

GIS-based models for environmental risk assessment of genetically modified plants: poplar case study in forest ecosystems in Mediterranean environment

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**Background**

Environmental risk assessment (ERA) and ecosystem monitoring associated with genetically modified (GM) organisms is a topic of broad interest. An essential step in the development of products based on genetically modified plants (GMPs) is an assessment of safety, including an evaluation of the potential impact of the crop and practices related to its cultivation on the environment and human or animal health. The literature describes several ways to complete a risk analysis, nevertheless, researches are still needed to implement the EU Directive within a standardized methodological reference framework. Geographical Information Systems (GIS) are a powerful tool for spatial analysis and modeling used to assist the decision-making process. GIS have been considered for ERA and monitoring of GMPs. However, the potential of GIS to assist the ERA as indicated in EFSA is an aspect to be further developed.

The aim of this work was the development of a method to assess the environmental risk generated by transgenic Bt-poplar plants. To this end, four areas of concern are considered: persistence and invasiveness of GMPs, interaction of GM plants with microorganisms, interaction of GM plants with target and non target organisms. In addition, we describe how GIS-based models might be used by risk assessors to support and complement the ERA of GMPs from local scale to landscape level taking into consideration a specific area of concern indicated in EFSA: persistence and invasiveness of the GMPs or its compatible relatives.

**Methods**

The proposed method integrates the quantitative approach developed by de Jesus et al. [1] with the guidelines on ERA provided by the EFSA [2]. It is performed in two steps: 1) complete a preformatted worksheet to compile the evidence of risks, 2) plot the outcome on the Matrix of Assessment. Potential hazard are grouped according to their source of exposure, along with at least one criterion for assessment of each one.

These items are predetermined on the worksheet to allow for an accurate evaluation of related risks. An index of risk and an index of significance were computed for each potential hazard. The index of risk is calculated as the product of: damage x exposure x precedent; the damage indicates the level or intensity of the impact that the GMP could have on the system, if the proposed adverse effect actually occurs, the exposure is related to the level that some components are exposed to the damage and precedent considers the previous occurrence of the adverse effect, as a consequence of the event. The index of Significance

takes into account the location where the GMP will be cultivated, the identification and evaluation of potential adverse effects, and the evaluation of the current environmental situation. The indexes were combined using a matrix in order to assess the risk for the environment and the measures required to prevent adverse effects of GMPs.

The study was carried out within the Regional Park of Migliarino, San Rossore, Massaduocoli (Italy). A GIS was used to collect spatial data for the study area. Topographic maps and thematic layers (soil map, land use map, forest type map, and crop map) were acquired to characterize the environment of the study area and its biodiversity at the landscape level. Aerial remote sensing data and GIS tools were used to assist field plot selection and field works planning to get data on local biodiversity (both plants and animals) in agricultural and forest ecosystems. A Global Positioning System was used to determine the geographic coordinates of the selected plots and of other instruments installed in the field (meteorological stations and pollen traps).

The spatial dataset was used to develop GIS-based models for ERA of GMPs. GM poplar cultivations were simulated in the study area and the environmental risk due to breeding between GM trees and poplar trees in the surrounding forest ecosystems was assessed. To do this, a spatially explicit analysis was performed taking into consideration the simulated distribution of GMPs (poplar), the potential distribution of wild relative species (poplar trees), and gene transfer due to pollen flow. The distribution of wild relative species at the landscape level was obtained extending local data from field plots. Gene transfer was modeled using data from pollen traps and literature data.

#### Results and Conclusions

We describe one case study on possible effects of *Bacillus thuringiensis* (Bt) poplars in the environment, taking into account data reported in literature and derived from the studied area. The potential hazards characterized in our case-study were related to four areas of interest and were coded with different letters.

The assigned values for the factors of moderation were based on literature data. Moreover, we observed a breeding event in the studied area (potential hazard c) in AREA1) between two poplars: P3 (*P. canadensis*, naturally originated poplar trees) x F1.1 (*P. euramericana*). This event has to be taken in account because it could be considered a consequence of gene flow and, in case of genetically modified plants the incorporation of transgenes could result in greater invasiveness or loss of biodiversity with related taxa, depending upon the amount of gene flow from generation to generation and the transgenic trait(s).

Considering the distribution of the "letters" inside the Matrix of Assessment, different risk management could be suggested. The most part of potential hazards analysed does not pose significant risk, so it does not require additional actions. Whereas, potential hazard coded as "n" denotes the effect on target organisms and the potential hazard coded as "c" points out the possible consequence of gene flow, which required some restrictions to monitor the risk.

A map was produced depicting the potential areas where a risk of breeding between GMPs and wild relative species could exist in agricultural and forest ecosystems.

In poplar scenario 1 (Area 1) the gene flow between GM trees and spontaneous poplar in the surrounding ecosystems was investigated as potential source for exposure, considering that the breeding between GMPs and non GMPs represents a potential hazard reducing the genetic diversity of wild population.

In poplar scenario 2 (Area 2) the environmental risk due root exudates released by transgenic poplar was investigated as potential source for exposure (Area 2), considering as potential hazard that root exudates might affect the rhizosphere and soil community. To map such a risk, which is a consequence of risk investigated in poplar scenario 1, we

supposed that gene transfer from GMPs to soil micro-organisms occur in those areas where a risk of breeding between GMPs and its wild relatives exist.

In poplar scenario 3 (Area 3) the interactions of the GM poplar cultivations with TOs (larvae of Diptera and Lepidopteran) were examined. The level of mitigation of this issue requires some management measure. These would be developed together with the measures required to mitigate the risk of breeding considering that these two potential hazards have the same distribution.

In poplar scenario 4 (Area 4) the interactions of the GM poplar cultivations with NTOs (micro-arthropods in the soil) were addressed. The assessment of this issue for the study area indicate that no restrictions are required to mitigate the potential adverse effects of GM poplar cultivations on NTOs.

Our results show how GIS might be used to assess the spatial interaction between GM plants and the receiving environment at the landscape level using data collected at the local scale. Additionally, our results show how geographic data might be used to select checkpoints for monitoring of GM crops. These results are important to further develop existing guidance on the environmental risk assessment and monitoring of GMPs according to the EU Directive 2001/18/EC on the deliberate release into the environment of genetically modified organisms.

#### **Competing interests**

The author declares that they have no competing interests.

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#### **References**

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