The HEAPS model as a framework for examining insecticide resistance management strategies.

Martin L. Dillon [1], Gary P. Fitt [1] and Joanne C. Daly [2]

1- CSIRO Entomology, Australian Cotton Research Institute, Narrabri, NSW.
2- CSIRO Entomology, Canberra, ACT.

Introduction

The summer crop insecticide resistance management (IRM) strategy has been operating very successfully in Eastern Australia since 1983/84 (Forrester et al., 1993). Adjustments to the IRM strategy have been periodically needed in response to changes in resistance frequencies and changes in available insect control technologies. Predicting the effects of changes to an IRM strategy, or predicting the efficacy of a given IRM strategy under a range of seasonal conditions is not easy. The incidence of resistance is intimately tied to the population dynamics of *H. armigera* both within and outside agricultural regions. *H. armigera* populations fluctuate in response to the availability of host crops, the levels of natural and applied mortality, the proportion of resistant individuals, and the rates of immigration and emigration. Resistance levels increase whenever insecticide controls exert differential mortality, by killing susceptible insects but allowing a higher number of resistant individuals to survive. Those survivors will promote resistant genes into the next generation, and they may spread resistant genes to populations in other areas. Resistance levels decrease only when non-selective controls are used and the frequency of resistant genes is diluted by immigration of susceptible individuals.

To understand and predict *Helicoverpa* dynamics on cotton, along with changes in levels of resistance, we must understand their dynamics on all hosts and the patterns of movement to and from cotton. The response of *H. armigera* populations to insecticidal controls, and the effect that resistance gene frequencies have on this response must be taken into account. The HEAPS simulation model (Dillon and Fitt, 1990) provides a framework for examining the potential impact of proposed IRM strategies that takes into account the dynamics, movement and gene frequencies of *H. armigera* populations over a regional or area-wide scale.

The HEAPS (*HElicoverpa Armigera* and *Punctigera* Simulation) model embodies all of our current knowledge on the ecology of *Helicoverpa* within cotton cropping regions. It differs from other models of *Helicoverpa* population dynamics in two main ways. Firstly it operates over an explicitly defined spatial representation of the agricultural landscape within the region being simulated, and secondly it simulates multiple sub-populations of *Helicoverpa*, each of which have their own demography and resistance gene frequencies. By necessity the model is a simplification of the real world, and there are many underlying assumptions governing its predictions. The HEAPS model is still in the process of being validated on a regional scale, and therefore the accuracy and precision of its predictions remain to be proven. However the model has already been a useful research tool for studying a range of issues relating to the regional population ecology of *Helicoverpa*. It is in this regard that we outline the use of the model to simulate the demographic and genetic response of *H. armigera* populations to IRM strategies (see Tabashnik, 1990).

Simulating insecticide resistance

The HEAPS model simulates insecticide resistance by keeping track of the allele and genotype frequencies in each of the sub-populations of *H. armigera* within the region being simulated. Separate tallies are kept for each life-stage. Genotype frequencies may change whenever each of the following events occur: (i) differential survival following a simulated insecticidal control, (ii) movement of adult moths between sub-populations, and (iii) moths mating and producing new batches of offspring. The initial frequencies of each genotype for each life-stage within each sub-population must be provided by the user. The resistance module within HEAPS incorporates the following assumptions:

1. Resistance is controlled by a single gene locus with 2 alleles, R (resistant) and S (susceptible). Thus three genotypes are possible, RR (homozygous resistant) , RS (heterozygous) and SS (homozygous susceptible).
2. Each *Helicoverpa* life stage of each genotype has a specific survivorship in relation to a given insecticide application and its residual effects. This results in differential survival of each genotype following a selective spray.

3. The relative "dominance" of the resistant allele is controlled by the survivorship that the user attributes to each genotype and life-stage combination.

4. Mating is random, so the allocation of offspring into each genotype is calculated on the basis of the allele frequencies within the parent population. Because the parent moths may have mixed origins, it is unlikely that a Hardy-Weinberg equilibrium will be maintained.

Fleshing out the framework

The HEAPS model has been designed as a flexible research tool. To run a simulation, the user must first define the scenario within which the model will operate. The spatial representation of the landscape within the region being simulated is described in terms of the type and size of each host patch and its distribution in space and time. Over the host patches are spread sub-populations of *Helicoverpa*, each with their own densities, demographic make-up, and initial genotype frequencies. As the simulation runs, the model needs to be able to access weather data as this effects the development and movement of the pests. The incidence and rate of immigration into the region, and the genetic make-up of the immigrants must be also be defined. The user must also define the efficacy of control applications and set rules that the model will use to trigger their use.

