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Poster paper

Genetic diversity among populations of soldier flies

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Soldier flies are a serious pest in several regions of the industry (Figure 1). Because they were often considered a localised problem, their impact has largely gone unrecognised. However, in recent years there has been a concerted research effort to gain more understanding of the biology of the pest and to develop better management solutions.

Figure 1. From left to right, soldier fly larvae of two sizes, a male and a female collected from Finch Hatton, Queensland. The scale bar represents 10 mm. (Picture by Manda Khudhir).

One important issue that needs resolving is the true species makeup of the soldier fly population in the Australian sugar industry. It has been assumed that there were two main species, *Inopus rubriceps* (sugarcane soldier fly) and *Inopus flavus* (yellow soldier fly). We undertook a pilot study where soldier fly larvae from around Queensland were collected and subjected to a technique known as DNA barcoding. Barcoding uses the DNA sequence of the mitochondrial cytochrome oxidase I (COI) gene to make identifications and to resolve genetic relationships among organisms. It is a well-established technique for identifying insects and has been used for other insect pests in the Australian sugar industry.

Larvae were collected from the Atherton Tablelands, Ayr, the Central region (Habana, Finch Hatton, Hay Point and Carmila) and the Southern region (Bingera, Gooburrum, South Kolan, Maryborough and Cordalba) between September 2017 and June 2018. They were sent to the SRA laboratory in Brisbane where DNA was extracted from 100 individual larvae and the COI gene amplified by PCR, then sequenced. Sequences were aligned using ClustalW and phylogenetic trees were generated using various models.

Phylogenetic results showed that there were five major genetic groups of soldier fly in Queensland cane fields, not two as expected. Figure 2 shows a phylogenetic tree generated from a subset of the collection (up to five larvae per location) using the Jukes-Cantor/UPGMA tree building models with 1000 bootstraps. While different phylogenetic models generated different tree-branching patterns, there were always five clusters. The clustering pattern was strongly linked to the geographic location for all larvae except for those collected from the Atherton Tablelands.

Adult soldier flies are currently in the process of being formally identified by an expert taxonomist. Their barcodes will then be included in the population study to complete the work.

Key words Soldier fly, cytochrome oxidase I, DNA barcode, *Inopus rubriceps*, *Inopus flavus*

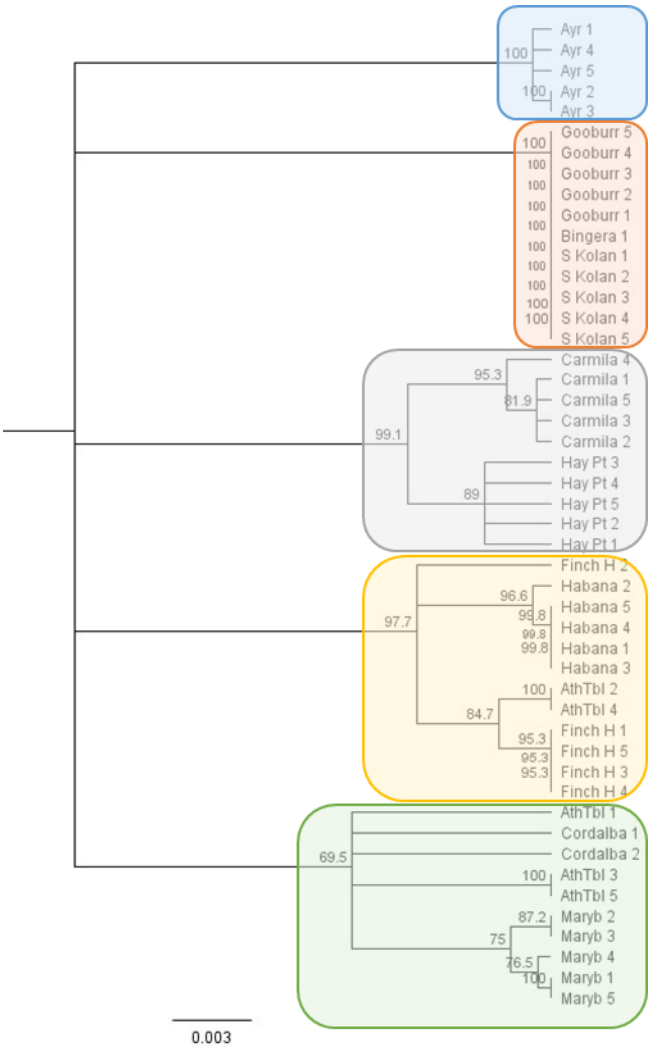

Figure 2. Phylogenetic tree of selected soldier fly larvae collected from 11 locations in Queensland. Mitochondrial cytochrome oxidase I gene sequences generated from 48 larvae were aligned using ClustalW. This tree was generated using Jukes-Cantor/UPGMA models with 1000 bootstraps. Larvae grouped into five DNA clusters representing, from top to bottom, the Burdekin (Ayr); the Southern districts of Gooburrum, Bingera and South Kolan; the Central districts of Carmila and Hay Point; the Central districts of Finch Hatton and Habana; and lastly the Southern districts of Maryborough and Cordalba. Only samples from the Atherton Tablelands were split across two clusters.