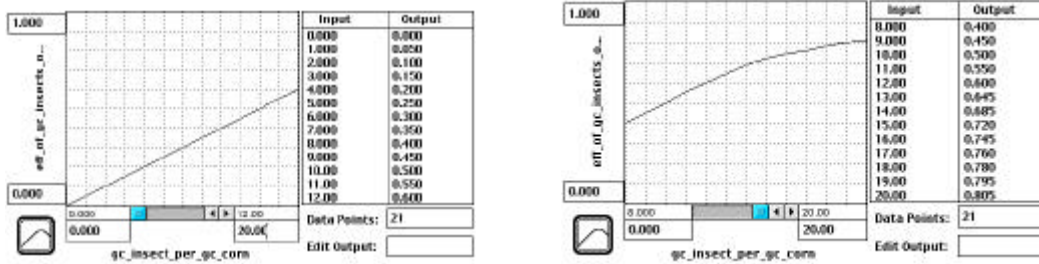


Figure 6-b) effect of gc insects on gc corn death fraction

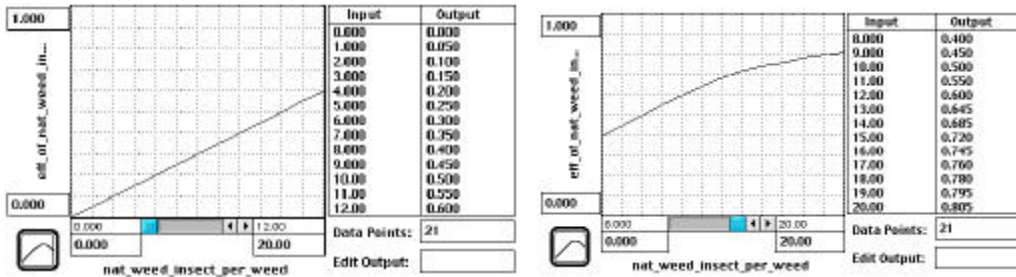


Figure 6-c) effect of natural weed insects on natural weed death fraction

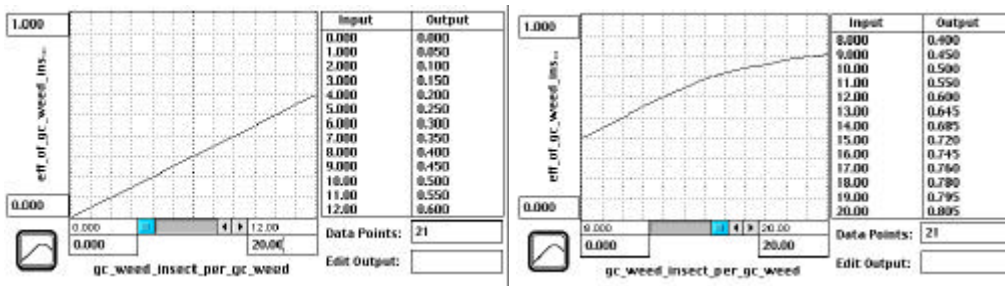


Figure 6-d) effect of gc weed insects on gc corn death fraction

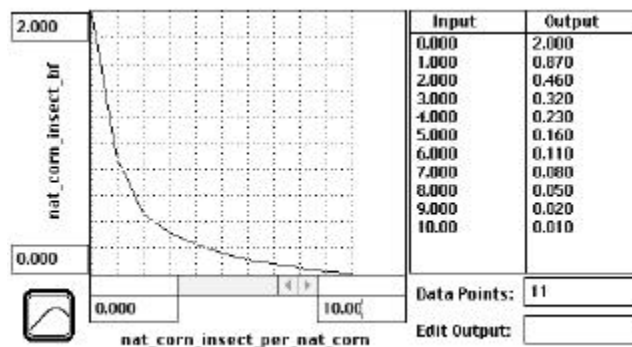


Figure 7-a) natural corn insect birth fraction

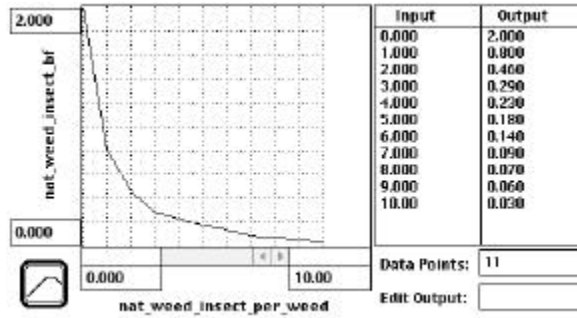


Figure 7-b) natural weed insect birth fraction

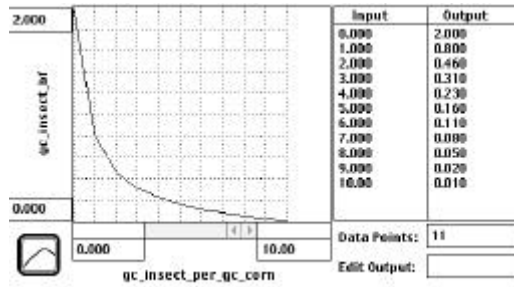


Figure 7-c) gc insect birth fraction

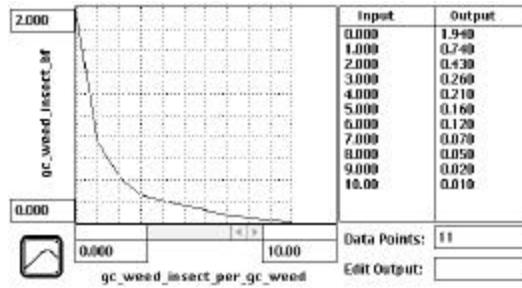


Figure 7-d) gc weed insect birth fraction

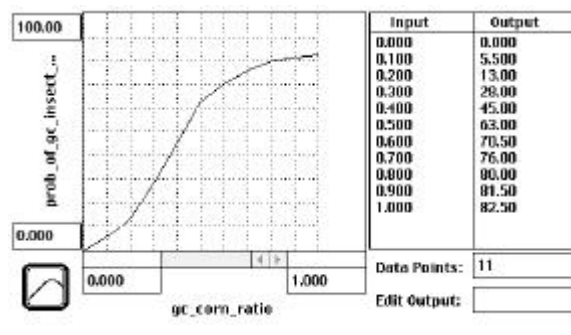


Figure 8-a) probability of gc insect mutation

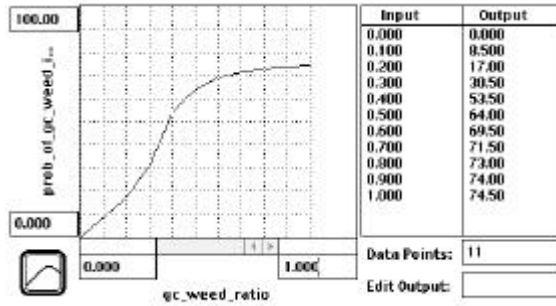


Figure 8-b) probability of gc weed insect mutation

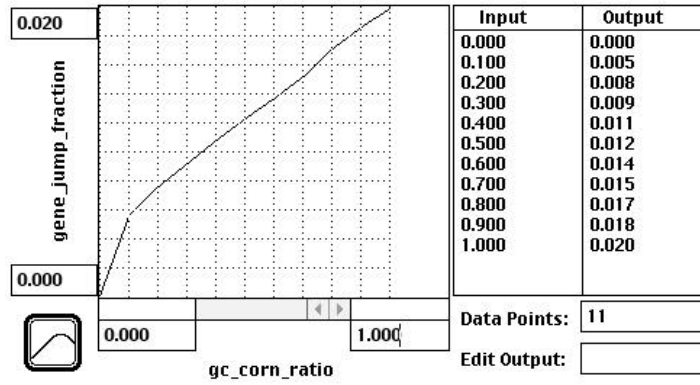
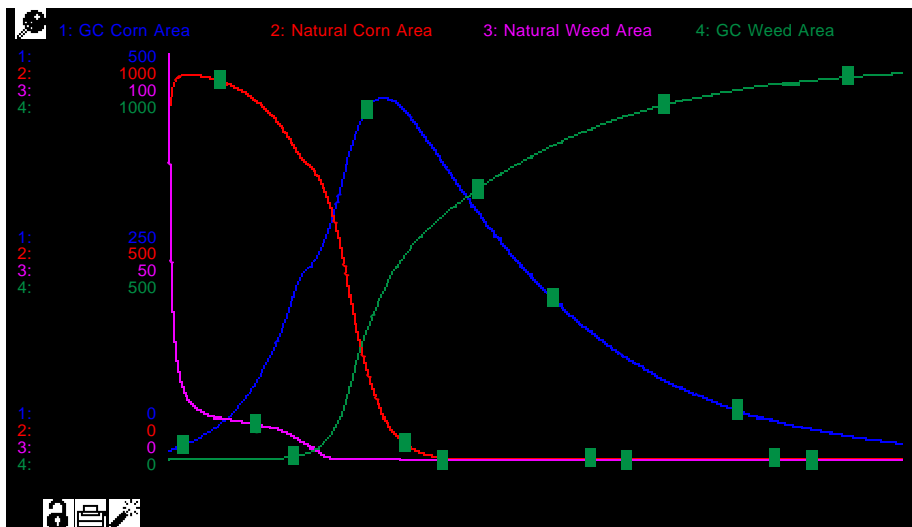


