

Simulation model on the coexistence between GM and non-GM supply chains based on the example of the starch maize simulation model

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Abstract

Coexistence between GM and non-GM supply chains is a complex issue, because adventitious mixing of GM material with non-GM product can occur at any one of the stages of production. In this paper, we present a simulation model of the coexistence between GM and non-GM products along supply chains. The aim of this model is to assess the ability of the supply chain to provide final non-GM product compliant with a required threshold. The model simulates GM and non-GM flows, and takes into account “real” admixture and dilution functions between GM and non-GM batches.

1. Introduction

Coexistence refers to the ability of farmers and consumers to make a practical choice between conventional, organic, and genetically modified (GM) products, based on compliance with the legal obligation for labelling and/or purity standards (European Commission, 2003a). Up to 0.9% of GM material in non-GM food and feed is authorised, provided these traces of GMOs are adventitious or otherwise technically unavoidable (European Commission, 2003b and c). Above this threshold, it must be labelled as consisting of, containing or being produced from a GMO.

One major facet of the coexistence between GM and non-GM supply chains is the fact that adventitious mixing of GM material with a non-GM product can occur at any one of the stages of production and anywhere along the supply chain, from the field where the crop is grown to its handling and processing. Hence, a batch intended to be non-GM can be rejected due to GM adventitious presence exceeding the required threshold. Stakeholders need to be able to anticipate such a risk. Some research has already been carried out to assess the risk of admixture between GM and non-GM material at the field level and at given stages of the supply chain. In particular, the cross-fertilisation between GM and non-GM crops has been widely studied (Devos *et al.*, 2005). Ingles *et al.* (2003) have focused on the handling effects on commingling in an elevator. To our knowledge, no study has assessed the risks of admixture at processing. Several economic studies have developed analytical models to investigate the coexistence between GM and non-GM products along supply chains (Lapan & Moschini, 2004, Wilson *et al.*, 2007, Hammoudi *et al.* 2008).

Another major facet of GM and non-GM coexistence is the fact that the GM content of a product is not a visible attribute. For instance, collecting firms do not know *a priori* the GM content of the non-GM harvest delivered to their county grain elevators. To bridge this gap in information, product testing can be carried out. Nonetheless, tests to detect adventitious presence are not accurate enough, and they may lead stakeholders to reach the wrong conclusion about GM content (Starbird, 2007). To what extent do these means to bridge the gap in information guarantee the probability that a non-GM labelled product is in fact compliant with the 0.9% threshold?

In this paper, we present a simulation model of the coexistence between GM and non-GM products along a supply chain. More specifically, the framework of the model is inspired by the starch maize supply chain. The aim of this model is to assess the probability of compliance with the labelling threshold of the final non-GM product, as a function of non-GM purity rate in the raw material. We also discuss the impact of the means to bridge the information gap on this probability of compliance.

In Section 2, the maize supply chain and the risks of commingling between GM and non-GM maize supply chain are presented. The model is described in Section 3 and the simulations carried out with the model are presented in Section 4.

2. Material flows and risks of commingling in the starch maize supply chain

At maize grain production level, the risks of commingling are related to the presence of GM seeds in non-GM seed lots (seed impurity), the occurrence of GM volunteers from a previous crop, natural pollen-flow between GM and non-GM fields, and admixture due to machinery (seedler, combine-harvester) and transport material (Devos *et al.*, 2005; Messéan *et al.*, 2006). Under the most common European conditions, due to cold winters and ploughing in the majority of the cropping systems, volunteers are rare and are deemed a negligible source of admixture (Angevin *et al.*, 2008).

The risks of commingling are also related to the flow of maize in the starch supply chain. Maize grain is collected (collection silos), dried, and stored (storage silos) by firms acting as middle-men, concentrating the maize grain supply in a limited amount of place while selling it over an extended period of time (Le Bail, 2003). Collection and storage silos are usually divided into bins, so that several types of product can be stored separately. Commingling between GM and non-GM maize can occur when non-GM maize is stored, transported or dried after GM maize since a certain amount of GM maize always remains in the equipment. To prevent commingling at collection level, two different segregation management strategies have been proposed: allocate silos to particular products on a spatial or on a temporal basis (Le Bail and Valceschini, 2004; Miraglia *et al.*, 2004).

