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A mechanistic model to predict transgenic seed contamination in bee-pollinated crops validated in an apple orchard

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ABSTRACT

The adventitious presence of transgene containing seed in conventional crops is an issue of considerable interest; a model to predict levels will aid regulators and help to address concerns of farmers and consumers. While outcrossing levels have been described in crops such as rape that are wind-pollinated, or both wind- and insect-pollinated, much less is known about pollen dispersal in exclusively insect-pollinated crops. In this paper, we develop a mechanistic model for pollen movement that is based on a description of bee movement through space. Our model is a system of diffusion-based partial differential equations that we use to predict percent transgenic seed at arbitrary distances from a transgenic source under different planting scenarios. We present a two-pronged study, in which the mathematical modelling work is informed by experimental work. The latter was carried out in an apple orchard with a row of 200 transgenic source trees carrying the GUS marker gene. Fruit from neighbouring conventional trees was gathered at distances ranging from 3.5 m to 183 m, and the seeds were extracted and germinated. Percent transgenic seed at each location was determined by testing the seedlings for the presence of the GUS marker gene. We use the experimental data to validate and parameterize the model, and then run model simulations to determine expected percent transgenic seed in various linear landscapes. We find that the percent transgenic seed in neighbouring conventional trees and orchards is a function of the size of each orchard block and the distance between them. The model explicitly shows the effect of overlapping transgenic and nontransgenic pollen distributions in setting seed distributions, and also shows the value of buffer rows in reducing outcrossing levels in neighbouring crops. The model parameters can be adjusted to suit particular crops and locations, and may be useful for determining plausible distributions on transgenic seed plantings needed to allow for an adventitious presence of, for example, 0.9%.

1. Introduction

Land planted with genetically modified crops has increased rapidly in recent years (Council for Agricultural Science and Technology, 2007). Simultaneously, widespread concern about the unintended spread of transgenes remains a public policy issue hindering further development of transgenic crops (Rieger et al., 2002; Chandler and Dunwell, 2008; Morris et al., 1994). Current regulations in Europe require that any crops with more than 0.9% presence of transgenes be labeled transgenic (Council for Agricultural Science and Technology, 2007; European Parliament, 2003), and thresholds as low as 0.1% have been suggested (Huygen et al., 2003). It is important then, that methods are available to predict the expected level of outcrossing in conventional crops grown in proximity to transgenic ones.

Plant pollen is dispersed either by wind or insects, usually bees. For plants using both dispersal methods, the relative importance of each is variable and not well-described (Hüsken and Dietz-Pfeilstetter, 2007), though pollinator-mediated pollination is thought to be the dominant mechanism and effective over longer distances, at least for oilseed rape (Hüsken and Dietz-Pfeilstetter, 2007). Most of the existing research on pollen gene flow from transgenic crops has been carried out with oilseed rape, and with exclusively wind-pollinated plants such as corn (Beckie et al., 2006). Empirical work has shown that most pollen falls within a distance of less than 20 m from the parent plant (Hüsken and Dietz-Pfeilstetter, 2007; Reboud, 2003) (though see (Messeguer et al., 2006)).

There is evidence that pollen spread is typically leptokurtic (Morris, 1993), but this may be an artefact of the observation methods used (Osborne et al., 1999). Indeed, Rieger (Rieger et al., 2002) did not observe a leptokurtic decline, or even an exponential decline, though their results are controversial since they did not check for adventitious presence of transgene in the planted seed. The amount of outcrossing between transgenic and conventional crops depends on the distance between the transgenic and