Figure 9: gene jump fraction



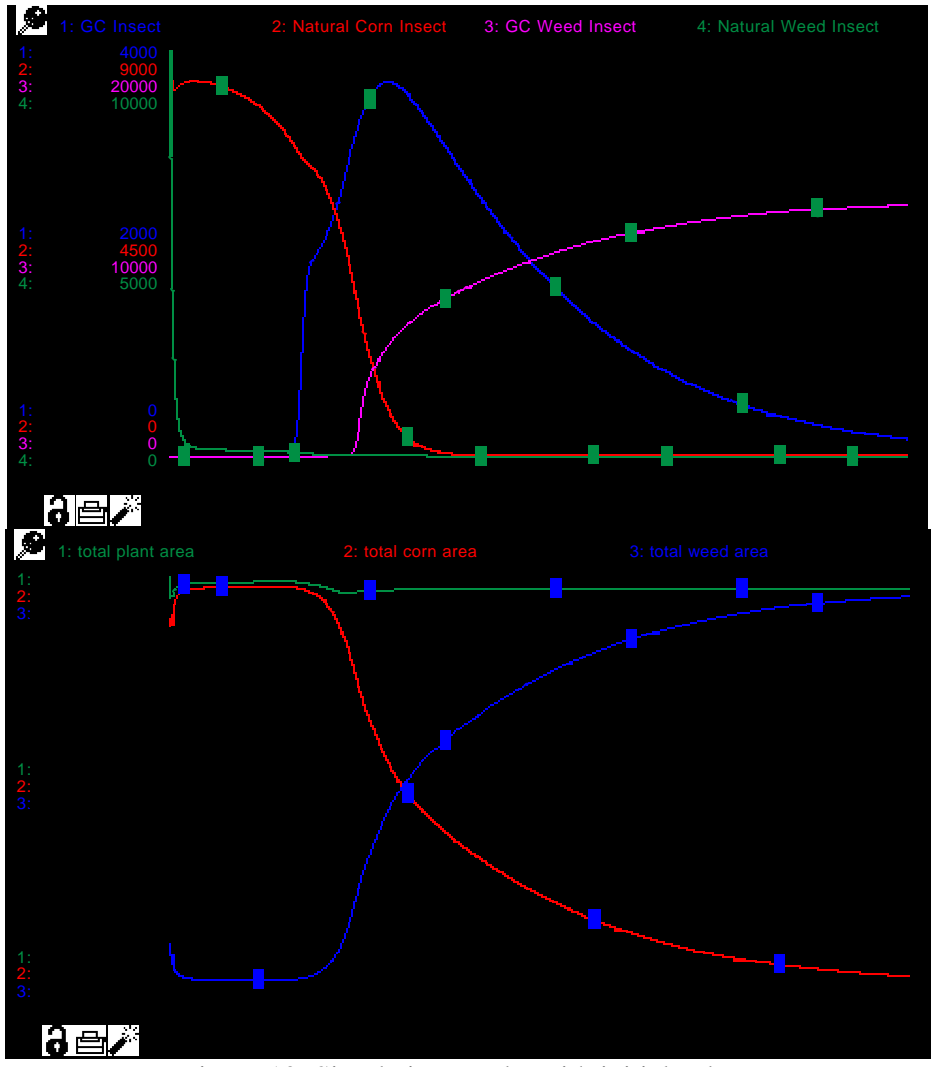


Figure 10: Simulation results with initial values

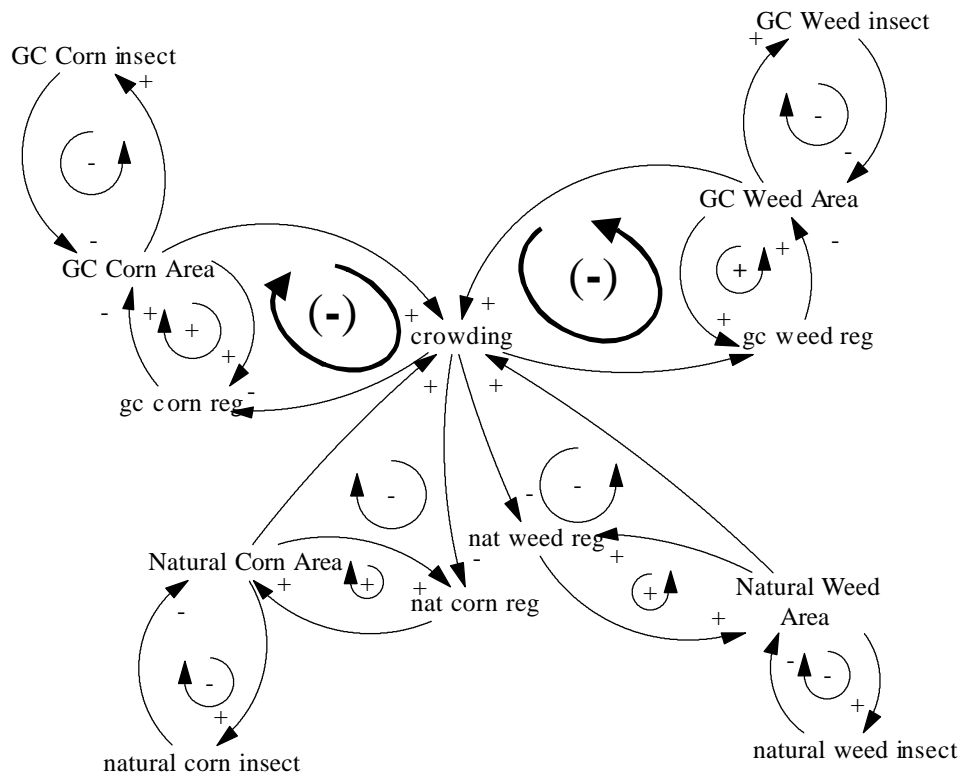
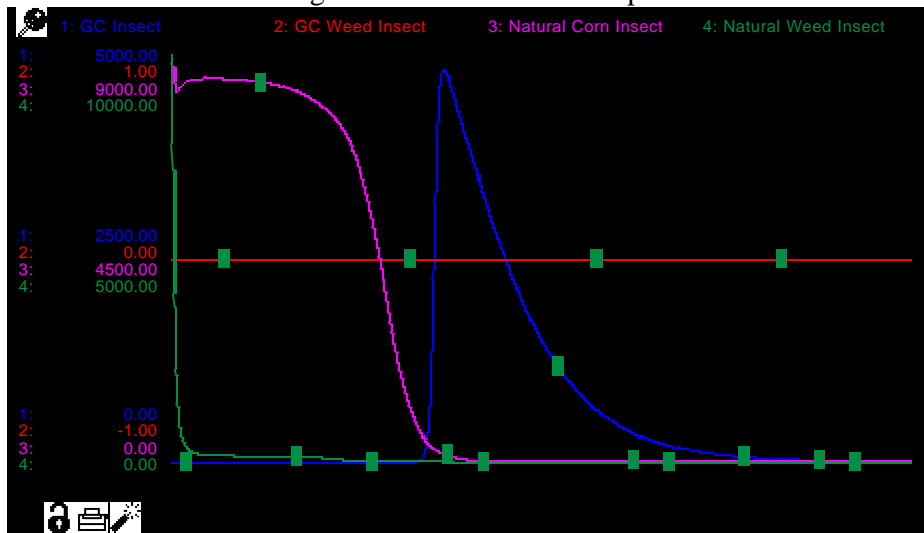


