

Genetically Modified Crops and Agricultural Landscapes: Spatial Patterns of Contamination

Ken Belcher

*Dept. of Agricultural Economics
University of Saskatchewan
51 Campus Drive
Saskatoon, Saskatchewan
S7N 5A8
Tel. (306) 966-4019
Fax. (306) 966-8413
E-mail: belcher@duke.usask.ca*

James Nolan

*Dept. of Agricultural Economics
University of Saskatchewan
51 Campus Drive
Saskatoon, Saskatchewan
S7N 5A8
Tel: (306) 966-8412
Fax: (306) 966-8413
E-mail: james.nolan@usask.ca*

Peter W.B. Phillips

*Dept. of Agricultural Economics
University of Saskatchewan
51 Campus Drive
Saskatoon, Saskatchewan
S7N 5A8
Tel: (306) 966-4021
Fax: (306) 966-8413
E-mail: phillips@duke.usask.ca*

Abstract

There is a growing concern in the global agri-food industry about the problem of genetically modified (GM) crop “field contamination” and its scope and duration at the farm level. The farm-level GM contamination problem needs to be better understood so as to ensure that crop identity preservation (IP) systems can be developed and maintained. Otherwise, the introduction of GM crops could prove very costly to the agri-food industry. These costs could more than offset the significant production benefits envisioned for producers and developers of GM crops. To help develop the kinds of policies necessary to maintain IP at the farm level, we develop and explore a spatial simulation model of farm level GM contamination. We find that unless careful attention is paid to where GM crops are grown in relation to non-GM crops, there is great potential for ubiquitous contamination of farmland wherever GM crops are introduced.

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1. Introduction

Public concerns over the introduction and proliferation of genetically modified¹ (GM) foods have focused on food safety, the rights of consumers to choose whether to expose themselves to risks associated with GM foods and the perceived environmental problems associated with the introduction of GM plant (and animal) varieties into ecosystems. In response to these concerns, some countries are starting enforce standards for GM food content by using food labeling systems that facilitate choice and help mitigate consumer fears about GM foods.

At present, the biotechnology and agri-food industries are developing policies and systems designed to cope with these issues. For example in Canada, at the request of Health Canada, the Canadian Food Inspection Agency and Environment Canada, the Royal Society of Canada appointed an expert panel to study the “Future of Food Biotechnology Policy Regulation”. This panel examined the scientific foundations of the technology and identified a number of policy and regulatory recommendations intended to address public concerns over GM food products (Royal Society of Canada 2001). Concurrently, a body called the Canadian Biotechnology Advisory Committee undertook a review of the governance mechanisms and recently released its advice on improvements to the system (Canadian Biotechnology Advisory Committee, 2002). Related efforts are now underway in the U.S., the European Union and New Zealand. All of these panels have encouraged more scientific review of the risks of cross-pollination and greater consideration of production and marketing systems to minimize potential “contamination” between different crop types.

¹ In this paper biotechnology and genetic modification (GM) refers exclusively to the direct transfer or modification of genetic material using recombinant DNA techniques and does not refer to other traditional breeding methods, such as hybridization and mutagenesis.

At the farm level, the cross-pollination of non-GM crops by nearby GM crops and seed translocation has made it difficult for producers of non-GM crops to offer a product that meets the low tolerances for GM content set by many domestic and international buyers. As of August 2001, 28 countries plus the E.U. had either adopted or announced plans to introduce labels for GM food, with allowable tolerances for GM content in non-labeled food ranging from 1% to 5% of content (Phillips and McNeill, 2001). As a result, producers are concerned about the level of GM crop “contamination” and its duration at the farm and field level (Lang, 2002). We assume in this work that contamination of non-GM fields through cross-pollination and seed translocation from GM crops will be costly to society, and hence there is a desire to ensure some isolation of GM and non-GM crops.

