Multitrophic factors influencing aphid vector competence in a spatially heterogeneous environment

Emily Clark[1], Dr Alison Karley[1] and Dr Steve Hubbard[2]
[1]Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA
[2]School of Life Sciences, University of Dundee, Nethergate, Dundee, DD1 4HN

Aphids harbour a number of different symbiotic bacteria that can have positive or negative effects on their survival and performance[1]. In addition, aphids are major insect pests of many agricultural crops, largely because they transmit a wide array of plant viruses. Aphid fitness and thus the competence of aphid clones to vector a plant virus may depend critically on the particular symbiont assemblages that they harbour, the spatial structure of the habitat, and the abiotic and biotic conditions (temperature, humidity, plant development stage, parasitism) of their environment (Figure 1).

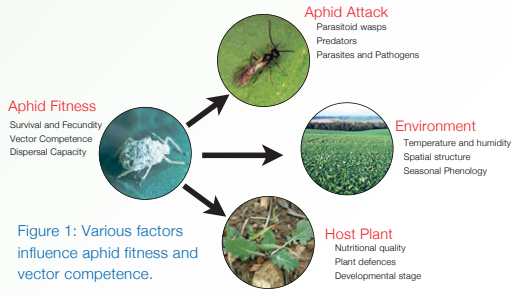

Figure 1: Various factors influence aphid fitness and vector competence.

Aim

To characterise and quantify the symbiont assemblage of the aphid, *Brevicoryne brassicae,* and to investigate the effect on their ability to vector a plant virus both directly and indirectly, by influencing aphid attack by parasitic wasps, aphid dispersal capacity and the aphid-host plant interaction.

Study System

The cabbage aphid *Brevicoryne brassicae* (Figure 2) feeding on the *Brassicaceae* and transmitting cauliflower mosaic virus (CaMV) is the chosen study system. *B. brassicae* feeds on a range of different *Brassica* crops many of which are economically important in Scotland, such as brussel sprout (*Brassica oleracea*) and oilseed rape (*Brassica napus*) (Figure 3). CaMV virus is also one of the most wide spread viruses of *Brassica* crops worldwide. *B. brassicae* populations are collected in the summer of each year from a range of different field locations and *Brassica* types and clonal lines are reared in culture for study.

Figure 2: *Brevicoryne brassicae* the cabbage aphid.

Figure 3: *B. brassicae* feeds on a range of different *Brassica* crops.

Methods

Molecular Techniques

Secondary symbiont diversity in the selected aphid clones will be investigated using a range of molecular techniques. DNA extracted from aphid samples from the different clonal lines is used as template for PCR amplification of a 2½ kb product incorporating the IGS (Inter-Genic Spacer) region between the 16S and 23S subunits (Figure 4). For most eubacteria other than *Buchnera* (the primary endosymbiont in aphids) the 16S gene is linked to the 23S gene by a region of IGS[2,3]. Amplifying this region using universal primer pairs (Figure 4) specific to the two genes excludes the primary symbiont *Buchnera* and can be used as means of detecting the other eubacteria harboured by aphids through gene cloning and sequence analysis[2,3] or T-RFLP[1,4].

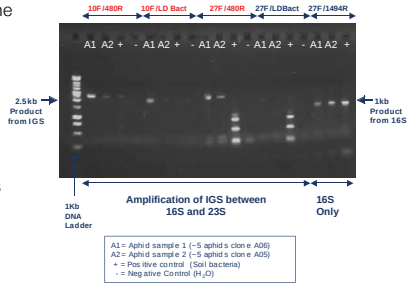

Figure 4: Gel image showing the 2.5kb product of interest. (Successful primer pairs are highlighted in red.)

Aphid Performance

A number of different experiments are being devised to test aphid performance according to endosymbiont complement. Life history traits being investigated for each aphid population on a range of different *Brassica* host plants and environmental conditions include fecundity, growth rate, intrinsic rate of population increase, dispersal capacity and development time.

Aphid- Parasitoid Interactions

Parasitised aphid material is collected from the field sites throughout the summer each year. The emergent wasps are used to routinely parasitise the *B. brassicae* clonal lines (Figure 5) to investigate both the interaction between parasitoid attack and endosymbiont complement and the fitness effects that influence the dynamics of parasitoid wasp populations.

Figure 5: A parasitoid wasp in culture with *B. brassicae*.

Application of Results

Data from the project will be used to construct mathematical and statistical models of the dynamics of the system[5,6], primarily to predict the spread of aphid-vectored plant disease in spatially heterogeneous arable crop systems.

These models will be a useful tool for the future management and control of aphid populations in arable crops giving the project a practical application within the agricultural industry.

References:
[1]Ferrari *et al.* (2004) *Ecol. Entomol.* 29, 60-65
[2]Unterman *et al.* (1989) *J. Bateriol.* 171, 2970-2974
[3]Sandstrom *et al.* (2001) *Mol. Ecol.* 10, 217-228
[4]Haynes *et al.* (2003) *Appl. Environ. Microbiol.* 69, 7216-7223
[5]Schofield *et al.* (2002). *J. Theor. Biol.* 214, 31-47
[6]Kot *et al.* (1996) *Ecology* 77(7), 2027–2042