Figure 11: Main Causal Loops



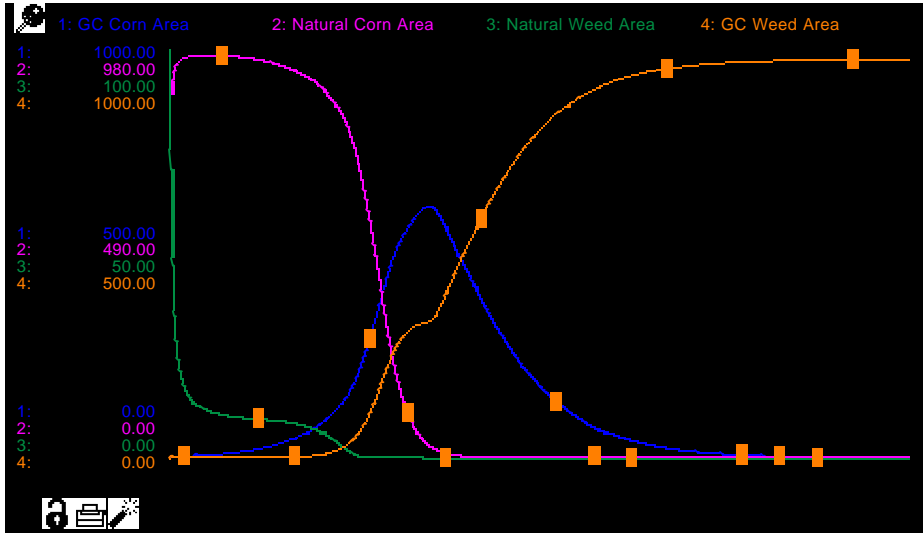


Figure 12: GC weed insects do not emerge but GC insects emerge

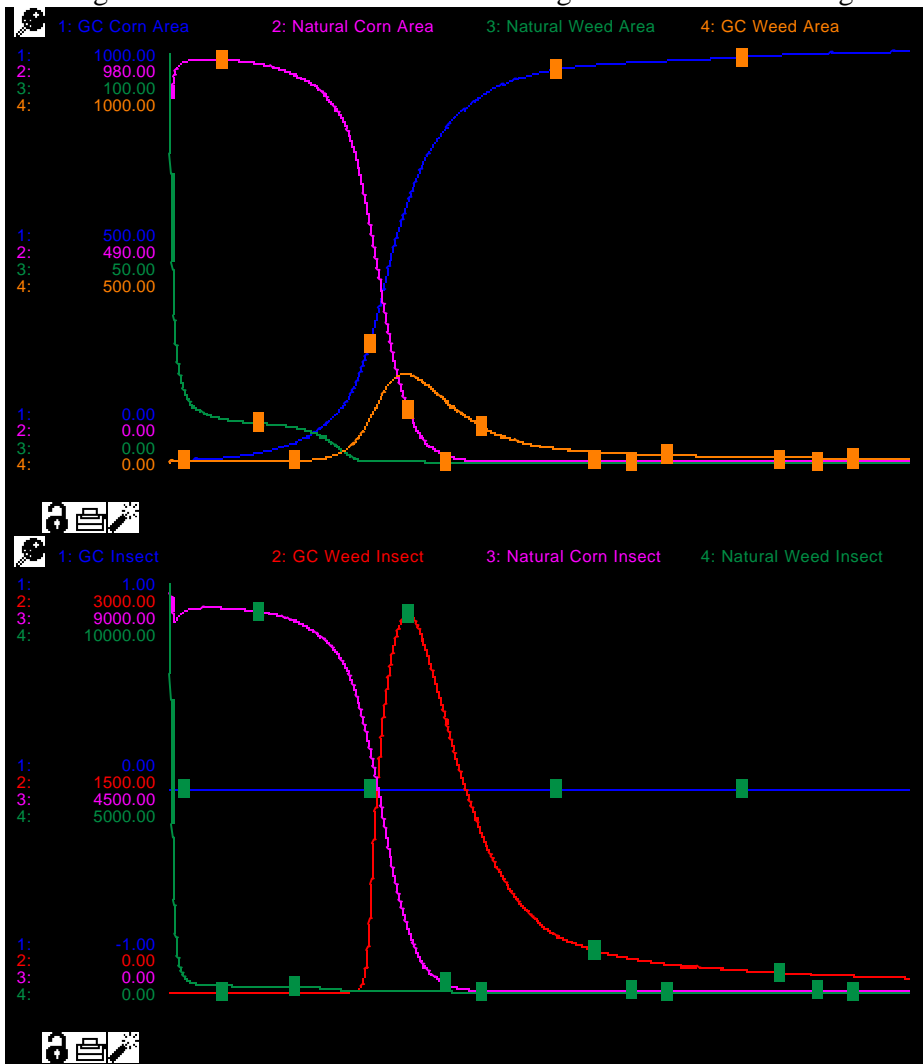


Figure 13: GC corn insects do not emerge but GC weed insects emerge

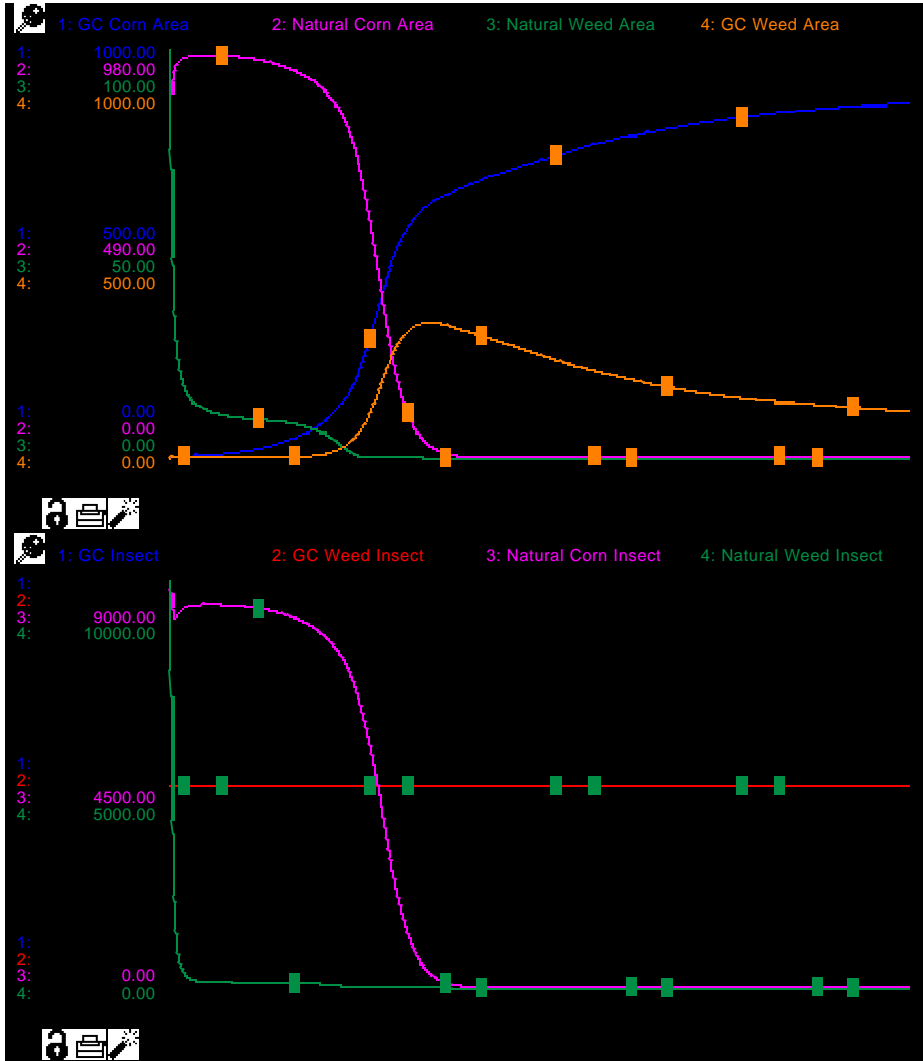
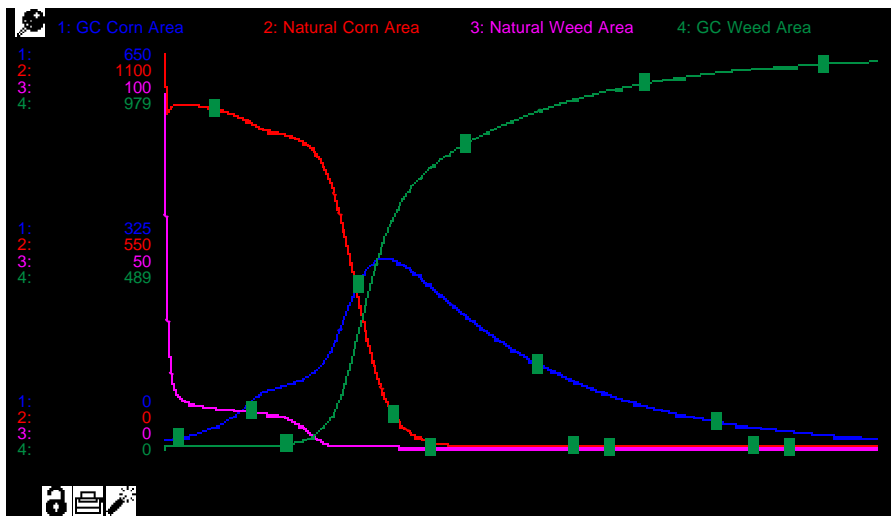


