## SUMMARISED REPORT

Modern molecular genetic techniques are used to examine *Helicoverpa armigera* for variation amongst individuals from different geographical locations around Australia. The prime objective has been to assess population structure: to find regionally diagnostic variation that will allow us, indirectly, to estimate the magnitude, direction and timing of movement patterns of these pest moths. This information would be valuable to the ecologists in their efforts to better predict moth movement into cropping areas and hence improve control. It would also help in planning strategies to minimise the spread of insecticide resistance and thus benefit the Cotton Industry.

Australia-wide mitochondrial DNA variation in *H. armigera* indicated a relatively homogeneous population, indicative of a species with high levels of mobility and gene exchange. Although some differentiation occurred in frequency of genetic types between samples from the south-east and both north-east and north-west Australia this was not at a magnitude that would be valuable or practical for estimating movement of moths into or out of the south-eastern area. Another genetic marker, a para sodium channel gene revealed a small but significant difference in frequency of genetic types between a Namoi Valley sample and one from St George, indicating some restriction to movement between these sites. Three hypervariable microsatellite loci are currently being sampled for geographic variation by our CRDC scholar, Ms Merrin Spackman, and the data will be reported later in 1996 when she submits her PhD thesis. Thus there are several genetic markers now known, including some described by Daly and Gregg (1985), that each show a level of regional differentiation. Each marker alone providing insufficient differentiation to be useful for the ecologists.

In future a multi-locus sampling programme (sampling individual moths from different localities for several genetic markers) will be the approach to use. The techniques and genetic markers are now available. To test the approach an intense sampling effort will be required in an important, though relatively isolated, cropping area. This would need to be carried out in close collaboration with ecologists and with accompanying ecological and climatic data. Exactly the same methodologies and approach will be valuable for *H. punctigera*.

By the end of 1996 we will know if the three microsatellite loci also hold promise for helping to diagnose moth origins. We will also report whether or not the DNA sequence of the mtDNA fragment used in our studies will be of taxonomic value for helping to sort out the Australian Heliothines (a recent side benefit of our work that is being carried out in collaboration with Dr Marcus Matthews). This will be of benefit to the Cotton Industry because it would speed up future trials of new insecticides and pest control biocides

This project has laid valuable technique foundations for future Helicoverpa research. The techniques can be used to study inbreeding and mating patterns, genetics of migration and in linkage and gene mapping studies. Such information will be valuable for understanding insecticide resistance genetics and mechanisms, that will inturn help in programmes that are designed to prevent development of resistance, or help decrease the spread of resistance.