The introduction of GM crops into the food chain could potentially impose a range of social costs. At present one of the most publicized issues is the perceived health hazard associated with the consumption of GM products. Even though regulators have judged those GM products in the market to be as safe as traditional foods, many consumers simply do not believe them. Regardless of who is right, from the farmers’ perspective if consumers of the future are willing to pay a premium for food derived from non-GM crops, then taking away their choice to grow non-GM crops becomes an opportunity cost to any farmer who wants to do so. If effective identity preservation (IP) systems are not forthcoming, the opportunity cost could rise dramatically as the number of GM-free markets declines, as disgruntled consumers would be more likely to avoid product lines with GM content (Dobson, 2002). Already there are examples of market disruption due to GM adoption. The European food market is now closed to all Canadian canola (*Brassica sp.*) because of the extensive adoption of GM varieties in Canada and lack of effective identity preservation and protection of non-GM produce for the EU market. Meanwhile, Canadian organic crop

producers have been unable to certify canola crops as organic for this market because of the extensive potential for cross-pollination between GM and organic crops; these producers are losing a lucrative and growing market. In addition, the removal of canola from organic crop rotations has economic as well as agronomic implications.

In spite of market concerns, adaptation and adoption of GM technology has continued to accelerate. As of June, 2002, 15 crops modified for one or more of 47 phenotypic traits have been commercialized (Phillips, 2002). Four main crops—soybeans (*Glycine max L.*), corn (*Zea mays L.*), cotton (*Gossypium hirsutum L.*) and canola—made up 99% of the total acreage planted to GM crops in 2001 (James, 2001). The geographic concentration of this production is quite high. In all, 16 countries have produced one or more transgenic crop, but the U.S., Argentina, Canada and China accounted for 99% of the acreage over the first seven years of production (James, 2001).

There are virtually no GM free agricultural regions. By 2001, there was at least one commercial introduction in each of the six arable continents and in all of the major agri-food producing and/or exporting countries in the world. Adoption by farmers is reaching a plateau in several product markets. In 2001, 46% of the global soybean acreage used GM seeds, as did 20% of global cotton, 11% of global canola and 7% of global maize production (James 2001). Adoption rates are highest in countries with unrestricted approval for new varieties, as in Argentina, the U.S. and Canada. More than 90% of Argentina's soybean crop in 2001 used GM seed, greater than 80% of Canada's canola acreage used herbicide tolerant seed and more than 70% of U.S. cotton acreage was transgenic. Recent approvals of GM cotton in China, India and Indonesia and GM corn and soybeans in South Africa increase the potential that fewer markets will be entirely GM free.

These trends and the ongoing development of new varieties of GM crops suggest that the production of GM crops will become increasingly common and widespread. In particular, a genetically modified herbicide tolerant wheat (*Triticum aestivum L.*) variety is currently being developed by Monsanto Co. and is at the field trial stage in North America. Wheat is an extremely important agricultural crop allocated to a significant proportion of the arable land in North America and western Canada in particular.

As the proliferation of GM crops continues, a small body of evidence has accumulated indicating that without careful precautions, it will be very difficult to prevent GM crops from cross-pollinating with similar non-GM crops grown nearby (e.g. Downey and Beckie 2002; Haslberger 2001). Ultimately, this situation could potentially render large amounts of (originally planted) non-GM crop unfit for consumption by that class of consumers who will demand that food products are certified as GM-free.

While it is expected that the contamination of non-GM crops by GM crops will impose costs on producers and consumers, how this problem will manifest itself across an agricultural landscape is poorly understood. To help understand this issue, we develop and analyze a simple spatial simulation model of GM crop introduction and expansion. Within this model we introduce a GM crop into a flat landscape of simulated fields. The GM crop has certain well-defined characteristics related to space and location relative to other crops which determine the rate at which individual farms become “contaminated” by the GM crop. Farms can also become “uncontaminated” in this model if conditions are right.