Figure 14: No GC corn insect and no GC weed insect emergence



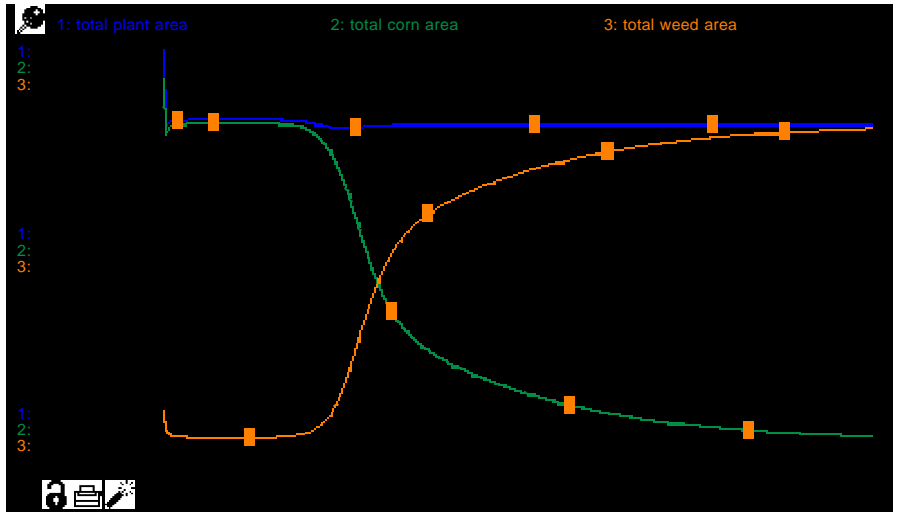


Figure 15: Simulation results for extreme condition tests-a

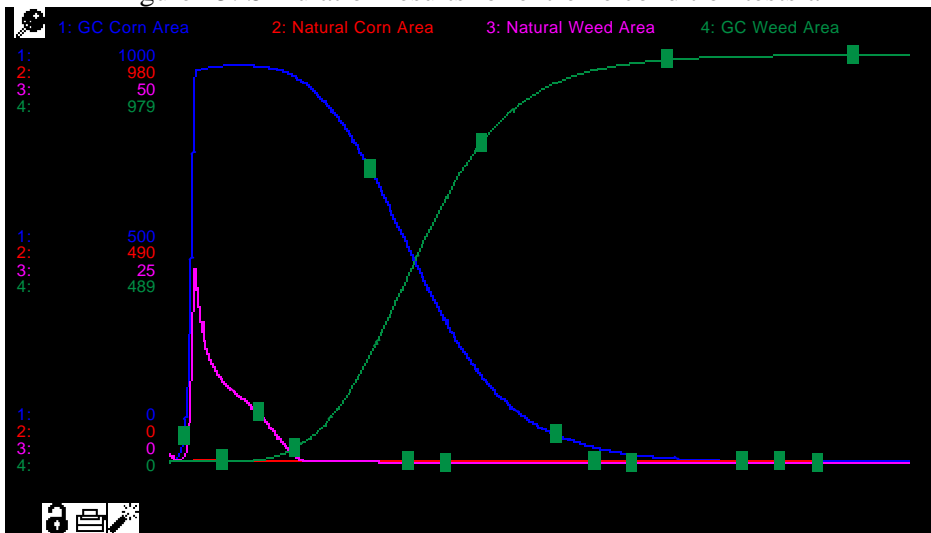
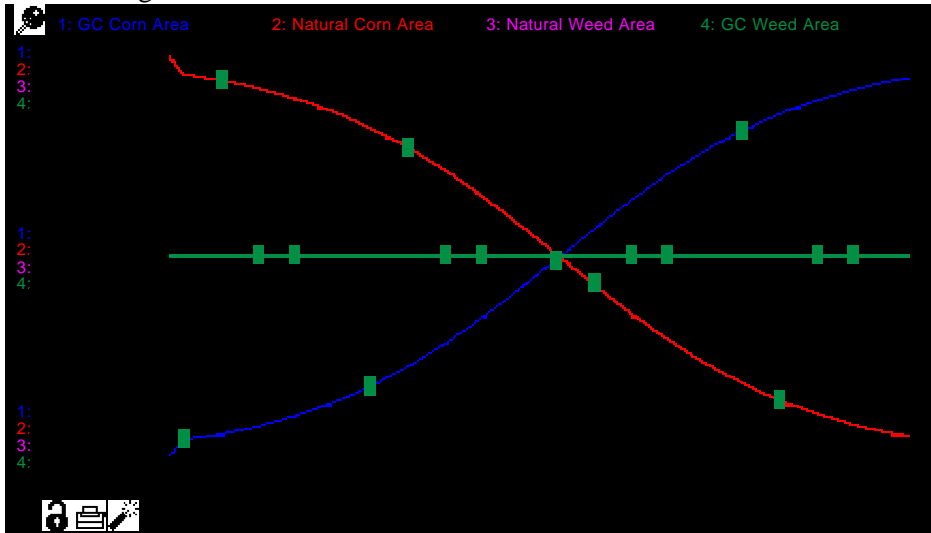


Figure 16: Simulation results for extreme condition tests-b



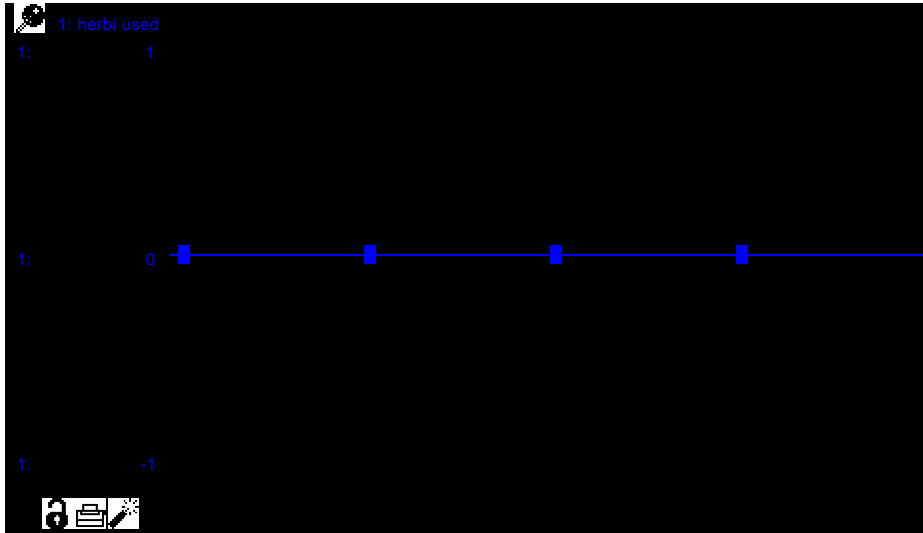
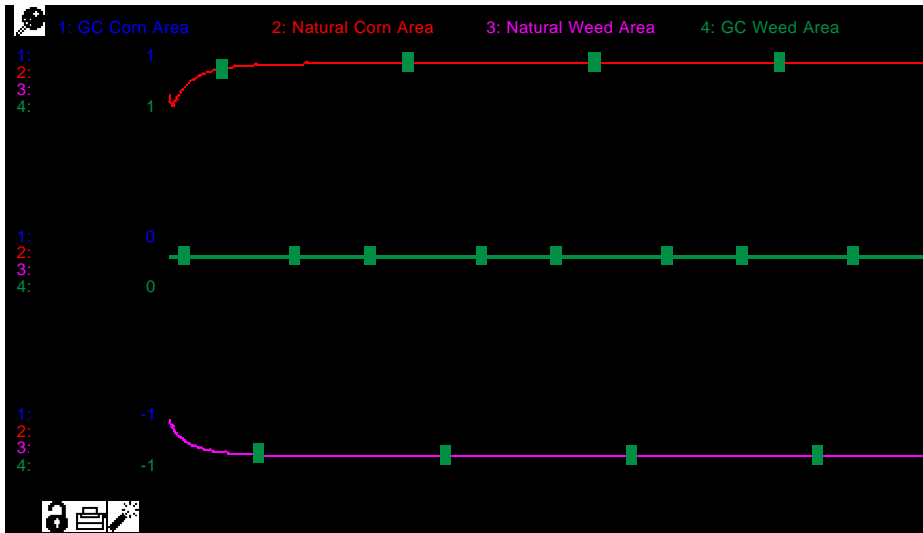