Once set up a wide range of aspects of the ecology and management of *Helicoverpa* can be studied. In particular the overall dynamics of *Helicoverpa* populations over the entire region can be observed in relation to the individual pest control regimes applied to each host patch being simulated. We have also been using the model as a test bed to take a closer look at some of the potential outcomes of the current IRM strategy. Some of the aspects studied include the renewed emphasis on the importance of cultivating over-wintering *H. armigera* pupae; the relaxation on the use of pyrethroids on spring crops other than cotton; the importance of the spring arrival of migratory moths in diluting local resistance levels; and the possible contamination of refuge areas with resistant genotypes.

Simulating insecticide applications

The HEAPS model allows the user to define control agents that can be applied onto a given host patch at any time. A control agent is given a specific efficacy for killing individuals of each genotype within each life-stage. This can then be 'applied' onto a given sub-population, and the densities and gene frequencies stored by the computer are automatically adjusted. The timing of such control applications can be set to happen on specific days, at regular intervals, or when a specified threshold is exceeded. The model always has an exact count of the number of pests that are present within the sub-populations in each host patch in the region.

By setting up a number of types of control agents and the rules governing their application, the user can run simulations to examine a range of issues relating to the resistance. Examples include: targeting different life-stages, application timing; the frequency of control applications; the proportion of the total population treated; the relative dominance of resistance; different rotation schedules; adjustments to dose rates; and the addition of synergists. One of the great benefits of using HEAPS to evaluate issues such as these is that although the model is simulating control applications on a patch by patch basis, the user can see the overall effects on *Helicoverpa* dynamics over the entire region. Meaningful trends cannot always be found by undertaking real or simulated experiments on a single field basis.

The cultivation of over-wintering pupae

Surveys of the abundance of *Helicoverpa* pupae under cotton residues have been undertaken in the Namoi/Gwydir for the past 7 years. Although there is a large range of variation, on average 39% of uncultivated cotton fields had over-wintering pupae present. The average density was over 2000 pupae/Hectare. All of these were *H.armigera*, and they represent the survivors of the previous seasons control program. Their level of resistance is very high, around 70% (Fitt et al., 1993).

We have set up HEAPS scenarios in which cultivation is 'applied' by the model to selected host patches in the same way as other insecticidal controls. Simulations showed that if left uncultivated, most of the pupae would survive to emerge in

October and November the following spring. A relatively small initial pulse of *H. armigera* usually arrive as immigrants in the Namoi/Gwydir in mid to late September. It is assumed that these originate from wild hosts on the same weather fronts that bring the spring migrations of *H. punctigera*, and that their resistance levels are very low. The emergence of the over-wintering pupae has a dramatic effect in bolstering the numbers of *H. armigera* present in the system and the frequency of resistant genotypes.

The gene frequency of resistance in refuge areas

The same set of simulations described above emphasised the importance of the spring immigration of susceptible moths in diluting resistance. Resistance levels decrease between the end of one cotton season and the beginning of the next only when the proportion of susceptible genotype individuals increases following the arrival of these migrants. It is assumed that they come from refuge areas in which they are not selected for resistance.

In recent years the magnitude of the inter-season decline in pyrethroid resistance has steadily decreased. Forrester et al. (1993) suggest that this is directly attributable to the 'contamination' of the refugia by resistant genotypes. As the level of resistance in refuge areas steadily rises each year, it results in increasingly poor dilution of resistance levels in the cropping regions by the arrival of spring immigrants.

With the anticipated release some years in the future of transgenic cotton expressing Bt toxins, we recognise that careful management of a refugia of susceptible *Helicoverpa* is going to be crucial. We intend to use simulation models to evaluate the pros and cons of a range of strategies for maintaining refugia both within and outside the cotton growing region. The spatial emphasis of the HEAPS model makes it ideal for many of these tasks.

References

Dillon, M.L & Fitt, G.P. (1990) HEAPS: A regional model of *Heliothis* population dynamics. Proceedings of the Fifth Australian Cotton Conference, Broadbeach, Qld. Australian Cotton Growers Research Association, Brisbane, pp. 337-344.

Forrester, N.W., Cahill, M., Bird, L.J. and Layland, J.K. (1993). Management of pyrethroid and endosulfan resistance in *Helicoverpa armigera* (Lepidoptera: Noctuidae) in Australia. Bulletin of Entomological Research Supplement Series: Supplement No. 1.

Fitt, G., Murray D., Dillon, M. & Daly, J. (1993) Overwintering *Heliothis* pupae and the importance of cotton stubble cultivation. The Australian Cotton Grower 14(4): 50-52.

Tabashnik, B.E. (1990). Modelling and evaluation of resistance management tactics. pp. 153-182 in R.T. Roush and B.E. Tabashnik (Eds): Pesticide Resistance in Arthropods. Chapman and Hall, New York.