CSE73C Executive Summary

## Plain English Summary

Resistance to both insecticides and Cry1Ac in Bt cotton is an ongoing concern in the management of *Helicoverpa armigera* in the Australian cotton industry. While management strategies for insecticides have been successful in slowing down the rate at which resistance has developed, the industry uses more insecticide to control *H. armigera* today than it did ten years ago. This, combined with the reduced bioefficacy of mature Bt cotton plants, means that there is an ongoing need to consider the resilience of the resistance management strategy in place for Bt cotton.

This project has examined the genetics of Bt resistance in *H. armigera.* This involved selecting for a resistant strain of insects and then seeing how many genes are contributing significantly to resistance and the relative contribution of each gene. Our work is linked closely with Dr Akhurst's project on the mechanisms of resistance. Such combined knowledge allows interpretation of the outcomes of resistance management strategies imposed on the cotton industry and their subsequent refinement to improve their effectiveness while reducing the cost to the grower.

A number of approaches for selecting a resistant strain were tried by various research groups. Five strains showing varying levels of resistance were obtained. This work concentrated on only one of these, the Bt resistant strain (called BX) from Dr Akhurst, because it showed high levels of resistance in bioassays and on Bt cotton. This strain was derived originally from field-collected material.

Genetic studies involved traditional crosses of the different strains and their analysis using dose-response bioassays. Results to date suggest that the BX resistant strain seems to be fixed for a major resistance gene that in heterozygotes is intermediate in expression between the susceptible (SS) and fully resistant (RR) individuals. The heterozgyous individuals (RS) represent the way the gene would most commonly exist in the field. The heterozygous and resistant strains showed significant survival on Bt cotton when compared with the susceptible strain.

Results from such studies can be ambiguous, so work on the genetic mapping of the putative genes, using the techniques developed by Dr David Heckel (Melbourne University) in an earlier CRDC-funded project has begun. Together these approaches will allow careful analysis of resistance. Genetic mapping techniques have been established with the help of Dr Heckel and Dr Wes Keys (CSIRO Plant Industry) after modifications, to utilise the newer, faster and safer technology of the DNA sequencer. DNA has been extracted from a Bt resistant strain and is being used to fine tune the AFLP mapping method. Using Dr Heckel's approach, we have begun the mapping of Bt resistance in *H. armigera* and this work will continue in a new joint project with Dr Heckel.

The research is a very important contribution to the TIMS strategy for Bt cotton. In particular, the results call into question the assumption that Bt resistance will be recessive because at this stage they suggest an incompletely dominant gene, which means resistance to Bt could develop faster in the field than originally thought.