

Summary:

The significant threat of *Heliothis* on the Darling Downs and elsewhere was demonstrated by the serious damage suffered by growers in the 1997/98/99 season. At present there is a need for a Management Strategy that considers the *Heliothis* problem at a population level across the entire Darling Downs.

The aim of this study was to construct a microsatellite library for the pest moth *Heliothis armigera* and to use this library to investigate temporal shifts in population structure. Specifically, the aim of the study was to determine whether 1998-1999 seasonal infestations of *H. armigera* in southwestern Queensland were the result of migration from an external source or were derived from previous populations. A secondary aim was to investigate the relationship between larval survivorship and source population.

Genotyping using microsatellite loci provides several advantages over other methods of measuring genetic variation in studies directed at determining relatedness between individuals and populations. These include high frequency of loci and occurrence in regions of low recombination; short length of sequences, which facilitates genotyping by automated techniques such as polymerase chain reaction (PCR); the ability to obtain results with small quantities of DNA; high levels of polymorphism which enables detection of small genetic variation; provides the highest probability of parentage determination and conservation of repeat sequences across related taxa, allowing use of primers developed for *H. armigera* to be used in *H. punctigera*.