

An integrative methodology to predict dispersal of genetically modified genotypes in oilseed rape at landscape-level—A study for the region of Schleswig-Holstein, Germany

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ABSTRACT

Potential environmental as well as socio-economic effects of the cultivation of genetically modified (GM) oilseed rape (OSR) may be caused by large-scale dispersal of transgenes. We present an up-scaling approach that was based on scenario assumptions concerning the percentage of GM cultivation and took into account natural and anthropogenic variation of involved dispersal processes. The applied methods include computer modelling and spatial analysis. A simulation model (GeneTraMP) was used to calculate the spatio-temporal pattern of the spread of a neutral transgene (without any specific function) in OSR. Basic scenario calculations were carried out for different spatial configurations covering 1 km² each and taking into account information on climate and cultivation systems of the region of the federal state of Schleswig-Holstein, Germany. For the exemplary regional study presented here, we analysed the numbers of flowering plants of GM OSR in different types of locations as predicted by the model. The results confirmed the expectation of a very high variability of GM occurrences at distinguishable intensity levels which were closely related to the proximity of areas of intended GM oilseed rape cultivation and may be described by a combination of management parameters and location type.

The up-scaling method included a spatial analysis of the target region. Based on satellite images and digital maps, the structure of the region was analysed resulting in a map of Schleswig-Holstein that represents each single field, also including information on crop rotation, ownership and production systems. Applying GIS queries to this database, we identified the area of relevant location types. Both, the model results and the spatial data were used to predict the total numbers of flowering GM OSR plants for the region of Schleswig-Holstein. As an important feature, the up-scaling of modelling results to a larger scale allows for a comprehensive analysis by also enclosing regional parameters, as, for example the cropping density. The presented methods can support decision making if they are incorporated into the planning of an environmental monitoring of commercial GM crops or into life cycle assessment and cost-benefit analyses of GMO cultivation.

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1. Introduction

Schleswig-Holstein is one of the leading regions of oilseed rape (OSR) cultivation and seed production in Germany. The world wide use of genetically modified (GM) crops (ISAAA, 2006) substantially strengthens the need to assess the consequences of large-scale cultivation of GM OSR. The global expansion in the development and cultivation of GM crops has also increased the concern about adventitious presence of GM materials in non-GM seeds and grains (Demeke et al., 2006). Van Acker (2004) showed that the presence of

GM herbicide resistant OSR volunteers in Canada largely increases, if the corresponding herbicide is used extensively in cultivation of other crops. A recent report indicates that intraspecific gene flow resulted in trait stacking of three different herbicide resistances in individual OSR plants of feral populations (Knispel et al., 2008). This might become economically or ecologically problematic because, for example multiple resistance against herbicides may lead to a rise in herbicide application (Benbrook, 2004) and related effects on biodiversity (Watkinson et al., 2000). Other issues of the large-scale cultivation of transgenic OSR are the likelihood and the consequences of the transfer of the transgenes to other fields where they would be undesired or to wild relatives (Dale, 1994). Spread of transgenes into feral populations and or wild relatives of crop plants is of special concern, because it may be difficult to predict whether the genetic modification will affect fitness, reproduction or other ecological parameters in the plants (Darmency, 1994).

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Large-scale dispersal of GM genotypes has already been a focus of several studies including different aspects of up-scaling and methodological approaches. Wilkinson et al. (2000) presented a procedure to quantify hybrid formation over large areas by using remote sensing to identify possible sites of sympatric occurrence of *Brassica napus* and *B. rapa* across 15,000 km² of South-East England and pollen dispersal profiles for a national assessment of hybridisation between these two species (Wilkinson et al., 2003). Perry (2002) calculated the amount of land available for the coexistent cultivation of both organic and GM crops, dependent of the separation distance between the two types of crop. Belcher et al. (2005) investigated how the presence of GM crops and changes in the likelihood of genetic transfer between crops on an agricultural landscape can result in contamination of conventional crops and discussed the results with respect to economical consequences.