The model allows us to examine certain macro-level characteristics of the spread of GM contamination, such as the speed and stability of GM crop

expansion or contraction on our farm landscape. The simulation is based upon the well-known “game of life” simulation model, one of the first simple attempts to create “virtual worlds” or cellular automata (CA) that are often used to study real world problems in a variety of research fields. By modifying the rules of this game to broadly emulate the real world process of GM cross-pollination and contamination, we create a necessarily simple but robust virtual world of GM crop contamination.

Given the gravity of these issues and the relative public uncertainty that surrounds them, labeling and identity preservation of GM crops will certainly remain important issues for the global agri-food industry. We postulate that in the absence of some formal control mechanism for the introduction of GM crops across agricultural landscapes in the near future, it is very likely that GM cross-pollination problem will be difficult to contain once a crop variety is introduced. Further, GM contamination will impose significant external costs on other sectors of the agri-food industry and consumers. We hope to show in this paper that these costs have significant potential to expand and potentially offset the production benefits associated with GM crops.

The next section discusses the original “game of life” and its relationship to the simulation model developed in this paper. Section 3 offers an overview of the limited research on modeling GM “contamination”, or the spread of GM crops in a GM-free landscape. Section 4 uses this biological information to develop a simple simulation algorithm describing the spread of GM crop over an agricultural landscape. The basic results of the simulation are presented in Section 5, while Section 6 concludes.

2. The “Game of Life”

The original game of life was one of the first popular computer simulation experiments. British mathematician John Conway designed the simulation in the late 1960s so as to emulate simple biological rules of “birth”, “death” and “survival”. In turn, the rules could be implemented on random initial patterns of simulated “populations” on a computer (Gardner, 1970). While the initial motivation for the design of the game was for simple amusement, even small versions of the game (including Conway’s original rules) generate fascinating and often chaotic patterns of evolution. As a research tool, the game of life has proven to be remarkably durable, as a number of individuals continue to analyze consequences of modifications to the original rules specified by Conway (Evans, 1996; Blok and Bergersen, 1999).

Even considering its simplicity, Conway was very careful to choose the rules for the game in order to keep the simulations interesting and unpredictable. In this light, the rules were designed to meet three basic criteria (Gardner, 1970).

- i. No initial population patterns in the simulation should transparently permit the population to grow without limit.
- ii. There ought to be initial patterns that apparently do grow without limit.
- iii. Simple initial patterns should be used that grow and evolve over time before coming to an end in three possible ways: i) fading away completely (i.e. overcrowding or sparseness), ii) settling into a stable configuration that remains unchanged, or iii) oscillating patterns, which repeat an endless cycle for two or more periods.

Conway envisioned the game being played on a flat and infinite plane with small square cells representing each “life”. When played in this manner, each cell has exactly eight neighbors and the rules are written relative to this design. The most commonly known version of the game of life is often referred to as the Conway configuration. Acting upon the randomized initial placement of the “population”, the Conway rules are as follows:

- 1) For a space that is presently 'populated':
 - a) Each cell with one or no neighbors dies, as if by loneliness.
 - b) Each cell with four or more neighbors dies, as if by overpopulation.
 - c) Each cell with two or three neighbors survives.
- 2) For a space that is presently 'empty' or 'unpopulated'
 - a) Each cell with three neighbors becomes populated.

This version of the game of life generates a variety of interesting temporal and spatial patterns. In fact, it has been shown to exhibit chaotic behavior in a mathematical sense; the final patterns and stability of the game solutions are dependent upon the initial configuration of the virtual population (Callahan, 2002).

While it is beyond the scope of this paper to detail the extensive research surrounding the game of life, we note that the Conway rules have been changed by various researchers to see how they impact the patterns that are generated when playing the game. Because of its use as a teaching tool for computer programmers, the basic game of life is probably the most programmed computer “game” in existence (Callahan, 2002).

This type of computer simulation research is formally known in applied mathematics as the field of cellular automata or CA. A cellular automaton is any discrete dynamical system based upon simple construction (i.e. identical components with rules defining local interactions) but which is capable of generating complex, self-organizing behavior (Wolfram, 1984). CA are often used to simulate physical systems evolution in the real world (Rauch, 2002).

