

SHORT, NON-REFEREED PAPER

OPTIMISING CROP REFUGE AREAS IN TRANSGENIC SUGARCANE FIELDS

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Abstract

Crops expressing genes from the bacterium *Bacillus thuringiensis* (Bt) produce a protein toxic to members of the order Lepidoptera and are a popular alternative to sprayed insecticides. Although these Bt crops are considered to be an effective pest control method, reckless usage adds environmental pressure on the pest population to develop resistance to the toxin over time. One method of limiting the rate of resistance development is to keep small portions of the cultivated land planted with the non-GMO crop which then acts as a refuge area for the pest, limiting its exposure to the toxin and removing the pressure to develop resistance. Strains of Bt sugarcane for the South African market that should limit the damage caused by the stalk borer moth, *Eldana Saccharina* Walker, are being developed, and a prerequisite to releasing such a product is a recommendation on the size and layout of the refuge areas to be planted, as too small an area may not curb the rate of resistance development enough, but too large an area may not be economically viable for the grower. A simulation-based model is presented where individual moths are modelled as agents on an underlying sugarcane field. To reduce the complexity of the model, the field is divided into a series of smaller cells that can interact with each other, which allows us to model the impact of a severe infestation on an area the size of an average sugarcane farm.

Keywords: sugarcane, *Eldana*, GMO, agent-based simulation, pest management, agricultural landscape

Introduction

A fundamental tool in modern integrated pest management (IPM) systems is the use of genetically modified organisms (GMOs) specifically developed to be resistant to target pests. One such organism in widespread use today contains genes from a ground dwelling bacterium known as *Bacillus thuringiensis* (Bt). Crystalline proteins produced by this bacterium at sporulation, when ingested by members of the Lepidoptera family, cause paralysis in the gut of the larvae, which leads to a cessation in feeding and eventually death (Ferré *et al.*, 2002).

A common pest in South African sugarcane is the stalk borer moth *Eldana saccharina* Walker (Lepidoptera: Pyralidae). These larvae feed on the sucrose-rich sugarcane stalks, resulting in significantly decreased yields where a serious infestation is present. Other Bt GM crops, such as the Herculex line of maize from Dow AgroSciences, have been developed and marketed successfully as pest suppressants (Siebert *et al.*, 2008). Bt maize has been used commercially in South Africa since the mid-1990s (Gouse *et al.*, 2005) and several studies have been published on both its efficacy and development of resistance in target pests (van Rensburg, 2007). The South African Sugarcane Research Institute (SASRI) is in the process of developing lines of Bt sugarcane that will form part of the overall IPM system against *E. saccharina*. To register a biotech sugarcane product that expresses the Bt gene for stalk borer protection, an Insect Resistance Management (IRM) plan must be submitted as part of the overall regulatory package, detailing how the developer plans to prevent or delay the development of resistance.

The most commonly implemented form of IRM in pest resistant plants is the use of refuge areas, which are portions of the farmed land planted with non-GM plants. This strategy creates a habitat for susceptible insects that would potentially mate with resistant insects from the transgenic crop. The resulting offspring would then be susceptible to the Bt toxin, limiting the rate of resistance development. An earlier study by Butterfield *et al.* (2002) suggested that the refuge requirements for sugarcane would be significantly higher than expected (50% of the planted area). The purpose of this project is to develop a computer simulation model that could predict the life cycle and evolution of Bt resistance in populations of *E. saccharina* in a modern sugarcane field. The output of this model would be used as a support tool to determine the size and layout of refuge areas. The final goal is to minimise the development of resistance in *E. saccharina* while minimising costs and losses incurred by the user due to higher losses in non-GM refuge areas.

Methodology

In the context of this study, a computer simulation known as an agent-based model is used to model an *E. saccharina* infestation in a sugarcane field. In an agent-based simulation, each individual is modelled as an autonomous agent that can make its own decisions (Helbing, 2012). The model takes a two-dimensional space as an input and divides the space into equal sized square cells. Each cell is its own simulation space and is responsible for managing everything within it, including the moths, eggs, larvae and the underlying sugarcane. Every cell can communicate with its eight neighbours as detailed in figure 1 and agents can move freely among them. The explicit location of any given agent is not stored, but given a small enough cell size, it can be assumed that any agent's interaction with another agent in the same cell could be considered realistic.

Female moths can find and mate with male moths in the same cell and can then lay batches of eggs while moving around in different cells or could lay all her eggs within a single cell. It is assumed that all eggs laid by a female share the genes of the same male parent, hence eggs and larvae are not stored as individual agents, but as clusters that share the same 'gene pool' inherited from the male and female parent. Once the moths emerge from the pupae, the moth's traits are generated from this gene pool. This significantly reduces complexity and allows for a far larger number of agents in the model. Some of the genes in the gene pool can confer resistance to *Bt* toxins and these genes will alter the mortality rate of larvae that bore into sugarcane that contains the toxin.

Preliminary results

Preliminary tests were performed on a small-scale test with a field of nine hectares and a population of moths uniformly distributed throughout the area. The resistant gene was randomly assigned to 1% of the population, which would represent a phenotype that was uncommon, but not rare.

Two batches of tests were run, one where resistance was a dominant trait and another where it is recessive. Where the trait is dominant, the size of the resistant population would increase rapidly over a period of two years until nearly half the population was resistant in cases where there was less than 60% refugia planted. In scenarios where the trait is recessive, having more than 40% refugia resulted in no resistance development in approximately 90% of the simulations run. Although the refuge area is large, it resulted in an approximately 60% reduction of the moth population when compared to a control scenario where no *Bt* crops were planted. In all cases refuge areas planted in a striped pattern performed better than planting all the refuge areas in a single block, which suggests that shorter distances between any point in the *Bt* crop and the refuge areas increased the efficacy of the refuge areas.

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