The wet milling process produces starch, oil-rich germs, and feed co-products (corn gluten feed and corn gluten meal). The wet-milling process includes many steps for the recovery and purification of starch and all coproducts (germ, gluten meal, and corn gluten feed). During the wet-milling process, the flow of corn is not linear, as a non negligible part of the flow is recycled upstream in order to optimise the purity of starch and all coproducts (Johnson & May, 2003; Ramirez *et al.*, 2008). This upstream flow induces a risk of admixture between succeeding lots with different purity levels.

The model described hereafter represents the flow of maize from grain maize production to starch recovery, considering only one dryer and one wet-milling plant. It takes into account the major factors involved in risks along the supply chain, including risks at the maize grain production level and risks at dryer and wet-milling process levels.

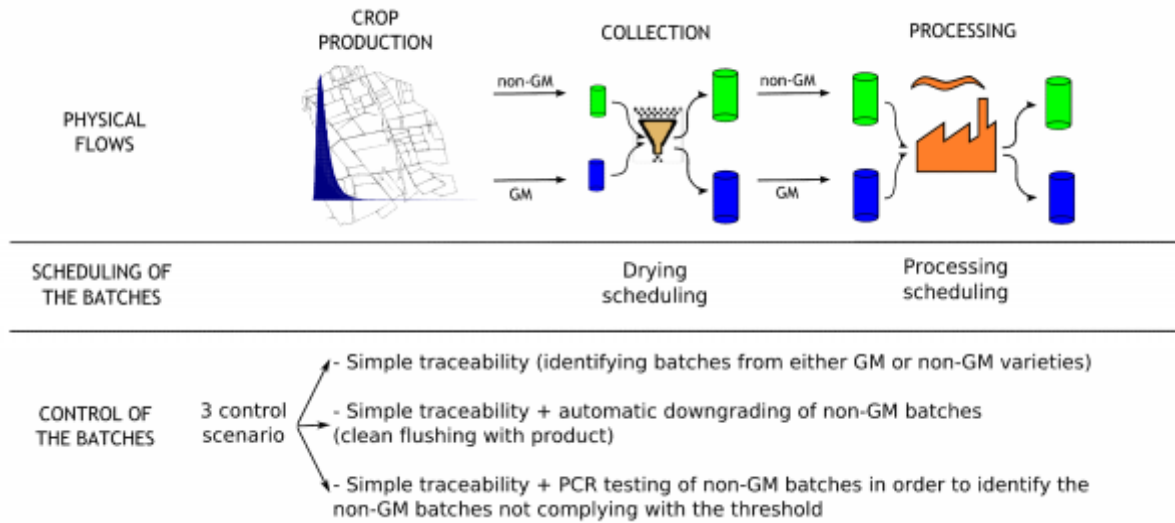
3. Model description

The simulation model simulates physical flows (GM and conventional) from field to processing. It takes into account admixture functions between GM and non-GM flows at each of the key stages of the supply chain.

In addition, the simulation model takes into account two kinds of decision which control GM and non-GM physical flows: (i) on the one hand scheduling of batches at collection (drying) and at processing and (ii) on the other hand control of these batches.

In this section, we present physical flows, scheduling and control of the batches. The model has been implemented using R2.8.1 software (R Development Core Team 2008).

Figure 1. Scheme of the maize simulation model.



a) Physical flows

Firstly, the model generates the GM content values of the harvests delivered to the county grain elevators. The number of field harvests delivered to the county grain elevators is given and noted N . If P_{GM} stands for the GM adoption rate by farmers, the number of GM maize harvests is equal to $P_{GM} \cdot N$. On the one hand, the model generates $P_{GM} \cdot N$ values equal to 1, representing the GM content of the GM maize harvests. On the other hand, the MAPOD model is used to generate the GM content of the harvest of the fields sown with a non-GM variety ($(1 - P_{GM}) \cdot N$ values).

MAPOD is a spatially explicit gene-flow model (Angevin *et al.*, 2008). It simulates pollen exchange between GM and non-GM maize in agricultural landscapes. It is divided into two modules: the flowering dynamics module aims at simulating pollen production and number of receptive silks, and the pollen dispersal module simulates pollen dispersal. The input variables include the field plan (form and size of the plants, location of GM and non-GM crops), climatic factors, traits of the varieties, and certain traits of the cropping system. The GM adventitious presence due to cross-pollination is computed as a percentage of grains carrying the transgene.