A recent related study worth highlighting involved the design of a CA to emulate citrus disease transmission by insects in Brazil (Martins et al., 2000). This work was founded upon a relatively complex stochastic algorithm because the particular transmission mechanisms under study were well documented. In

contrast, we hope to convince the reader that our relatively simple modifications to the basic “game of life” represent a reasonable foundation upon which to usefully analyze the processes of “birth”, “death” and “survival” with respect to the planting of genetically modified crops and their interaction with non-GM varieties and other species.

3. Genetically Modified Crops and their Potential Impact on an Agricultural Landscape

Much of the recent policy research on GM crops has focussed on consumer and demand related issues, which address the growing public concern about genetic modification of food products (e.g. Hobbs and Plunkett 2000; Knoppers and Mathios 1998). While some effort has been made to quantify the impact of averse consumer responses (e.g. Kuntz, 2001) and the costs of identity preserving GM crops (Smyth and Phillips, 2002), very little academic research to date has been conducted on trying to assess the risks associated with growing GM crops.

Why must GM crops be regulated differently from other crops? The answer to this question comes down to the value consumers will eventually place on purity of various crop varieties. As alluded to earlier, a strong backlash against any form of genetic modification in the human food chain is gaining momentum, especially in Europe. These concerns have been at least partly strengthened by the fact that the first generation of GM crop varieties have focused on developing traits such as herbicide tolerance and insect resistance and not on traits that confer direct, visible benefits to consumers.

Incidents like StarLink corn (*Zea mays*)² suggest that very little is understood at present about the potential for GM products to spread in an undesirable fashion through the food chain. In Canada, anecdotal evidence has already emerged about cross-pollination between GM and non-GM crops and seed translocation between fields. For instance, since the adoption of GM canola in western Canada, organic crop producers have been unable to meet organic certification standards for organic canola. This is due to concerns about cross-pollination from GM canola fields. As a result, organic producers are no longer producing this crop. A continued pattern of contamination would likely negate any organic certification for many growers and ruin consumer confidence in the industry (Saskatchewan Organic Directorate, 2002c). The adoption of other GM crop varieties would likely have similar impacts on both organic and conventional non-GM crop producers.

On top of this problem is layered the legal issue of whether farmers are liable for crops that have accidentally cross-pollinated with patented GM crops. A recent and very public lawsuit in the province of Saskatchewan involved a farmer who grew and marketed a patented crop without paying the Technology Use Agreement (TUA) Fee to a biotechnology firm. In this case, the farmer claimed that the GM canola came onto his field through cross-pollination and/or seed translocation and should not be liable for the TUA fee. In the end, the case was decided in favor of the biotechnology firm (Western Producer, 2001) but is currently under appeal in a higher court. The case has already both fascinated and frightened the regional farm community about the planting of new generation GM crops (Western Producer, 2000).

² StarLink was a genetically modified corn developed as an animal feed. The developing firm, Aventis, decided that it should be produced in special segregated areas to ensure that it did not contaminate corn destined for human consumption. Eventually, the GM trait in StarLink was found in the food chain and several manufacturers of corn products (including TacoBell) withdrew product lines that were thought to be contaminated (Smyth et al., 2002)

A related legal question is whether the biotechnology companies responsible for the development of the GM crop are responsible for their property if it does show up in a non-GM field through cross-pollination or seed displacement. If the presence of this crop imposes extra costs on the farmer, for instance, through increased weed control costs or precludes a producer from selling his product in a premium market (e.g. organic crops), should the company be required to compensate the affected producer? If the GM crop is the company's property, are they responsible for it wherever it shows up?³

We assume in this paper that consumers will continue to value the ability to distinguish between GM and non-GM derived food products. In turn, this demand for identity preservation means farmers will continue to plant some non-GM products, and these products will require certification that they do not contain a level of GM contamination above a benchmark value. There is still a great deal of academic and policy debate as to what this optimal contamination level should be. For an overview of these issues, see Hobbs and Plunkett (2000).

