

## EPSRC Mathematics CASE PhD Studentship

Start Date: September/October 2008

Duration: 3.5 years

Enhanced stipend of £15,940

### Mathematical modelling of the spatio-temporal dynamics of aphid-parasitoid-plant-virus interactions

#### Supervisors:

Prof. Mark Chaplain, Division of Mathematics

Dr. Alison Karley, Scottish Crop Research Institute

#### Introduction

Intensive agricultural practises are a feature of the highly productive arable systems that prevail in the EU, with effective control of many crop pests achieved by combinations of synthetic chemical pesticides, efficient cultural practices and the use of resistant plant varieties. Aphids are a group of crop pests that represent an exception to this general pattern. These insects can cause many millions of pounds of damage to crops annually, largely due to the capacity of aphids to transmit an enormous range of plant virus diseases to multiple plant species. Efficient virus transmission can lead to considerable crop damage even at low aphid population densities. Thus disease transmission, and the underlying population processes which affect it, are much less tightly coupled to the densities of both the aphid vector and the plants which harbour the infection. A reduced emphasis on the role of traditional density-dependent processes in virus transmission in aphid-plant associations presents special challenges in the modelling of plant disease dynamics, particularly because stochastic processes are likely to have a greater influence on the spatio-temporal patterns of virus transmission in a field crop. In addition to the viruses which they vector, aphids harbour one to several types of symbiotic bacteria which can have considerable influence on their fitness and therefore upon their capacity to transmit disease. Most aphid species host an obligate endosymbiont, *Buchnera aphidicola*, which has an extremely important physiological function in synthesising essential amino acids that the aphids cannot otherwise produce. As there is increasing evidence that pea aphid (*Acyrtosiphon pisum*) secondary symbionts influence the interaction between the aphid and its natural enemies (for example, parasitoid wasps), it is particularly important to assess the contribution of secondary bacteria to the control of the trophic dynamics of the arable system.

#### Project Objectives

- To develop and analyse ordinary differential equation models of multi-species aphid-parasitoid-plant-virus systems
- To develop and analyse partial differential equation models of multi-species aphid-parasitoid-plant-virus systems
- To develop and analyse individual-based models of multi-species aphid-parasitoid-plant-virus systems
- To compare the results of the three modelling approaches

The model development will be carried out in close collaboration with the CASE partner Dr. A. Karley (SCRI) and Dr. S. Hubbard (College of Life Sciences). The mathematical modelling will develop previous work in this general area by Chaplain and Hubbard (References [1]–[6]).

## Programme of Work

Initially, we will consider a (spatially-homogeneous) system of one aphid, one parasitoid and one virus denoted  $A$ ,  $P$ ,  $v$  respectively. The initial model to be studied is:

$$\frac{dA}{dt} = f(A, P, v) \quad (1)$$

$$\frac{dP}{dt} = g(A, P, v) \quad (2)$$

$$\frac{dv}{dt} = h(A, P, v) \quad (3)$$

where  $f, g, h$  are appropriate functions modelling the interactions between the aphid, parasitoid and virus. An analysis of a similar model of host-parasitoid dynamics [5] (Preedy et al., 2007) has revealed very interesting temporal dynamics with the existence of a chaotic attractor as well as quasi-chaotic transient dynamics. We would expect similar behaviour here. The model will then be extended to account for multi-species interactions cf. References [4]–[6].

In order to examine the situation where the aphids and parasitoids can move freely and interact with each other within a given spatial domain, the model will then be extended to include spatial effects in both aphids and parasitoids through the inclusion of (nonlinear) random motility (cf. diffusion) i.e.

$$\frac{dA}{dt} = \nabla \cdot (D_A(A, P)\nabla A) + f(A, P, v) \quad (4)$$

$$\frac{dP}{dt} = \nabla \cdot (D_P(A, P)\nabla A) + g(A, P, v) \quad (5)$$

$$\frac{dv}{dt} = h(A, P, v) \quad (6)$$

Further development of the model will include extending to multi-species interactions and investigating the effect of the explicit inclusion of plants  $X$  into the model. Since the plants are non-motile, this will mean including an ODE of the form:

$$\frac{dX}{dt} = k(A, P, v, X) \quad (7)$$

Modelling the effect of the plants on the aphids, parasitoids and virus will be achieved by computationally simulating equations (4)–(7) on a 2-dimensional spatial domain where the spatial configuration of the plants in the domain reflects the actual experimental spatial configuration used in the field-work. In this case, the diffusion coefficients  $D_A$ ,  $D_P$  and kinetic functions  $f, g, h$  will be modified accordingly i.e.  $D_A(A, P, X)$ ,  $D_P(A, P, X)$ ,  $f(A, P, v, X)$ ,  $g(A, P, v, X)$ ,  $h(A, P, v, X)$ .

