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A first step for modelling pollen dispersal at the landscape level: determining the shape of dispersal functions at long-distance. The case of oilseed rape

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Abstract

Simulation outputs from an oilseed rape pollen dispersal model compared to experimental data allowed us to show (1) that the individual pollen dispersal function of oilseed rape that is to be used at the landscape level to predict the consequences of the large scale cultivation of genetically modified plants has a fatter tail than an exponential curve and therefore (2) that pollen coming from different cultivars may be mixed at the landscape level.

Introduction

Modelling pollen dispersal at the landscape level is crucial for predicting the possibility of the co-existence of genetically modified (GM) and non-GM crops. Such modelling can be done on an individual plant basis by integrating the individual dispersal function of all pollen-emitting plants over the landscape. This individual dispersal function describes the probability that a pollen grain emitted at the (0,0) coordinates fertilizes a plant at any (x,y) coordinates (e.g. Lavigne *et al.*, 1996; Klein *et al.*, 2003). Determining the weight of the tail of that function (i.e. its shape for long distance dispersal events) is essential because it changes the composition of the pollen cloud over the landscape and thus may change the pattern of pollution of non-GM crops. However, pollen dispersal experiments are usually conducted on too small distances to enable researchers to discriminate between different types of function tails.

We therefore performed computer simulations and, from them, designed an experiment that allows us to determine the individual dispersal function family, according to the weight of its tail, in the case of oilseed rape. The choice of the function family is based on the comparison between the model and the experiment of the diversity and the differentiation of pollen clouds sampled randomly over the landscape.

Material and methods

Computer simulations

We built a landscape level pollen dispersal model that considers oilseed rape fields as point sources of pollen. Pollen is dispersed from every field with the same function but the quantity of pollen is adjusted from field to field according to its area. The landscape for this model was calibrated on a survey concerning the 2002 distribution of oilseed rape fields in a 10 * 10 km area surrounding the village of Selommes (Loir-et-Cher, France). Cultivars were determined for all fields. Dispersal functions were estimated from a prior experiment conducted on a one-ha field of oilseed rape (dispersal data in Lavigne *et al.*, 1998). After pollen dispersal was simulated, the virtual pollen cloud was sampled randomly over the landscape and its composition in terms of oilseed rape cultivars was determined.

Field and laboratory experiments

Field experiments were conducted during the 2002 spring to sample real pollen clouds in the region of Selommes. We placed 50 male-sterile oilseed rape plants, divided into two temporal repetitions at 13 controlled scattered sites in the Selommes area during the flowering period. Mature seeds from each plant were sampled for genetic analyses using 4 microsatellites markers to determine the fertilising pollen genotype of each seed. These genotypes allow us to characterize the pollen cloud, in terms of cultivar composition, at each site and to compare it to that expected from the computer simulations.

Results

A geometric fat-tailed individual dispersal function generated pollen clouds that were diverse but little differentiated – clouds were composed of a mean of 6.5 (sd 3.2) cultivars - and therefore should produce high diversity between descents collected on male-sterile plants scattered across the landscape but little differentiation among the groups of these descents. In contrast, an exponential individual dispersal function would generate little diversity within seeds collected on traps but high differentiation among them – clouds were composed of a mean of 1.2 (sd 0.8) cultivars.

The 4 markers allowed us to obtain the genotypes of 1834 of the 1967 seeds sampled on 19 of the 38 surviving male-sterile plants from the two repetitions. The pollen clouds above these 19 plants were all diverse: pollen clouds were all composed of more than 2 cultivars.

Conclusion and perspectives

These preliminary results performed on a sample of the 2002 seeds suggest that the individual dispersal function has a fatter tail than an exponential curve. Consequently, exponential functions may be inadequate for modelling long-distance pollen dispersal because they severely underestimate long- distance events. Rigorous statistical analyses will be lead to formally assess this result and they could be obtained from an adaptation of classical methods of parentage analysis.

We reconducted the experiment on a larger scale in 2003 and in regards to the 2002 results.

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