Furthermore, GM products will be assumed to confer production benefits to crop producers, benefits that include crop immunity to destruction from certain insects and weeds. Because of this, GM crops will continue to be planted in order to serve other agricultural markets (such as feed markets), most often in the same regions or possibly even on the same farms as non-GM products. The likelihood of this situation means that there is value in understanding the dispersion of GM products at the farm level.

³ A class action lawsuit has recently been launched by Saskatchewan organic producers on Monsanto and Aventis seeking compensation from damages caused by the release of GM canola and seeking to restrict the release of GM wheat (Saskatchewan Organic Directorate, 2002a).

In order to help set up the simulation rules as they apply to GM contamination, we must incorporate evidence concerning the potential for spreading GM characteristics to other, non-GM crops. This process is known as “cross-pollination”, and is a function of the distance that GM and non-GM crops are located from each other (Moyes and Dale, 1999). Table 1 is derived from a recent compendium of the best available biological research to date about the potential for cross-pollination of non-GM products by commonly planted GM crops. There is not one common safe distance that holds for all crops, but certain similarities in pollen dispersal can be found. For example, each of the three crops shown here appears to need at least 50 meters of separation from other non-GM crops to improve the chances of non-contamination. Regulatory systems in most countries have established isolation distances for confined field trials (up to 600 meters for some crops in the U.S.) and buffer zones for production of foundation, certified and registered seed (ranging from 1 meter to 100 meters in Canada). Finally, these distances are varied based on the potential for outcrossing (Altman and Phillips, 2001).

Clearly, there is considerable variation in the best estimates of how far GM pollen can travel to contaminate other non-GM crops. The level of uncertainty in these estimates indicates that we need to develop a set of conservative cross-pollination or contamination rules for the basic simulations. The model also abstracts from any other potential “vectors” for GM contamination – including wind, birds or other animals (both domestic and wild).

While it is not critical to the interpretation of the results, each iteration of the simulation may be thought of as a single crop year. Spatially, we assume that GM contamination of a given parcel of land (one cell) is determined by the likelihood that an individual cell is contaminated by its neighbors (adjacent cells). In turn, this likelihood is exactly determined by the total number of

neighbors for a given cell that are already contaminated. Under certain conditions, a contaminated cell can become uncontaminated after a single iteration of the model. Once contaminated by a GM crop, farm output is restricted to producing only the GM version of that particular crop until the farm becomes uncontaminated. As we shall discuss later, this last assumption may be unrealistic and overly generous considering the time frame assumed for each iteration, but it allows for the possibility that technology could permit full decontamination of cells if a particular area can be adequately isolated from contaminated land.

The production of GM crops creates an economic externality. In this paper we will treat the planting of GM crops as a negative externality for the agricultural landscape as a whole. We seek to assess the viability of GM products as part of crop production and their potential impact on those producers who wish to grow and market non-GM crops.

4. Developing an algorithm for GM contamination based upon the Game of Life

To maintain consistency with the structure of the original game of life, a single cell in this study represents one farm. However, it is likely that interpretation of the results would change little by assuming that the system is at a smaller scale (i.e. one cell represents a field) or a larger scale (one cell represents a municipality or county). The simulations are restricted to a finite number of virtual farmers, each of whom are assumed to grow either GM or non-GM crops on their land. The initial conditions are always set up so that some farmers choose to grow GM crops and some do not. Cells where GM crops are grown will be referred to as “contaminated” cells. A final restriction we impose

for realism is that at the beginning of each simulation, the number of contaminated cells is small compared to the number of uncontaminated cells.

The average size of a farm in Western Canada is approximately 325 cultivated hectares (800 acres) (SAF, 2001); cells represent farms of this size. Considering this fact and the available data on cross-pollination, we assume that non-GM farms can only be cross-pollinated by adjacent neighbors. However in the simulation, proximity alone does not guarantee cross-pollination. We also set a threshold describing the number of GM-growing neighbors necessary to guarantee cross-pollination or contamination of an uncontaminated farm.