The rate of transgene flow into natural populations and resulting risk levels are affected by spatial and temporal variability of factors, which control relevant processes of persistence and dispersal (Burke and Rieseberg, 2003; Kelly et al., 2005; Ammitzbohl and Jorgensen, 2006) and most of them are highly affected by large-scale spatial patterns like topography, distances between fields or more generally the spatial sink–source relationship. Hence, the consideration of specific regional conditions as well as large-scale land use pattern is required for reliable predictions of GM cost–benefit scenarios. In this study, computer modelling and spatial analysis aimed at a small-scale description of relevant processes and a large-scale transfer of results according to a specific regionalization approach (Faivre et al., 2004). We describe the combination of methods used and present as an example estimates of total number of flowering OSR plants carrying a neutral transgene in the region of Schleswig-Holstein. This is accomplished by a spatial analysis of GM cropping density on the spatial extension of contamination levels in conventional OSR crops. Such predictions are relevant for assessing consequences for post-market release monitoring activities as prescribed by European law (EC, 2001) or effects on alternative cultivation systems.

2. Methods

The development of cultivated, volunteer and feral OSR plants as well as related species was calculated with a spatially explicit computer model taking into account information on location, climate, cultivation intensity and regional cultivation systems. Model calculations (Box 1 in Fig. 1) integrate growth and pollen transfer processes on the plant level on single fields covering a mixed landscape up to units of 1 km². In order to estimate the

impact of GM OSR cultivation for the region of Schleswig-Holstein with an area of about 15,000 km², large-scale processes and variability (Box 2 in Fig. 1) were incorporated in model calculations by considering information of a scenario building process, which is described below.

Up-scaling from model calculations of 1 km² size considered different cropping schemes due to soil quality, local climate and prevailing farm types with a spatial database containing detailed information of the entire region of Schleswig-Holstein (Box 3 in Fig. 1), providing for each field site, size, shape, length of borders, and validated information for the years 1995, 1998 and 2000 if cropped with OSR. Model results like distant-dependent density of GM OSR plants growing up beyond the designed GM cropping situations were analysed in order to identify and rank specific spatial situations according to simulated frequencies of GM OSR plants.

Two up-scaling levels were used which of one aims at the regional level (Box 4 in Fig. 1) at which spread and dispersal of GM plants can be monitored. The second up-scaling level is the farm level (Box 5 in Fig. 1) where economic implications of gene flow may force the farmers to specific responses.

We achieved an area-wide estimate of transgene frequencies for Schleswig-Holstein by implementing two up-scaling steps. The first step was to identify spatial situations that could be related to different ranges of transgene frequencies within the target region and was done applying GIS queries to the spatial database of Schleswig-Holstein. The second step leading to the region-wide estimation was achieved by simply relating the total area of identified spatial situations (received from the GIS queries) to calculated ranges of transgene numbers (received from the model calculations).

In the following sections we give a detailed description of the methods and present as an example estimates of the total number of flowering OSR plants in Schleswig-Holstein that carry a neutral transgene.

2.1. Model calculations

We developed a mechanistic model GeneTraMP (Generic Transgene Movement and Persistence, Middelhoff et al., 2011), which allowed to represent and analyse persistence and dispersal of genetically modified OSR in heterogeneous landscapes. The selected support unit (Faivre et al., 2004) for simulation covers an area of 1 km². The applied object oriented modelling approach focused on a spatially explicit and individual representation of plants and reproduction units. This enabled to represent genetic interactions in relation to variable spatial cropping density and neighbourhood as well as environmental situations. Process

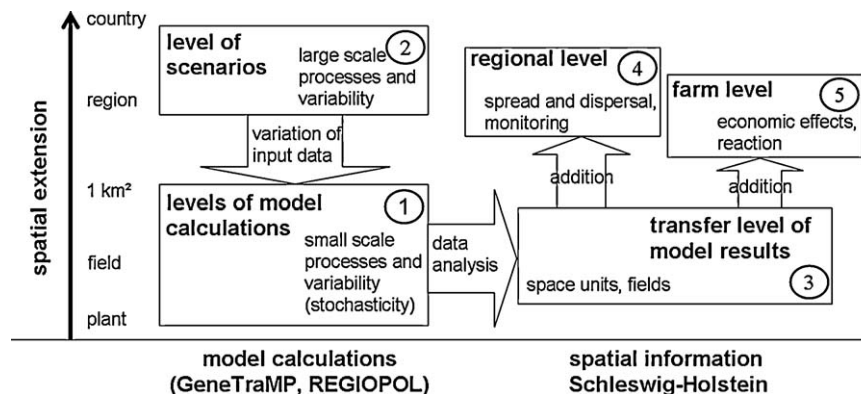


Fig. 1. Overview on information flow, involved levels of spatial extension and ecological organisation of the presented up-scaling method (Boxes no. 1–3) and accessible contents (Boxes no. 4 and 5) for the region of Schleswig-Holstein, Germany.

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