Figure 17: Simulation results for extreme condition tests-c



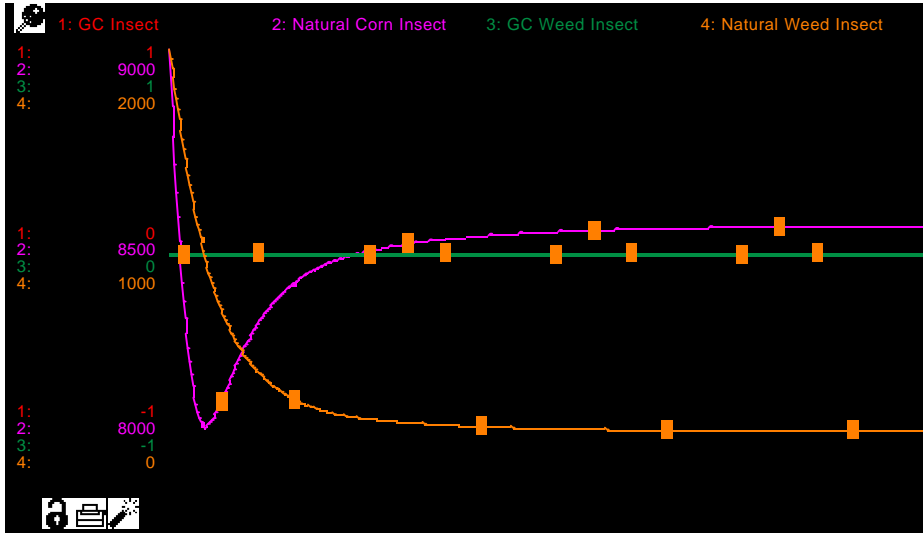


Figure 18: Simulation results for extreme condition tests-d

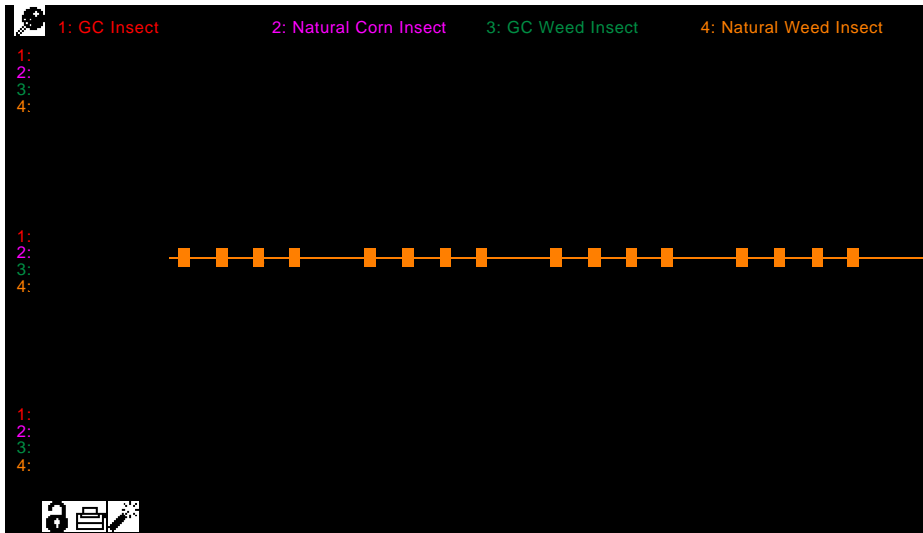


Figure 19: Simulation results for extreme condition tests-e

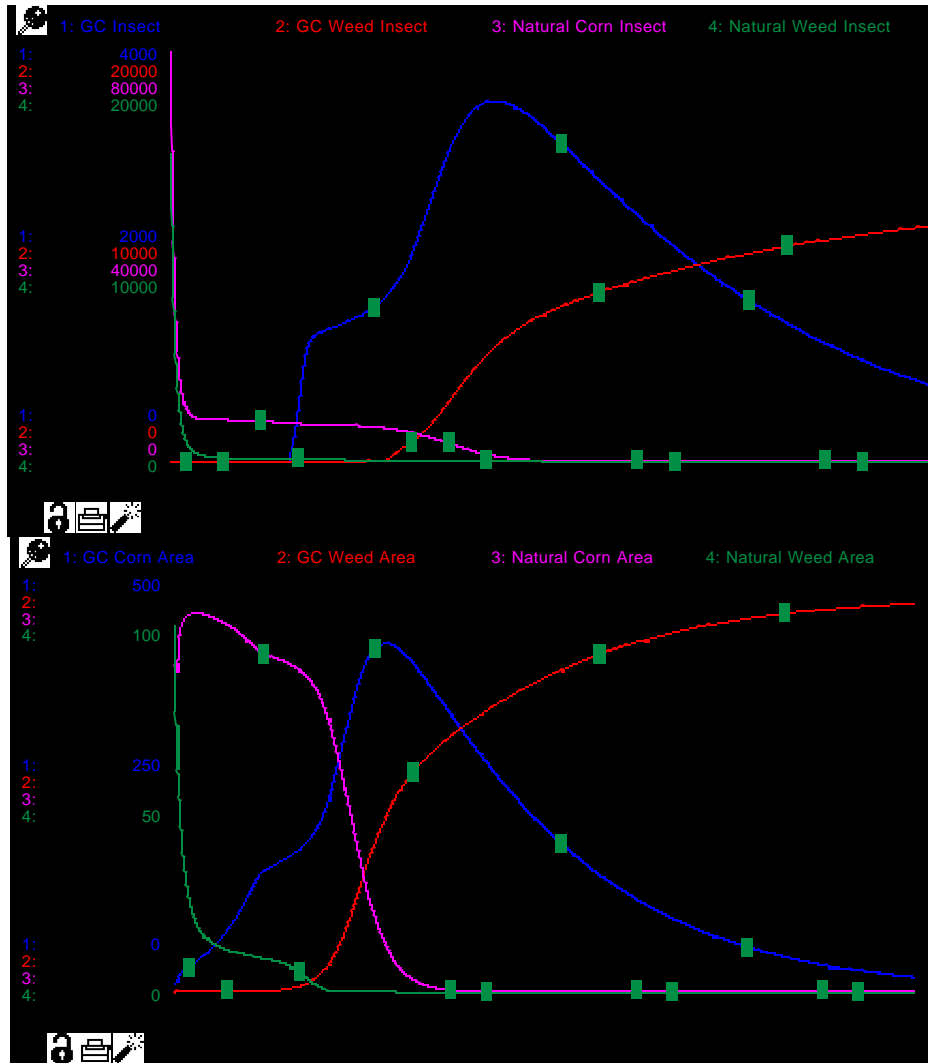


Figure 20: Simulation results for extreme condition tests-f

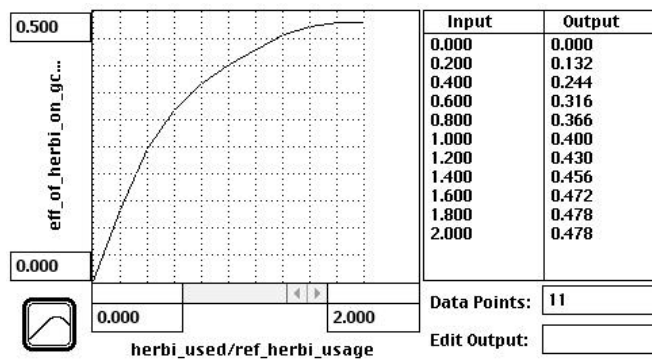


Figure 21: Effect of herbicide on GC weed df-Sensitivity Analysis1

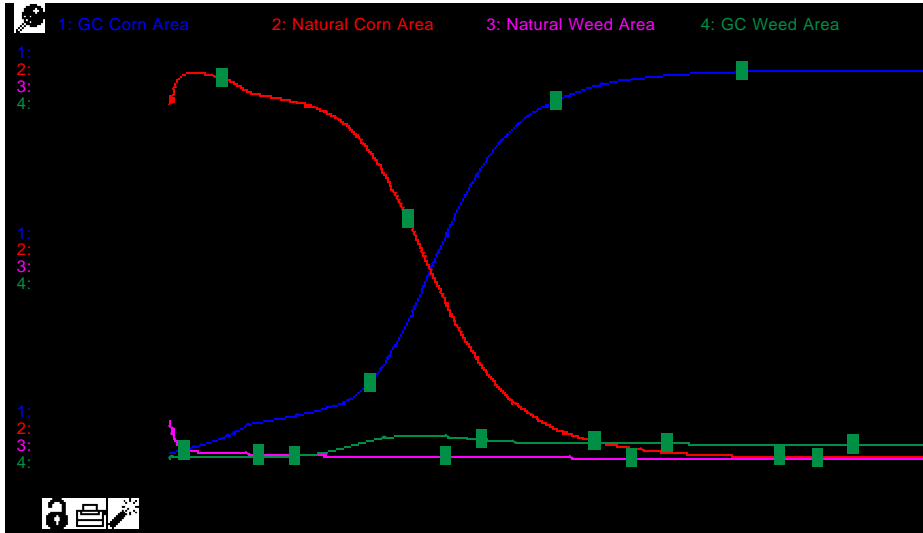


Figure 22: Simulation results for sensitivity analysis-1

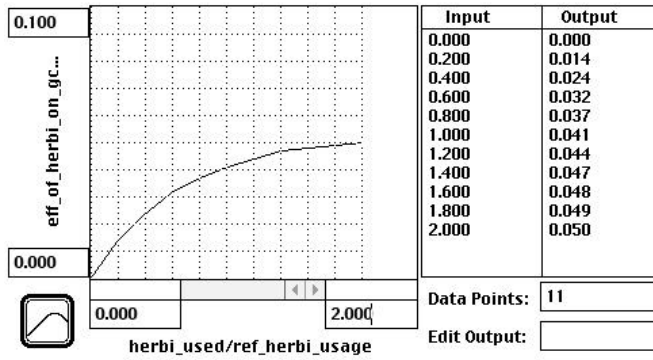


Figure 23: Effect of herbicide on GC corn df -Sensitivity Analysis2

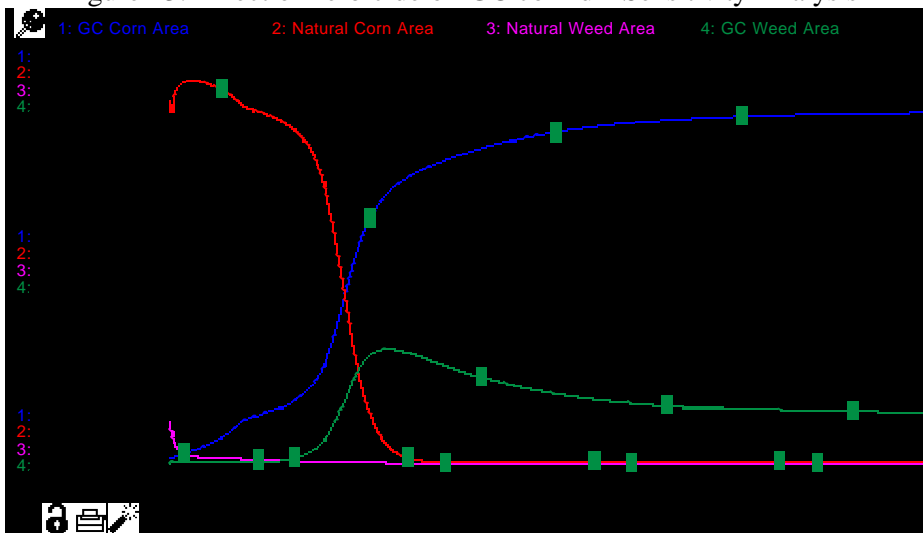


Figure 24: Simulation results for sensitivity analysis-2

References:

1. Teitel, Martin and Kimberly A. Wilson, 1999. *Genetically Engineered Food: Changing the Nature of Nature*. Rochester: Park Street Press.
2. Dalton, Rex, 2001. Transgenic corn found growing in Mexico. *Nature* 413: 337.
3. Kendall, H., R. Beachy, T. Eisner, F. Gould, R. Herdt, P.H. Raven, J.S. Schell and M.S. Swaminathan, 1997. *Bioengineering of Crops-Report of the World Bank Panel on Transgenic Crops*. Washington: The World Bank
4. Potrykus, Ingo, and German Spangenberg, eds. 1995. *Gene Transfer to Plants*. Germany: Springer.
5. Quist, David and I. H. Chapela, 2001. Transgenic DNA intogressed into traditional maize landraces in Oaxaca, Mexico. *Nature*, Volume 414: 541-542
6. Barlas, Yaman, 1996. Formal Aspects of Model Validity and Validation in System Dynamics. *System Dynamics Review* Vol.12, no.3 ,Fall 1996.
7. http://www.truefoodnow.org/take_action/supermarket_tours.html, cited [20 March 2002].
8. Willson, Harold R., 1989. *European Corn Borer* [online]. Ohio: Ohio State University. [cited 20 March 2002]. Available from World Wide Web: (<http://ohioline.osu.edu/icm-fact/fc-15.html>)

Appendix 1:

$GC_Corn_Area(t) = GC_Corn_Area(t - dt) + (gc_corn_reg - gc_corn_death) * dt$

INIT GC_Corn_Area = 10

INFLOWS:

$gc_corn_reg = gc_corn_rf * GC_Corn_Area$

OUTFLOWS:

$gc_corn_death = GC_Corn_Area * gc_corn_df$

$GC_Insect(t) = GC_Insect(t - dt) + (gc_insect_births + insect_mutation - gc_insect_deaths) * dt$

INIT GC_Insect = 0

INFLOWS:

$gc_insect_births = gc_insect_bf * GC_Insect$