As is clear from Table 1, a single neighbor growing a GM version of a crop should not necessarily guarantee cross-pollination because the detectable cross-pollination distances are very small for some crops. We decided that a realistic threshold for guaranteed cross-pollination with farms of this size that would also exhibit interesting properties on a macro level is three contaminated neighbors out of eight total neighbors. Thus, for all farms if less than three neighbors grow GM crop, then the farm remains uncontaminated for the next time period. However, if three or more neighbors grow GM crop, then this farm also becomes contaminated for the next time period.

The algorithm describing the cross-pollination of genetically modified organisms through our farming “universe”, written in the language of the “game of life” is as follows;

I) For a cell that is contaminated:

- a) If such a cell has 0-2 contaminated neighbors, it becomes uncontaminated the next time period.
- b) If such a cell has 3-8 contaminated neighbors, it stays contaminated for the next time period.

II) For a cell that is uncontaminated -

- a) If such a cell has 3 - 8 contaminated neighbors, it becomes contaminated for the next time period.

The results described in the next section are derived from the application of this algorithm. However, slight changes in these rules (e.g. increasing or decreasing the likelihood of contamination in the algorithm by a single neighbor) do not significantly alter the qualitative results described here.

We will focus on three possible scenarios for the farming landscape; 1) those situations where GM contamination explodes and eventually, all cells in the landscape become contaminated; 2) those situations where GM contamination contracts and eventually, all cells become uncontaminated; and 3) those unusual situations where the landscape evolves into a long run equilibrium, characterized by stable areas of contaminated cells co-existing with areas of uncontaminated cells. As might be expected, all of the simulation findings are sensitive to initial population conditions.

5. Simulation Results

Using both *Stella* 7.0.2 (see Appendix for the *Stella* pseudo-code of the algorithm) and Life 32 (Bontes, 1999) simulation software, we developed the basic GM-crop contamination algorithm described in Section 4. Within only a few iterations of running the model, several interesting patterns began to emerge.

Most critically, we found that with an initial arrangement of just 7 adjacent contaminated cells (Figure 2), only a few iterations were required (in most cases less than 10) to observe that full GM contamination of the farming

landscape was taking place. While the “speed” of this contamination varied depending on the initial alignment of the contaminated cells, using a 7 contaminated cell configuration meant that approximately 1000 cells became contaminated for every 30-40 iterations of the model.

Conversely, if the initial set of contaminated cells are arranged so that no more than 6 neighboring contaminated cells have appropriate spacing (i.e. two rows or columns must separate the grouping of contaminated cells, see Figure 3) on the grid, then a “stable” equilibrium results (Figure 1). This particular equilibrium contains a mix of contaminated and uncontaminated cells; the contaminated cells are self-sustaining, but the configuration does not allow any further contamination of surrounding cells. These “stable” configurations are not easy to sustain; they are quite fragile and are easily destroyed by the presence of just one other adjacent contaminated cell. This can be observed by comparing the contaminated cell configurations in Figures 1 and 2.

Finally, Figure 3 illustrates an initial alignment of contaminated cells that, in just a few time steps, turn into a completely uncontaminated landscape; two rows (columns) of alternating cells across the grid, while the next set of alternating cells must be placed at least 2 rows (columns) above or below (to the right or left of) the nearest neighbors. From this alignment, we conclude that at most approximately 16 percent of all cells (e.g. in Figure 3, 16 of 100 cells are contaminated), arranged in such a precise spatial arrangement, could begin life as contaminated cells without fully contaminating the farming landscape. Clearly, the system is extremely sensitive to initial contaminated cell placement once 7 or more adjacent contaminated cells are placed on the grid; we find that virtually any initial group of 7 or more contaminated, neighboring cells will eventually lead to universal contamination.