Even if the preliminary evaluation of MAPOD concluded that MAPOD provides good average predictive values, we may assume that GM content estimation with MAPOD is not completely accurate. MAPOD estimation uncertainty is represented by a normal distribution with a mean of μ_M and a variance of σ_M , where $\mu_M = \hat{p} + \eta$ and $\sigma_M = k_M \cdot \hat{p}$ (\hat{p} is the GM content estimated with MAPOD, η the estimation bias and k_M is a constant). MAPOD simulation results are input for the maize simulation

maize model which then generates $P_{GM} \cdot N$ values of GM adventitious presence of the harvest delivered to the county elevators.

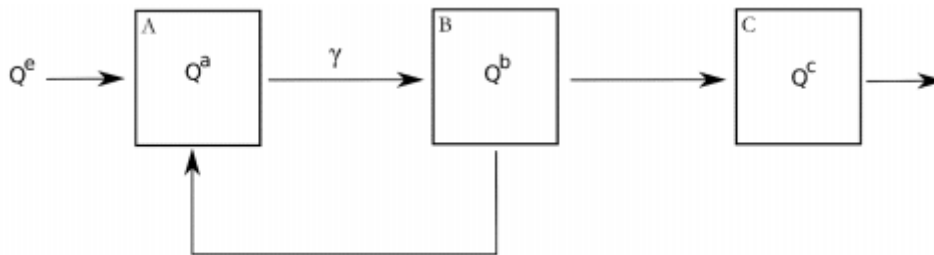
Secondly, the model simulates grain collection and drying. After temporary storage in collection bins, all the maize batches are dried in the same dryer and then are stored in storage bins. n_{pi} fields and n_{is} collection bins are blended respectively in one collection bin and one storage bin, assuming that all the field harvests and collection bins have the same weight. The resulting GM content of the collection bins and the storage bins is equal to the mean of the GM content of the batches blended together. The storage capacities are considered non-limiting in this module (see Coléno (2008) for a modelling approach on storage capacity constraints). In the model, the GM content of each batch is affected by the previous and following batches in the drying sequence. Thus, the admixture function at drying is formulated by the following equation:

$$p_i^c = \alpha \cdot p_{i-1}^c + \beta \cdot p_{i+1}^c + (1 - \alpha - \beta) \cdot p_i^c \quad (1)$$

where p_i^c and $p_i^{c'}$ are the GM content of the batches respectively before and after drying.

Finally, the model simulates the wet-milling process. In this study, we have adopted a compartmental modelling approach of the wet-milling process to quantify risks of admixture. A transfer of biomass takes place between 3 compartments: tank A, tank B, and tank C. Biomass is stocked temporarily in tanks A and C. After being processed in tank B, a proportion of biomass flow is sent back to the first tank A (Figure 2). Each maize lot entering the wet-milling plant is divided into d lots.

Figure 2. Scheme of the wet-milling module



A set of three discrete equations formulates the transfer of biomass between the three compartments between times i and $i+1$:

$$Q_{i+1}^a = Q_i^a + Q_{i+1}^e - \gamma \cdot Q_i^a + x \cdot Q_i^b \quad (2)$$

$$Q_{i+1}^b = Q_i^b + \gamma \cdot Q_i^a - x \cdot Q_i^b - y \cdot Q_i^b \quad (3)$$

$$Q_{i+1}^c = Q_i^c + y \cdot Q_i^b - z \cdot Q_i^c \quad (4)$$

where Q_i^e is the amount of biomass entering the plant at time i , Q_i^a , Q_i^b and Q_i^c are the amount of biomass respectively in tanks A, B and C at time i .

We assumed that the system works at equilibrium, thus :

$$x = \gamma \cdot \frac{r_b}{r_a} - r_b \quad y = r_b \quad z = r_c$$

where γ is the proportion of starch transferred from batch A to batch B, and r_a , r_b and r_c are the ratio of the amount of starch entering the system over respectively the amount of biomass in tanks A, B, and C ($r_a = \frac{Q_e}{Q_a}$, $r_b = \frac{Q_e}{Q_b}$, $r_c = \frac{Q_e}{Q_c}$).

Based on the equations 2-4, we obtained, as follows, 3 deterministic equations for the proportion of GM starch in the tanks:

$$p_{i+1}^a = p_i^a + r_a \cdot p_i^e - \gamma \cdot p_i^a + (\gamma - r_a) \cdot p_i^b \quad (5)$$

$$p_{i+1}^b = p_i^b + \gamma \cdot \frac{r_b}{r_a} \cdot (p_i^a - p_i^b) \quad (6)$$

$$p_{i+1}^c = p_i^c + r_c \cdot p_i^b - r_c \cdot p_i^c \quad (7)$$

where p_i^a , p_i^b and p_i^c are the GM content of respectively tanks A, B and C at time i .