$insect_mutation =$

$IF(GC_Insect > 0) THEN(0) ELSE(IF(Natural_Corn_Insect > 10) THEN(MUTATEORNO T * Natural_Corn_Insect * insect_mutation_coeff) ELSE(0))$

OUTFLOWS:

$gc_insect_deaths = GC_Insect * gc_insect_df$

$GC_Weed_Area(t) = GC_Weed_Area(t - dt) + (gc_weed_reg + gc_weed_produced_by_gene_jump - gc_weed_deaths) * dt$

INIT GC_Weed_Area = 0

INFLOWS:

$gc_weed_reg = GC_Weed_Area * gc_weed_rf$

$gc_weed_produced_by_gene_jump = Gene_Jump$

OUTFLOWS:

$gc_weed_deaths = GC_Weed_Area * gc_weed_df$

```

GC_Weed_Insect(t) = GC_Weed_Insect(t - dt) + (gc_weed_insect_births +
weed_insect_mutation - gc_weed_insect_deaths) * dt
INIT GC_Weed_Insect = 0
INFLOWS:
gc_weed_insect_births = GC_Weed_Insect*gc_weed_insect_bf
weed_insect_mutation =
IF(GC_Weed_Insect>0)THEN(0)ELSE(IF(Natural_Weed_Insect>10)THEN(MUTATE
ORNOT2*Natural_Weed_Insect*weed_insect_mutation_coeff)ELSE(0))
OUTFLOWS:
gc_weed_insect_deaths = gc_weed_insect_df*GC_Weed_Insect
Gene_Jump(t) = Gene_Jump(t - dt) + (delay3) * dt
INIT Gene_Jump = 0
INFLOWS:
delay3 = (Gene_jump2-Gene_Jump)/gene_jump_delay_time
Gene_jump1(t) = Gene_jump1(t - dt) + (delay1) * dt
INIT Gene_jump1 = 0
INFLOWS:
delay1 = (possible_gene_jump-Gene_jump1)/gene_jump_delay_time
Gene_jump2(t) = Gene_jump2(t - dt) + (delay2) * dt
INIT Gene_jump2 = 0
INFLOWS:
delay2 = (Gene_jump1-Gene_jump2)/gene_jump_delay_time
Natural_Corn_Area(t) = Natural_Corn_Area(t - dt) + (nat_corn_reg - nat_corn_deaths)
* dt
INIT Natural_Corn_Area = 890
INFLOWS:
nat_corn_reg = Natural_Corn_Area*nat_corn_rf
OUTFLOWS:
nat_corn_deaths = Natural_Corn_Area*nat_corn_df
Natural_Corn_Insect(t) = Natural_Corn_Insect(t - dt) + (nat_corn_insect_births -
nat_corn_insect_deaths) * dt
INIT Natural_Corn_Insect = 9000
INFLOWS:
nat_corn_insect_births = nat_corn_insect_bf*Natural_Corn_Insect
OUTFLOWS:
nat_corn_insect_deaths = Natural_Corn_Insect*nat_corn_insect_df
Natural_Weed_Area(t) = Natural_Weed_Area(t - dt) + (nat_weed_reg -
nat_weed_deaths) * dt
INIT Natural_Weed_Area = 100
INFLOWS:
nat_weed_reg = Natural_Weed_Area*nat_weed_rf
OUTFLOWS:
nat_weed_deaths = Natural_Weed_Area*nat_weed_df
Natural_Weed_Insect(t) = Natural_Weed_Insect(t - dt) + (nat_weed_insect_births -
nat_weed_insect_deaths) * dt
INIT Natural_Weed_Insect = 10000
INFLOWS:
nat_weed_insect_births = Natural_Weed_Insect*nat_weed_insect_bf