The rules implemented in the simulations assume that if left alone, a GM-contaminated farm could possibly become uncontaminated after a single time step. But preliminary research in plant biology has indicated that it will likely take longer than a single year for a producer to be able to meet the existing standards for non-GM markets on a field contaminated by a GM version of the crop (Canadian Broadcasting Corporation 2001; Saskatchewan Organic Directorate, 2002b). Therefore, the length of time necessary for crops to meet more rigorous standards, such as organic certification, after a field has been contaminated will be somewhat longer than a single year. The main implication for increasing this interval for GM decontamination in the simulation model is that it would be even more difficult to find initial conditions (using the simulation algorithm specified here) that will eventually result in a stable contaminated or completely uncontaminated farm landscape.

The primary regulatory implication of our findings is that the spatial arrangement (planting) of GM crops matters to the eventual number of uncontaminated farms in a particular region. Simply put, where there are significant safety or market concerns, regulatory oversight will likely be needed to ensure that GM crops are not planted in such concentrations that would generate full GM contamination across the entire agricultural landscape. At a minimum, the results are strongly suggestive that a policy of carefully planting small areas of GM crops in dispersed locations is well advised until further research on GM cross-pollination can be undertaken.

Agricultural regulators may find this model provides them with useful information for setting sites in confined field trials for unapproved out-crossing GM varieties in order to ensure undesired traits do not escape. The model could also be used by various commodity groups to ensure that appropriate identity preservation systems evolve to preserve and support product and market

differentiation. The model could also help determine the potential benefits of scientifically based isolation methods, such as genetic use restriction technologies (GURTs), often called “terminator” systems. Such systems would largely halt gene flow due to cross-pollination and thereby increase the potential for diversified production of GM and non-GM crops.

6. Conclusions

The simulation model presented in this paper illustrates several important features about the introduction of GM products into agriculture. The type of system-wide cross-pollination or contamination of farmland by GM crops demonstrated here indicates that a significant external cost could be imposed on farmers because they would be incapable of growing produce to sell in potentially lucrative GM-free markets. In addition, the loss of the ability of consumers to choose non-GM foods, or to only have access to much higher priced imported non-GM foods, would be another significant external cost stemming from careless adoption of GM crops. Further, if there are significant environmental costs associated with widespread contamination by GM crops, the scenarios outlined in this paper could be serious. Such analysis is desperately needed for society to be able to sustainably benefit from this new technology. The presence of these major potential externalities could cause GM technologies to be either over or under used relative to the social optimum. The challenge is to use this new evidence to sort out how to ensure optimal use of the new technology.

At this stage, our analysis does not incorporate notions of prices or markets for GM and non-GM crops, factors that will certainly affect adaptation and adoption rates for different crops. Our results do, however, help to define the potential scope of the externality associated with the planting of GM crops.

This will be especially important as new GM varieties are introduced (such as GM wheat) or existing GM varieties are adapted and adopted in new markets (e.g. India, China or Brazil).

Markets will certainly have a major role in deciding how and where to plant GM and non-GM crops, but this study suggests that the potential scope of GM contamination may make it impossible for markets to effectively price any related externalities of the new crops. If consumers are willing to pay a premium for non-GM derived foods (or possibly for some output trait GM foods) and GM contamination at any given location is temporary, it should be possible to develop a pricing mechanism (e.g. a tax on GM growers on behalf of non-GM growers) to address the externalities. Such a scheme could compensate non-GM growers for any loss of income that would have been available from consumers paying premiums for identity preserved crops, while allowing the new GM technologies to be optimally adopted.

Finally, the issue of property rights associated with GM crops, currently the focus of a legal challenge to certain biotechnology companies from organic producers in Western Canada, may be significantly affected by this analysis. Depending on the potential for cross-pollination externalities, this analysis suggests there may be a number of different patterns of compensation appropriate for this industry. Ultimately, the analysis suggests that the market may need to be assisted by some government action. While the costs of a zoning or regulatory system that ensures some pre-set level of uncontaminated land is maintained within the agricultural landscape may be significant, the social benefits of maintaining a non-GM agricultural sector may be great enough to justify these costs.