At the beginning, the proportion of GM starch in the 3 tanks is null so that $p_0^a = 0$, $p_0^b = 0$ and $p_0^c = 0$. The proportion of biomass transferred must be between 0 and 1. In addition, between batches A and B and between batches B and C, the proportion of biomass transferred must be strictly positive. Therefore, the constraints are:

$$\min\left\{\frac{r_a}{r_b}, 1\right\} \geq \gamma \geq r_a > 0, 1 \geq r_b > 0 \text{ and } 1 \geq r_c > 0.$$

b) Scheduling of the batches

In the temporal specialisation strategy, on which the model focuses, GM and non-GM material are successively handled in the same equipment. Stakeholders define the frequency at which GM and non-GM flow alternates within equipment. In relation with admixture functions, the model takes into account sequence of GM and non-GM batches at drying and wet-milling level. The frequency of alternating between GM and non-GM flows are represented by two stakeholders' decision variables: k_{sech} and k_{am} . They represent the minimum number of batches with the same attribute (GM or not) successively dried (k_{sech}) or processed in the wet milling industry (k_{am}).

At drying level, these GM and non-GM batches are randomly ordered according to k_{sech} [respectively k_{am} at wet-milling process level]:

- The order of the sequence is randomly sampled: at the beginning of the sequence and every k_{sech} [resp. k_{am}] batches, the type of material (GM or not) is randomly sampled, according to the proportion of each type,
- The order of the batches within the sequences are then randomly sampled (draw without replacement).

c) Control of the batches

Once the sequence of batches has been scheduled, how do stakeholders manage the risks of admixture between GM and non-GM batches? We assume that the information on the type of variety sown (GM or not) is available for all the stakeholders at each stage. Consequently, there is no risk of error that a GM batch might be blended in a non-GM bin. Nonetheless, for non-GM batches, uncertainty

remains about the GM adventitious content, due to various sources of commingling between GM and non-GM material. Three kinds of control system might be set up in the model:

- In the first control system, stakeholders implement a simple traceability system, which allows them to identify whether the batches come from either GM or non-GM varieties.
- In the second control system, the simple traceability system is supplemented by rules on automatic downgrading of non-GM batches. Stakeholders downgrade automatically some non-GM batches, at drying and/or processing level.
- In the third control system, the simple traceability system is also implemented. In addition, testing is used to gather information on the non-GM batches. The model takes into account the fact that testing can be inaccurate.

The testing procedure is subject to two types of error: a diagnostic error and a sampling error (Starbird, 2008). We assumed that the sample is representative of the lot from which it was drawn. In this model, we took advantage of recent studies which have investigated the measurement error in analytical chemistry (Durbin *et al.*, 2002; Durbin and Rocke, 2004; Macarthur, *comm. pers.*). Thus, we assumed a proportional error by simulating measurement uncertainty with a lognormal distribution. Despite difficulties encountered in the determination of GM% in processed food from maize, mainly associated with the use of PCRs targeting sequences of unequal length (Yoshimura *et al.*, 2005), we considered that DNA-based quantification of the GM content in starch using PCR methodology is possible, with the same measurement uncertainty that for maize grains.

d) Way of quantification of GM adventitious presence

The GM adventitious presence in batches can be quantified either as the proportion of material carrying the transgene or material produced from grain carrying the transgene, or as the proportion of DNA carrying the transgene. These two ways of quantification are not directly equivalent, more particularly for maize. Indeed, maize kernels are made mainly of a tegument, an embryo and an endosperm. Throughout this study, GM content has been evaluated as the percentage of material carrying the transgene. Based on Trifa and Zhang (2004), we assumed that, in average, the percentage of DNA carrying the transgene in the grain is then 40.3% (Messéan *et al.*, 2006). Nevertheless, for more complex genetic structures, such as stacked genes, case-by-case studies should be performed to relate the percentage of GM seeds to the DNA quantification by PCR. Holst-Jensen *et al.* (2006) and Paul (2009) discussed these problems of quantification in more detail.



4. Simulations carried out

a) Input data

Previous studies have shown that not only does the risk associated with GM adventitious presence in non-GM harvest depend on the GM variety use, but it also varies between regions. This variation depends on structural variables of the landscape as well as cropping system (Le Bail *et al.*, submitted; Lécroart *et al.*, 2007). To take into account this variability, we considered several distributions of the GM adventitious presence in non-GM field harvests.

