

SHORT, NON-REFEREED PAPER

TOWARDS OPTIMISING CROP REFUGE AREAS IN TRANSGENIC SUGARCANE FIELDS

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Abstract

Genetically modified (GM) crops expressing genes from the bacterium *Bacillus thuringiensis* (Bt) produce a protein toxic to members of the insect order Lepidoptera and are a popular alternative to chemical insecticides. Although Bt crops are considered to be an effective pest control method, poor management adds environmental pressure and the pest population may 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 act as a refuge area for the pest, limiting its exposure to the toxin and removing the pressure to develop resistance. Lines of Bt sugarcane for the South African market that will limit the damage caused by the stalk borer moth, *Eldana saccharina* Walker are being developed. A prerequisite to releasing such GM genotypes 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, but a large area may not be economically viable for the grower. The requirements for building a computer simulation-based system that can model the population dynamics and resistance development of a moth population in Bt sugarcane with various sizes and layouts of refuge areas are presented, with insects being modelled as individuals on a farm-sized scale using a simulation technique known as agent-based simulation.

Keywords: sugarcane, eldana, GMO, agent-based simulation, pest management, agricultural landscape, computer modelling, cellular automata

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, 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, 2008). Bt maize has been used commercially in South Africa since the mid-1990s (Gouse, 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 delay or 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 allows for 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 is used to model an *E. saccharina* infestation in a sugarcane field. A highly-detailed model, simulating the entire lifecycle of *E. saccharina* was developed by Van Vuuren *et al.* (2014). The model included details such as the dispersal of larvae across the sugarcane canopy, the formation of 'leks'¹ by male moths and approximated rules and logic females would follow to lay eggs. Although very detailed, the model is too large to realistically simulate the entire extent of a commercial sugarcane plantation. The simulation model must be able to accommodate for several hectares containing roughly a million moths in various life stages and run over several planting and harvesting cycles.

In traditional agent-based simulation, individuals in a population are modelled explicitly, meaning that every individual is an autonomous agent that can interact with its environment and other agents (Helbing, 2012). In the context of this project, a full agent-based simulation could include simulating the entire lifecycle of individual moths as well as the growth of the sugarcane they feed on, as demonstrated by Van Vuuren *et al.* (2014). To accommodate for the scale of the problem considered, it is necessary to make several simplifications to ensure that the running time of the simulation is within reasonable bounds. One approach to reducing the complexity of the model is to overlay an n by n grid over the simulated space and to treat every block or cell in the grid as a separate subpopulation. Using this approach greatly reduces the number of possible interactions between agents as it only considers agents within its own cell, greatly decreasing the number of calculations the simulation has to perform at each time step.

Within the cells agents are free to interact with each other, their environment and can move to another of the eight adjacent cells in its neighbourhood, as seen in Figure 1. Each moth agent is given a set of traits in the form of parameters that influence its decision making and general behaviour, acting as the moth's 'genes'. Traits that an agent can possess include age, sex, propensity to fly longer distances and resistance to the Bt toxin. Whilst age and sex are not inherent genetic traits, resistance to the Bt toxin will form part of the moth's genome and can be passed on to future progeny. If the gene is recessive, it requires copies from both parents to be expressed, and maintaining pockets of non-resistant moths should, according to several studies including work by Jin *et al.* (2015), limit the development of a resistant population effectively. In the simulation, each cell would contain subpopulations of

¹ Leks are groups of about three to five males that display together to attract females.

resistant and non-resistant agents. These subpopulations would be allowed to interact over several simulated years and their sizes logged. The smaller the overall resistant population will likely point to a more effective refuge strategy. The simulation would also be able to show where in a field higher concentrations of resistant individuals are likely to develop.