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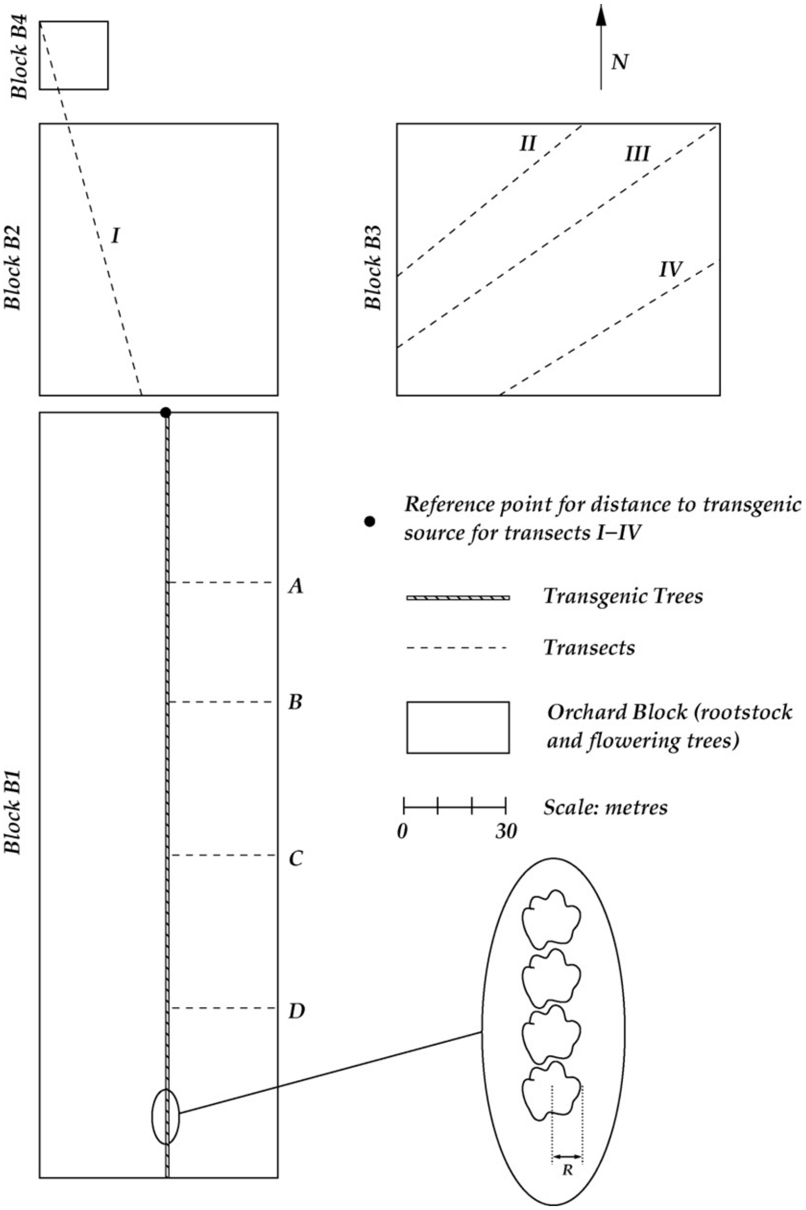

Fig. 1. Diagram of the study site showing the location of transgenic trees, conventional trees, and transects along which apple seeds were gathered. The zoom panel in the lower right shows R, the half-canopy width of the row of transgenic trees. The study site consisted of 4 blocks planted with apple trees, shown as rectangles in the diagram and labeled as blocks B1–B4. The transgenic trees occurred as a single row of 200 trees in the longest orchard block. In addition to the transgenic trees, which were of type gala, Orchard block B1 consisted of a single cultivar (Cripp's Pink, also called Pink Lady), while the other blocks were composed of a large number (≈50) of mixed cultivars. The transgenic trees and cross-compatible with all of the other trees in blocks B1–B4. The areas between the orchard blocks were empty of floral resource. Eight transects, labeled A–D and I–IV, were placed across the orchard blocks, and apples were gathered at 3.5 m (12 ft) intervals along these transects.

conventional crop blocks, the nature of any vegetation in the gap between them, and the size of the area planted (Hüsken and Dietz-Pfeilstetter, 2007; Messeguer et al., 2006; Reboud, 2003). Other factors such as flowering time and weather conditions also affect outcrossing level; we focus here on the primary factors of distance and flower presence.

In practice, farmers and regulators need to know isolation distances resulting in predictable levels of transgene containing seed (Rong et al., 2010). Research with oilseed rape indicates that some characteristics of pollen dispersal are predictable. Since oilseed rape pollen is dispersed by both wind and a host of natural insect pollinators, it is difficult to separate the effects of different pollination agents, and limits the extent to which the results can be applied to other types of crops, particularly bee-pollinated ones. The oilseed rape research however, suggests that pollen from other plants will be dispersed according to patterns that can be quantified. A mechanistic model for pollen dispersal based on these observed patterns and that can be used to predict outcrossing levels would be very useful to growers and regulators (Rong et al., 2010).

In this paper, we examine the bee-mediated spread of transgenes in a crop that is exclusively pollinated by bees; wind is not a pollination agent. We develop a mechanistic model for bee-mediated pollen movement, and so our approach is general and can be used to predict bee-mediated pollen movement in a variety of crops. Most outcrossing models to date are empirical and focus chiefly on wind-mediated pollen dispersal (Beckie and Hall, 2008), and so the framework we present here represents a significant step forward. As a practical application, we place our work in the context of outcrossing in apple. Only a few reports have described the extent of outcrossing or spread of pollen by wild or honey bees