Various simulations were carried out with MAPOD model. Two areas of simulation with contrasted field pattern were selected in Aragon (Table 1). Various proportions of agricultural used area under conventional maize and under GM maize were simulated. GM and non-GM maize were allocated at random either with or without spatial constraints, such as separation distance between GM and non-GM maize and clustering of GM and non-GM maize. For the simulations with MAPOD, GM and non-GM varieties were sown at same density and produced similar amount of pollen. We assumed that all maize flowered simultaneously.

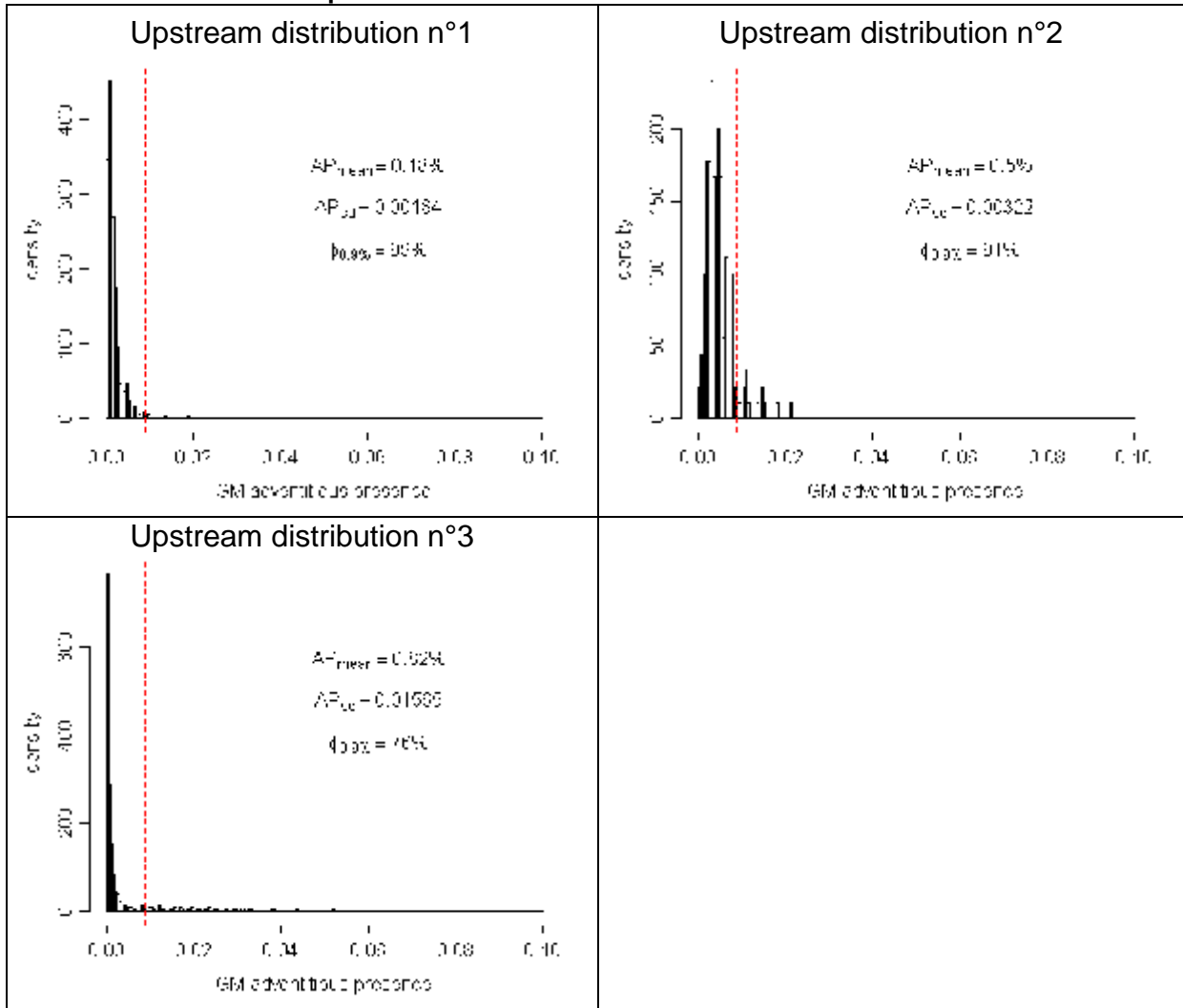
Table 1. Areas of simulation

| Aragon 1 | Aragon 2 |
|---|---|
|  |  |
| 964 ha 489 fields | 1081 ha 106 fields |

Original maps: Courtesy of the Institute for the Protection and Security of the Citizen, Joint Research Centre of the European Union.