```

OUTFLOWS:

```
nat_weed_insect_deaths = Natural_Weed_Insect*nat_weed_insect_df
crowding = total_plant_area/total_field
gc_corn_df =
gc_corn_normal_df+eff_of_gc_insects_on_gc_corn_df+eff_of_herbi_on_gc_corn_df
gc_corn_normal_df = .08
gc_corn_per_m2 = 9
gc_corn_ratio = GC_Corn_Area/total_plant_area
gc_insect_df = .9
gc_insect_per_gc_corn =
IF(GC_Corn_Area=0)THEN(999999)ELSE(GC_Insect/(GC_Corn_Area*gc_corn_per_
m2))
gc_weed_df =
gc_weed_normal_df+eff_of_herbi_on_gc_weed_df+eff_of_gc_weed_insect_on_gc_we
ed_df
gc_weed_insect_df = 0.9
gc_weed_insect_per_gc_weed =
IF(GC_Weed_Area=0)THEN(999999)ELSE(GC_Weed_Insect/(GC_Weed_Area*super
weed_per_m2))
gc_weed_normal_df = .08
gc_weed_ratio = GC_Weed_Area/total_plant_area
gene_jump_delay_time = 40/3
herbi_usage_for_1000_m2_and_10%_weed = 10
herbi_used = ref_herbi_usage*eff_of_weed_%_on_herbi_used
herbi_used\_ref_herbi_usage = herbi_used/ref_herbi_usage
insect_mutation_coeff = .1
MUTATEORNOT = MONTECARLO(prob_of_gc_insect_mutation)
MUTATEORNOT2 = MONTECARLO(prob_of_gc_weed_insect_mutation)
nat_corn_df =
nat_corn_normal_df+eff_of_herbi_on_nat_corn_df+eff_of_nat_insects_on_nat_corn_df
nat_corn_insect_df = .9
nat_corn_insect_per_nat_corn =
IF(Natural_Corn_Area=0)THEN(999999)ELSE(Natural_Corn_Insect/(Natural_Corn_A
rea*nat_corn_per_m2))
nat_corn_normal_df = .08
nat_corn_per_m2 = 9
nat_weed_df =
eff_of_herbi_on_nat_weed_df+nat_weed_normal_df+eff_of_nat_weed_insects_on_nat
_weed_df
nat_weed_insect_df = .9
nat_weed_insect_per_weed =
IF(Natural_Weed_Area=0)THEN(999999)ELSE(Natural_Weed_Insect/(Natural_Weed
_Area*nat_weed_per_m2))
nat_weed_normal_df = .08
nat_weed_per_m2 = 15
possible_gene_jump = gene_jump_fraction*Natural_Weed_Area
ref_field = 1000
ref_herbi_usage = herbi_usage_for_1000_m2_and_10%_weed*(total_field/ref_field)
```

```

ref_weed_% = 0.1
superweed_per_m2 = 15
total_corn_area = GC_Corn_Area+Natural_Corn_Area
total_field = 1000
total_plant_area =
GC_Corn_Area+Natural_Corn_Area+Natural_Weed_Area+GC_Weed_Area
total_weed_area = GC_Weed_Area+Natural_Weed_Area
weed_% = total_weed_area/total_plant_area
weed_insect_mutation_coeff = .1
eff_of_gc_insects_on_gc_corn_df = GRAPH(gc_insect_per_gc_corn)
(0.00, 0.00), (1.00, 0.05), (2.00, 0.1), (3.00, 0.15), (4.00, 0.2), (5.00, 0.25), (6.00, 0.3),
(7.00, 0.35), (8.00, 0.4), (9.00, 0.45), (10.0, 0.5), (11.0, 0.55), (12.0, 0.6), (13.0, 0.645),
(14.0, 0.685), (15.0, 0.72), (16.0, 0.745), (17.0, 0.76), (18.0, 0.78), (19.0, 0.795), (20.0,
0.805)
eff_of_gc_weed_insect_on_gc_weed_df = GRAPH(gc_weed_insect_per_gc_weed)
(0.00, 0.00), (1.00, 0.05), (2.00, 0.1), (3.00, 0.15), (4.00, 0.2), (5.00, 0.25), (6.00, 0.3),
(7.00, 0.35), (8.00, 0.4), (9.00, 0.45), (10.0, 0.5), (11.0, 0.55), (12.0, 0.6), (13.0, 0.645),
(14.0, 0.685), (15.0, 0.72), (16.0, 0.745), (17.0, 0.76), (18.0, 0.78), (19.0, 0.795), (20.0,
0.805)
eff_of_herbi_on_gc_corn_df = GRAPH(herbi_used_\ref_herbi_usage)
(0.00, 0.00), (0.2, 0.0285), (0.4, 0.0475), (0.6, 0.0635), (0.8, 0.075), (1.00, 0.083), (1.20,
0.089), (1.40, 0.0935), (1.60, 0.097), (1.80, 0.099), (2.00, 0.1)
eff_of_herbi_on_gc_weed_df = GRAPH(herbi_used_\ref_herbi_usage)
(0.00, 0.00), (0.2, 0.066), (0.4, 0.122), (0.6, 0.158), (0.8, 0.183), (1.00, 0.2), (1.20,
0.215), (1.40, 0.228), (1.60, 0.236), (1.80, 0.239), (2.00, 0.239)
eff_of_herbi_on_nat_corn_df = GRAPH(herbi_used_\ref_herbi_usage)
(0.00, 0.00), (0.2, 0.046), (0.4, 0.09), (0.6, 0.122), (0.8, 0.149), (1.00, 0.167), (1.20,
0.18), (1.40, 0.189), (1.60, 0.195), (1.80, 0.199), (2.00, 0.2)
eff_of_herbi_on_nat_weed_df = GRAPH(herbi_used_\ref_herbi_usage)
(0.00, 0.00), (0.2, 0.27), (0.4, 0.48), (0.6, 0.645), (0.8, 0.765), (1.00, 0.85), (1.20, 0.91),
(1.40, 0.955), (1.60, 0.975), (1.80, 0.99), (2.00, 1.00)
eff_of_nat_insects_on_nat_corn_df = GRAPH(nat_corn_insect_per_nat_corn)
(0.00, 0.00), (1.00, 0.05), (2.00, 0.1), (3.00, 0.15), (4.00, 0.2), (5.00, 0.25), (6.00, 0.3),
(7.00, 0.35), (8.00, 0.4), (9.00, 0.45), (10.0, 0.5), (11.0, 0.55), (12.0, 0.6), (13.0, 0.645),
(14.0, 0.685), (15.0, 0.72), (16.0, 0.745), (17.0, 0.76), (18.0, 0.78), (19.0, 0.795), (20.0,
0.805)
eff_of_nat_weed_insects_on_nat_weed_df = GRAPH(nat_weed_insect_per_weed)
(0.00, 0.00), (1.00, 0.05), (2.00, 0.1), (3.00, 0.15), (4.00, 0.2), (5.00, 0.25), (6.00, 0.3),
(7.00, 0.35), (8.00, 0.4), (9.00, 0.45), (10.0, 0.5), (11.0, 0.55), (12.0, 0.6), (13.0, 0.645),
(14.0, 0.685), (15.0, 0.72), (16.0, 0.745), (17.0, 0.76), (18.0, 0.78), (19.0, 0.795), (20.0,
0.805)
eff_of_weed_%_on_herbi_used = GRAPH(weed_%/ref_weed_%)
(0.00, 0.00), (1.00, 1.00), (2.00, 1.35), (3.00, 1.54), (4.00, 1.68), (5.00, 1.77), (6.00,
1.85), (7.00, 1.89), (8.00, 1.91), (9.00, 1.92), (10.0, 1.92)
gc_corn_rf = GRAPH(crowding)
(0.00, 0.877), (0.1, 0.855), (0.2, 0.825), (0.3, 0.787), (0.4, 0.75), (0.5, 0.713), (0.6, 0.69),
(0.7, 0.66), (0.8, 0.615), (0.9, 0.5), (1, 0.1), (1.10, 0.0375), (1.20, 0.0225), (1.30, 0.015)
gc_insect_bf = GRAPH(gc_insect_per_gc_corn)

