Summary

This project helped to identify the factors that affected the efficacy of transgenic Bt cotton plants to control *Helicoverpa punctigera* and *H. armigera*. This knowledge contributes the design and refinement of the resistance management strategy for the commercial use of transgenic cotton plants.

We have demonstrated, through several sets of experiments, that the plant growth stage itself has a major effect on efficacy. That is, a compound(s) in the plant appear to alter the availability of the Bt protein to the insect, after ingestion. Our results suggest that condensed tannins, accumulated in the leaves under field conditions, could decrease the efficacy of Bt. Changes in environmental conditions seemed to affect efficacy, particularly through changes in growth rate, seen in two major experiments. Thus, stresses of different kinds may impact on efficacy because generally stress alters the growth rate of the plant.

We quantified season long variation in efficacy of Bt cotton grown under field conditions. Initial bioassays, on field samples taken from individual Bt plants, over two seasons, showed that there was a significant difference in efficacy between plants. Bioassays on bulked, freeze-dried field samples of two commercial Bt varieties, over the 96/97 and 97/98 seasons, quantified changes in efficacy over the season and illustrated differences between the two varieties and the two seasons. Efficacy was measured as dropping over 50 fold for V2i by early February in both seasons and 276 fold for V15i by mid March1997, 82 fold by mid January 1998.

We selected for strains of *H. armigera* resistant to Bt. Two laboratory and two field generated resistant strains have been selected, over several generations, in the laboratory and tested with diet incorporation bioassays of Cry1Ac as MVP and Bt leaf material. Most strains showed resistance to both sources of Bt, with the field strains showing the highest resistance, of over 20 fold, compared to the susceptible strain.

Preliminary genetic studies were carried out on two strains, by Dr David Heckel, during his sabbatical, in preparation for developing a genetic map of *H. armigera* chromosomes.