Three contrasted distributions of the GM adventitious presence in non-GM harvest, each based on five simulations results, were selected in order to assess the effect of the maize grain purity rate on the starch maize purity rate (Table 2). Three mean levels of the GM content were selected (~0.18%, ~0.5%, ~0.82%).

Table 2. GM adventitious presence distribution in the non-GM harvest used for the simulations



b) Parameters

For each simulation, $N = 100000$ maize fields were delivered to the collection silos. We assumed that MAPOD estimated the cross-pollination rate without bias ($\eta = 0$) and with a coefficient of variation $k_M = 0.2$. The number of fields blended in a collection bin and the number of collection bins blended in a storage bin were equal to 10.

For each of the parameters of the commingling between batches in the dryer and the processing plant, two values were considered for the simulations, as summed up in table 3. In the plant, each lot was divided into $d = 10$ sub-lots.

Table 3. Value of the various parameters of commingling between two consecutive lots at drying and processing levels

| | | Admixture parameters at drying level | |
|--|--|--------------------------------------|-------------------------|
| | | low = 0.02 – = 0.02 | high = 0.17 – = 0.17 |
| Admixture parameters at processing level | low $r_a = 0.1$ $r_b = 0.8$ $r_c = 0.1$ | (low, low) | (low, high) |
| | High $r_a = 0.01$ $r_b = 0.01$ $r_c = 0.01$ | (high, low) | (high, high) |

In addition, γ is equal to $\gamma = \frac{r_a + \min\left\{\frac{r_a}{r_b}, 1\right\}}{2}$

c) Scenarios

One scheduling scenario was considered: $k_{sech} = 100$ and $k_{am} = 10$.

We assumed that the information on the type of variety sown was known without error by all the stakeholders. Three types of scenario were simulated:

- (i) simple traceability,
- (ii) automatic downgrading,
- (iii) downgrading according to PCR test.

For each of the scenario (ii) and (iii), several modalities were considered (number of batches downgraded before and after GM sequence at drying and processing levels, localisation of tests along supply chain).

According to Roy MacArthur, the accuracy level of PCR test is equal to 0.3 for *Round up ready*® soybean and 0.62 for other events. We simulated with an intermediate value ($\sigma = 0.4$).

Other things being equal, 30 repetitions were simulated.

d) Outputs

The model calculates the true GM adventitious presence of non-GM batches at each step.

In addition, three outputs indicators were used to compare the different contexts and scenarios at the various steps of the maize supply chain (maize harvest, collection bins, storage bins and starch bins):

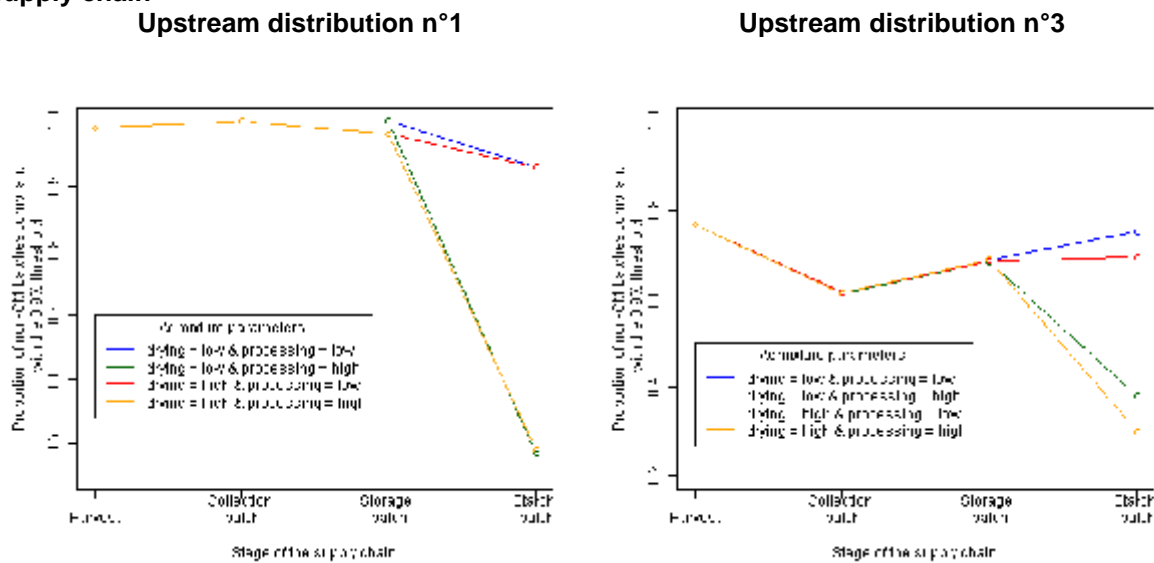
- the number of batches deemed as non-GM,
- the mean GM adventitious presence over all the batches deemed as non-GM,
- and the proportion of batches deemed as non-GM which are compliant with the 0.9% threshold.