```

(0.00, 2.00), (1.00, 0.8), (2.00, 0.46), (3.00, 0.31), (4.00, 0.23), (5.00, 0.16), (6.00, 0.11), (7.00, 0.08), (8.00, 0.05), (9.00, 0.02), (10.0, 0.01)

gc_weed_insect_bf = GRAPH(gc_weed_insect_per_gc_weed)
(0.00, 1.94), (1.00, 0.74), (2.00, 0.43), (3.00, 0.26), (4.00, 0.21), (5.00, 0.16), (6.00, 0.12), (7.00, 0.07), (8.00, 0.05), (9.00, 0.02), (10.0, 0.01)

gc_weed_rf = GRAPH(crowding)
(0.00, 1.30), (0.1, 1.29), (0.2, 1.29), (0.3, 1.29), (0.4, 1.27), (0.5, 1.27), (0.6, 1.26), (0.7, 1.17), (0.8, 1.05), (0.9, 0.9), (1, 0.16), (1.10, 0.0375), (1.20, 0.0225), (1.30, 0.0225)

gene_jump_fraction = GRAPH(gc_corn_ratio)
(0.00, 0.00), (0.1, 0.0055), (0.2, 0.0076), (0.3, 0.0092), (0.4, 0.0107), (0.5, 0.0122), (0.6, 0.0136), (0.7, 0.0151), (0.8, 0.017), (0.9, 0.0185), (1, 0.0198)

nat_corn_insect_bf = GRAPH(nat_corn_insect_per_nat_corn)
(0.00, 2.00), (1.00, 0.87), (2.00, 0.46), (3.00, 0.32), (4.00, 0.23), (5.00, 0.16), (6.00, 0.11), (7.00, 0.08), (8.00, 0.05), (9.00, 0.02), (10.0, 0.01)

nat_corn_rf = GRAPH(crowding)
(0.00, 0.877), (0.1, 0.855), (0.2, 0.825), (0.3, 0.787), (0.4, 0.75), (0.5, 0.713), (0.6, 0.69), (0.7, 0.66), (0.8, 0.615), (0.9, 0.5), (1, 0.1), (1.10, 0.0375), (1.20, 0.0225), (1.30, 0.015)

nat_weed_insect_bf = GRAPH(nat_weed_insect_per_weed)
(0.00, 2.00), (1.00, 0.8), (2.00, 0.46), (3.00, 0.29), (4.00, 0.23), (5.00, 0.18), (6.00, 0.14), (7.00, 0.09), (8.00, 0.07), (9.00, 0.06), (10.0, 0.03)

nat_weed_rf = GRAPH(crowding)
(0.00, 1.30), (0.1, 1.29), (0.2, 1.29), (0.3, 1.29), (0.4, 1.27), (0.5, 1.27), (0.6, 1.26), (0.7, 1.17), (0.8, 1.05), (0.9, 0.9), (1, 0.16), (1.10, 0.0375), (1.20, 0.0225), (1.30, 0.0225)

prob_of_gc_insect_mutation = GRAPH(gc_corn_ratio)
(0.00, 0.00), (0.1, 5.50), (0.2, 13.0), (0.3, 28.0), (0.4, 45.0), (0.5, 63.0), (0.6, 70.5), (0.7, 76.0), (0.8, 80.0), (0.9, 81.5), (1, 82.5)

prob_of_gc_weed_insect_mutation = GRAPH(gc_weed_ratio)
(0.00, 0.00), (0.1, 8.50), (0.2, 17.0), (0.3, 30.5), (0.4, 53.5), (0.5, 64.0), (0.6, 69.5), (0.7, 71.5), (0.8, 73.0), (0.9, 74.0), (1, 74.5)

Appendix 2

Variable	dim	variable	dim
GC_Corn_Area	m2	prob_of_gc_weed_insect_mutation	dim.less
gc_corn_reg	m2/ yr	prob_of_gc_insect_mutation	dim.less
gc_corn_rf	1/yr	gc_weed_ratio	dim.less
gc_corn_death	m2/ yr	gc_corn_ratio	dim.less
gc_corn_df	1/ yr	crowding	dim.less
GC_Corn_Insect	insect	nat_weed_insect_per_weed	insect/ plant
gc_insect_births	insect/ yr	nat_weed_rf	m2/ yr
gc_insect_bf	1/ yr	nat_weed_insect_bf	1/ yr
gc_insect_deaths	insect/ yr	nat_corn_rf	1/ yr
gc_insect_df	1/ yr	nat_corn_insect_bf	1/ yr
GC_Weed_Area	m2	nat_corn_insect_per_nat_corn	insect/ corn cob
gc_weed_reg	m2/ yr	gene_jump_fraction	1/ yr
gc_weed_rf	1/ yr	gc_corn_ratio	dim.less

gc_weed_produced_by_gene_jump	m2/ yr	gc_weed_rf	1/ yr
Gene_Jump	m2/ yr	gc_weed_insect_bf	1/ yr
gc_weed_deaths	m2/ yr	gc_weed_insect_per_gc_weed	insect/ plant
gc_weed_df	1/ yr	gc_insect_per_gc_corn	insect/ corn cob
GC_Weed_Insect	insect	gc_insect_bf	1/ yr
gc_weed_insect_births	insect/ yr	gc_corn_rf	1/ yr
gc_weed_insect_bf	1/ yr	weed_%/ref_weed_%	dim.less
weed_insect_mutation	insect/ yr	eff_of_weed_%_on_herbi_used	dim.less
Natural_Weed_Insect	insect	eff_of_nat_weed_insects_on_nat_weed_df	1/ yr
weed_insect_mutation_coeff	1/ yr	nat_weed_insect_per_weed	insect/ plant
gc_weed_insect_deaths	insect/ yr	eff_of_nat_insects_on_nat_corn_df	1/ yr
gc_weed_insect_df	1/ yr	nat_corn_insect_per_nat_corn	insect/ corn cob
MUTATEORNOT	dim.less	herbi_used	grams
MUTATEORNOT2	dim.less	ref_herbi_usage	grams
delay1	m2/ yr*yr	eff_of_herbi_on_nat_weed_df	1/ yr
delay2	m2/ yr*yr	eff_of_herbi_on_nat_corn_df	1/ yr
delay3	m2/ yr*yr	eff_of_herbi_on_gc_weed_df	1/ yr
Gene_jump1	m2/ yr	eff_of_herbi_on_gc_corn_df	1/ yr
Gene_jump2	m2/ yr	eff_of_gc_weed_insect_on_gc_weed_df	1/ yr
weed_%	dim. less	gc_weed_insect_per_gc_weed	insect/ plant
total_weed_area	m2	eff_of_gc_insects_on_gc_corn_df	1/ yr
total_plant_area	m2	nat_weed_normal_df	1/ yr
ref_herbi_usage	grams	gc weed per m2	plant/ m2
nat_weed_per_m2	plant/ m2	nat_corn_per_m2	corn cob /m2
herbi used \ ref herbi usage	dim. less		

Appendix 3

total_plant_area=

GC_Corn_Area+Natural_Corn_Area+Natural_Weed_Area+

[m2]	GC Weed Area [m2]+[m2]+[m2]+[m2]
crowding= [dimensionless]	total_plant_area/ total_field [m2]/ [m2]
weed_%= [dimensionless]	[Natural_Weed_Area+GC Weed Area]/[total_weed_area] ([m2]+[m2])/[m2]
possible_gene_jump= [m2/ year]	gene_jump_fraction*Natural_Weed_Area [1/ year]*[m2]
gc_corn_df= [1/ year]	gc_corn_normal_df+eff_of_gc_insects_on_gc_corn_df+ eff_of_herbi_on_gc_corn_df [1/ year]+[1/ year]+ [1/ year]
delay1= [m2/year*year]	(possible_gene_jump-Gene_jump1)/gene_jump_delay_time ([m2/year]-[m2/year])/ year
nat_corn_insect_births= [insect/ year]	nat_corn_insect_bf*Natural_Corn_Insect [1/ year]*[insect]
nat_weed_reg= [m2/ year]	Natural_Weed_Area*nat_weed_rf [m2]*[1/year]
herbi_used= [grams]	ref_herbi_usage*eff_of_weed_%_on_herbi_used [grams]*[dimensionless]
ref_herbi_usage= [grams]	herbi_usage_for_1000_m2_and_10%_weed* (total_field/ref_field) [grams]*[dimensionless]
insect_mutation= [insect / year]	IF(GC_Insect>0)THEN(0)ELSE(IF(Natural_Corn_Insect>10) THEN(MUTATEORNOT*Natural_Corn_Insect* insect_mutation_coeff)ELSE(0)) [dimensionless]*[insect]*[1/year]
gc_insect_per_gc_corn= [insect/ corncob] MUTATEORNOT= [dimensionless] (0 or 1)	IF(GC_Corn_Area=0)THEN(999999)ELSE (GC_Insect/(GC_Corn_Area*gc_corn_per_m2)) [insect]/[m2]*[corncob/m2] MONTECARLO(prob_of_gc_insect_mutation) [dimensionless]