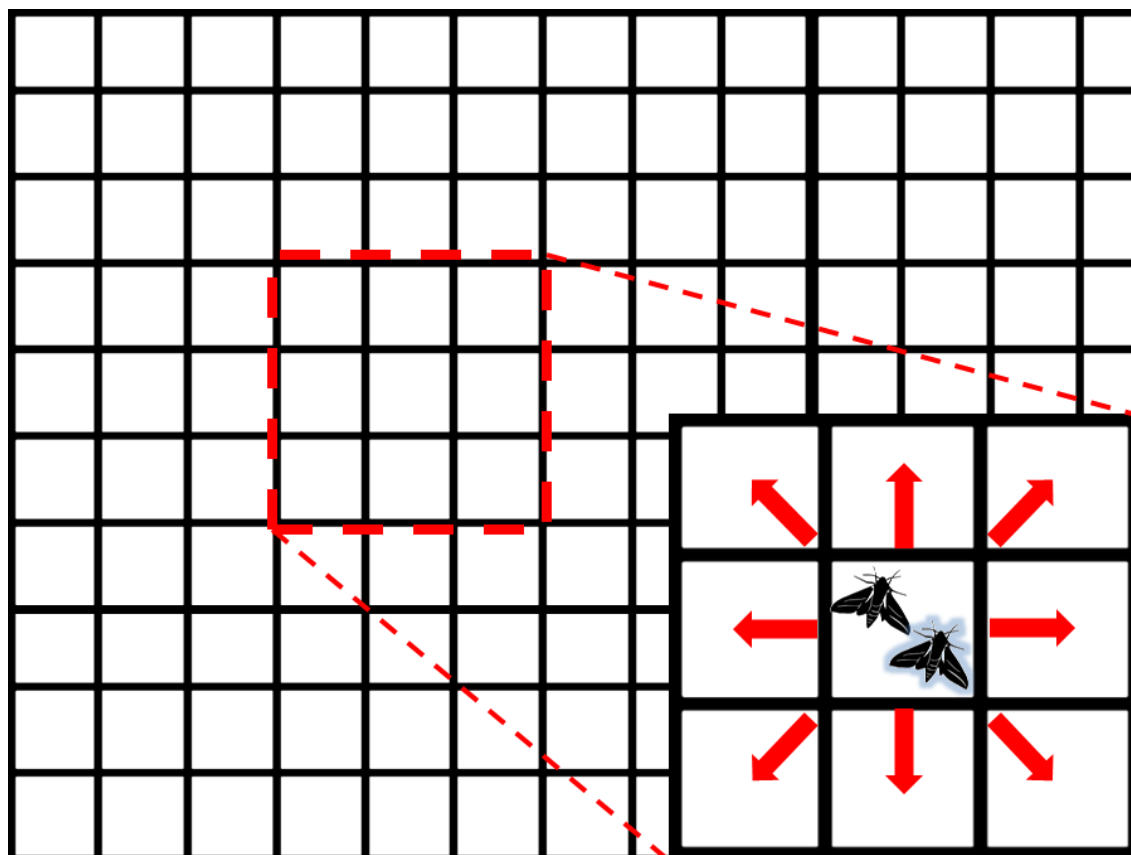


Figure 1: The grid overlay that allows for simplified simulation by only ever considering smaller subsets of the total area when calculating moth behaviour.

Conclusion

A simulation model of the development of Bt resistance in *E. saccharina* is being developed, utilising a cellular structure to reduce complexity and decrease computational time compared with previously developed models to predict insect movement. The model is currently a work in progress, with many complexities and functionalities that still need to be added. The output of the model is to be used in setting recommendations for the size and layout of refuge areas to be planted in newly developed sugarcane germplasm as part of the regulatory package development phase of the GMO development lifecycle.

REFERENCES

- Butterfield MK, Brokensha MA and Wood RA (2002). Genetic models to assess the development of counter-resistance in insect pests exposed to Bt-sugarcane. *Proc S Afr Sug Technol Ass* 76: 329-335.
- Chien K (n.d.) (2017). *Bacillus thuringiensis*. Retrieved March 30, 2017, from <http://www.bt.ucsd.edu/index.html>
- Ferré J and Van Rie J (2002). Biochemistry and Genetics of Insect Resistance to *Bacillus thuringiensis*. *Annual review of Entomology* 47(1): 501-533.

- Gouse M *et al.* (2005). A GM subsistence crop in Africa: The case of Bt white maize in South Africa. *International Journal of Biotechnology* 7(1-3): 84-94.
- Helbing D (2012). Agent-based modeling. *Social self-organization*. Springer Berlin Heidelberg, pp 25-70.
- Jin L *et al.* (2015). Large-scale test of the natural refuge strategy for delaying insect resistance to transgenic Bt crops. *Nature Biotechnology* 33(2): 169-174.
- Siebert MW *et al.* (2008). Evaluation of corn hybrids expressing CryIF (Herculex® I insect protection) against fall armyworm (Lepidoptera: Noctuidae) in the southern United States. *Journal of Entomological Science* 43(1): 41-51.
- Van Rensburg JBJ (2007). First report of field resistance by the stem borer, *Busseola fusca* (Fuller) to Bt-transgenic maize. *South African Journal of Plant and Soil* 24(3): 147-151.
- Van Vuuren BJ, Potgieter L and Van Vuuren JH (2014). Prerequisites for the design of an agent-based model for simulating the population dynamics of *Eldana saccharina* Walker. Proceedings of the 2014 Operations Research Society of South Africa (ORSSA) Annual Conference.