5. Results and Discussion

Result 1

Results of simulation underline the fact that the whole supply chain, from the upstream producers to the downstream stakeholders, had a strong effect on non-GM purity rate of conventional products. At various stages within supply chain, there was admixture between batches with different characteristics – origin (GM or non-GM) and non-GM purity rate for conventional product. Focusing on three stages of supply chain (crop production, collection, and processing), the model allowed two underlying mechanisms (Figure 3):

Figure 3. Probability of compliance of non-GM products with the 0.9% threshold along the supply chain



10% of GM and simple traceability scenario

- **Admixture between GM and non-GM products:** It occurred first at crop production level, through pollen-flow. Downstream in the supply chain, it also occurred when alternating GM and non-GM products at drying and processing levels. Sources of admixture were additive which is why the mean GM adventitious presence in non-GM batches increased along supply chain.
- **Admixture between non-GM products:** There was admixture between succeeding non-GM batches at drying and processing levels. In addition, at collection level, several non-GM batches were blended into the same batch. Hence, standard deviation of GM content decreased. What was the effect on the probability of compliance of non-GM batches? Results of simulation show that here were two possibilities:
 - If the mean GM content was much lower than the threshold, then the probability of compliance increased. It was due to a dilution effect: few batches were not complying with the threshold. When blended in large volume, these non-compliant batches were diluted, so that the resulting batch was compliant with the threshold. This mechanism was observed between harvest batches and collection batches for the upstream distribution n°1 and n°2.

- If the mean GM content was higher (near the threshold), then the probability of compliance decreased. In this situation, the number of initial batches not complying with the threshold was too high, so that they could not be diluted in a larger volume. The resulting batch was also not compliant with the threshold.

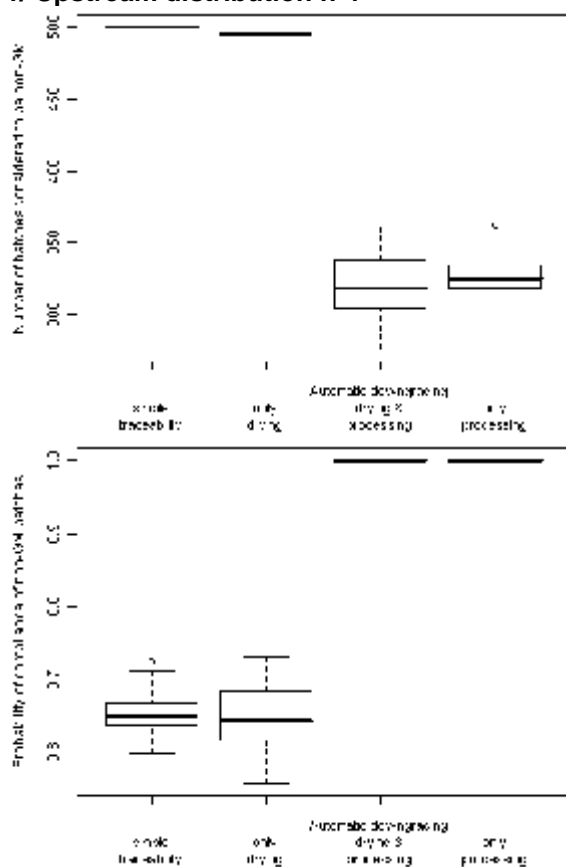
As a consequence, there was a threshold effect: dilution induced an increase of the probability of compliance only for distributions whose mean was below a threshold. Nevertheless, this dilution effect should be considered carefully with respect to regulation. Indeed, European regulation (European Commission, 2003b) authorises up to 0.9% of GM material in non-GM food and feed, provided these traces of GMOs are adventitious or otherwise technically unavoidable. One could argue that the dilution effect is no longer adventitious. This aspect still needs to be clarified.