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Table 1.
Pollen dispersal from three selected GM crops (from Smyth et al., 2002)

Property	Canola	Wheat	Corn
<i>Potential to Outcross</i>	Yes	Yes (limited)	Yes (limited)
<i>Detected distance of pollen drift</i>	2.5-25,000 metres	48-400 metres	50 metres

		X					
		X		X			
	X		X		X		

Fig. 1. A stable initial configuration of 6 contaminated cells (each designated with an *X*).

		X					
		X		X		X	
	X		X		X		

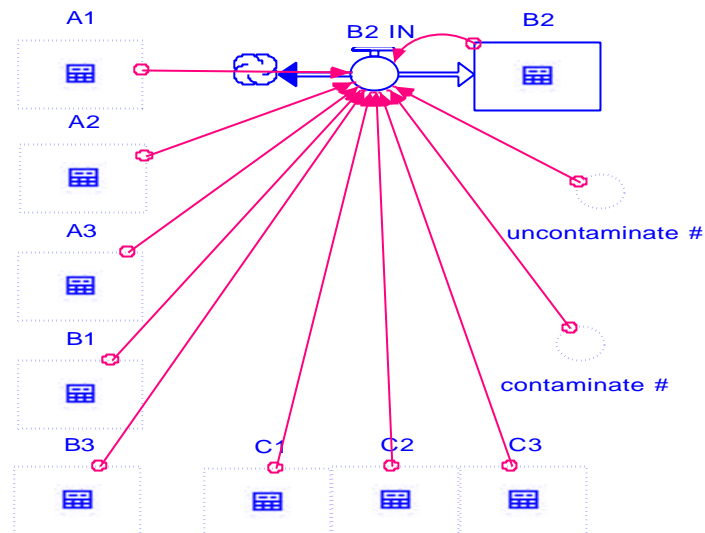
Fig. 2. An explosive initial configuration of just 7 contaminated cells (each designated with an *X*).

...X		X		X		X...	
	...X		X		X		X...
...X		X		X		X...	
	...X		X		X		X...

Fig. 3. An initial configuration of contaminated cells (each designated with an X) that will produce an uncontaminated landscape.

Appendix

Representation of the GM simulation model in *Stella*⁴



$$B2(t) = B2(t - dt) + (B2_IN) * dt$$

$$\text{INIT } B2 = 0$$

INFLOWS:

$$B2_IN = \text{IF } (A1+A2+A3+B1+B3+C1+C2+C3) > \text{contaminate_# and } B2=0 \text{ THEN } 1 \text{ ELSE IF } (A1+A2+A3+B1+B3+C1+C2+C3) < \text{uncontaminate_# AND } B2=1 \text{ THEN } -1 \text{ ELSE } 0$$

$$A1(t) = A1(t - dt)$$

$$\text{INIT } A1 = 0$$

$$A2(t) = A2(t - dt)$$

$$\text{INIT } A2 = 0$$

$$A3(t) = A3(t - dt)$$

$$\text{INIT } A3 = 0$$

$$B1(t) = B1(t - dt)$$

$$\text{INIT } B1 = 0$$

$$B3(t) = B3(t - dt)$$

$$\text{INIT } B3 = 0$$

$$C1(t) = C1(t - dt)$$

$$\text{INIT } C1 = 0$$

$$C2(t) = C2(t - dt)$$

$$\text{INIT } C2 = 1$$

$$C3(t) = C3(t - dt)$$

$$\text{INIT } C3 = 0$$

contaminate_# = 2 {minimum number of neighbor cells required to contaminate an uncontaminated cell}

uncontaminate_# = 3 {minimum number of contaminated cells below which the cell becomes uncontaminated}

⁴ The Stella[®] simulation model was developed following a Game of Life model presented in Hannon and Ruth (1997).