Finally a discrete (stochastic) individual-based model (IBM) will also be developed. This modelling technique is ideally suited for tracking individuals which interact in a spatial domain and has been very successfully applied to model host-parasitoid interactions (cf. References [1] [2] [3] Schofield et al. 2002; 2005a,b). Modelling the transmission of disease/virus between interacting individuals is modelled particularly well using this technique. This technique also lends itself very well to the explicit inclusion of (stationary) plants into the system. The models will be posed on 2-dimensional spatial domains and different plant configurations and multiple plant species will be incorporated into the model. Extensions of the model to include multiple spatial domains (i.e. more than one “patch”) will also be considered. Chaplain and Hubbard have pioneered the use of the individual-based model for host-parasitoid systems (References [1]–[3]) and now have considerable expertise in this area. The computational simulation results from the IBM will be compared and contrasted with the results and analysis obtained from the differential equation approach.

The mathematical approach (particularly the individual-based model) adopted by this project is especially amenable to novel Integrated Pest and Disease Management (IPDM) practises which are

currently being developed at SCRI. IPDM is viewed as the favoured option for short-medium term control (meeting consumer acceptance, environmental sustainability, development costs and agricultural policy). In particular, the generic models developed in the project describing the spatial and temporal population dynamics of aphids and parasitoids will link into specific experimental work at SCRI. This work investigates how the bacterial symbiota of the cabbage aphid, *Brevicoryne brassicae*, influence aphid interactions with parasitic wasps and aphid ability to vector viruses. Extension of this approach to investigate potato-aphid-natural enemy interactions could be beneficial for understanding the genetic and environmental factors influencing disease transmission by insect pests. Mathematical models will therefore be crucial for gaining a deeper understanding of the complex interactions and the effect of spatial heterogeneities. The program of complementary experimental work at SCRI will allow such models to be validated and developed in an iterative manner.

To parameterise the models we will need a suitable experimental system where the basic elements outlined above are known to be present. The aphid species *Macrosiphum euphorbiae*, transmitting potato leaf roll virus and attacked by its parasitoid *Aphidius ervi*, is deemed to be the most appropriate. The diagnostic molecular techniques already developed for the pea aphid secondary symbionts will be suitable for the detection of secondary symbiont types in *M. euphorbiae* (we have already demonstrated the presence of one common secondary symbiont type in a culture of *Macrosiphum* collected locally). In addition, the species is amenable to both field and laboratory experimentation, which will make it relatively easy to investigate the potential for within-field parasitoid transfer of secondary bacteria between aphids with different symbiont assemblages, which would be the first demonstration of such an effect. It will also allow realistic, field-based parameters to be estimated for the purposes of inclusion into the mathematical models.

The results of the analysis of the models have implications therefore not only for understanding the role of infection in determining the structure of ecological communities, but also for the effective application of biological control in agro-ecosystems, the impact such methods might have on the ability of farmland habitats to sustain biodiversity, and the general dynamics of disease processes.

### Other Relevant Information

The project will also involve the supervision of Dr. Steve Hubbard, Division of Environmental and Applied Biology, College of Life Sciences, who has collaborated successfully with Prof. Chaplain over the last 7 years, co-supervising 4 PhD students in the area of host-parasitoid models (P.G. Schofield, I. Pearce, K. Preedy, A. Burgess). Relevant publications in the area are as follows:

- [1] Schofield, P.G., Chaplain, M.A.J. and Hubbard, S.F. (2002) "Mathematical modelling of host-parasitoid systems: effects of chemically mediated parasitoid foraging strategies on within- and between-generation spatio-temporal dynamics" *J. Theor. Biol.* **214**, 31-47.
- [2] Schofield, P.G., Chaplain, M.A.J., Hubbard, S.F. (2005) "Dynamic heterogeneous spatio-temporal pattern formation in host-parasitoid systems with synchronised generations" *J. Math. Biol.* **50**, 559-583.
- [3] Schofield, P.G., Chaplain, M.A.J., Hubbard, S.F. (2005) "Evolution of searching and life history characteristics in individual-based models of host-parasitoid-microbe associations" *J. theor. Biol.* **237**, 1-16.
- [4] Pearce, I.G., Chaplain, M.A.J., Schofield, P.G., Anderson, A.R.A., Hubbard, S.F. (2006) "Modelling the spatio-temporal dynamics of multi-species host-parasitoid interactions: heterogeneous patterns and ecological implications" *J. theor. Biol.* **241**, 876-886.
- [5] Preedy, K., Schofield, P.G., Chaplain, M.A.J., Hubbard, S.F. (2007) "Disease induced dynamics in host-parasitoid systems: Chaos and coexistence" *Roy. Soc. Interface* **4**, 463-471.
- [6] Pearce I.G., Chaplain, M.A.J., Schofield, P.G., Anderson A.R.A., Hubbard S.F. (2007) "Chemotaxis-induced spatio-temporal heterogeneity in multi-species host-parasitoid systems" *J. Math. Biol.* **55**, 365-388.

Applications, with full CV and the names of two academic referees should be addressed to:

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