Result 2

In this part, we assumed that stakeholders had information on the number of batches to downgrade at the processing level. In fact, an *ex-post* decision-making rule was simulated: conventional batches processed before and after GM sequence were downgraded so that the first batch still considered to be non-GM was compliant with the threshold. In addition, two modalities were considered at drying level:

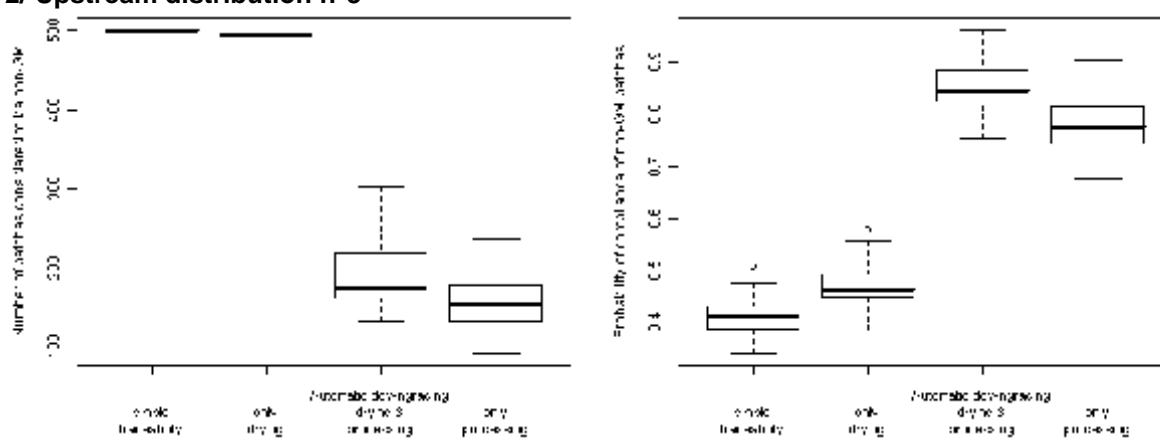
- no downgrading,
- the last and first non-GM batches respectively before and after GM sequence were downgraded.

Figure 4. Number of final batches considered to be non-GM and probability of compliance of non-GM products with the 0.9% threshold according to the downgrading scenario 1/ Upstream distribution n°1



50% of GM and low level of admixture parameters at drying and processing levels

2/ Upstream distribution n°3



50% of GM and low level of admixture parameters at drying and processing levels

The number of batches at the end of the supply chain was quite variable, other things being equals. This was due to sampling at drying and mainly at processing levels.

As shown in figure 4, automatic downgrading allowed increasing the compliance probability of non-GM batches with the 0.9% threshold. There was a trade-off between the number of non-downgraded non-GM batches and the compliance probability of these batches at the end of the supply chain. The more non-GM batches were downgraded, the higher the probability of compliance.

For the first upstream distribution, downgrading only at processing level was sufficient to achieve a high rate of compliance of non-GM on-downgraded batches. There was no need for downgrading both at drying and processing levels. On the contrary, the highest compliance probability was observed with the automatic scenario at drying and processing levels for the third upstream distribution. Thus, this result shows that information on the distribution of GM adventitious presence in raw material may help in implementing the best automatic downgrading strategy.

Result 3

What is the effect of PCR testing? We considered three different testing scenarios:

- testing at collection level,
- testing at processing level,
- and testing at collection and storage levels.

As expected, the probability of compliance of non-GM batches was almost always lower with a testing scenario than with an optimal automatic downgrading scenario, assuming stakeholders had information on the number of batches to downgrade. We calculated the ratio of compliance probability between the better automatic downgrading scenario and the better testing scenario: this ratio varied from 0% to 13.3%. In addition, in two situations, the PCR testing strategy was more effective in terms of compliance probability (negative ratio). It was due to the fact that the mean GM adventitious presence in conventional batches was close to the threshold value. Within these conditions, PCR testing allowed better distinguish between compliant and non-compliant batches.

6. Conclusion

As a conclusion, the simulation model presented in this report allows analysing mechanisms along supply chains. According to the model, the chain organisation, from the upstream producers to the downstream stakeholders, plays a crucial role in maintaining or improving the non-GM product compliance with a given threshold. The model allows also comparing various scenarios. Acquiring information on the quality of the upstream non-GM batches (farm gate) helps implementing better automatic strategies and may therefore save PCR testing. This implies a strong vertical coordination but increases the overall profit.

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