Final report

CRDC code: RRDP2108

Final report – Public Summary only

Project title:

iMapPESTS: Assess biosecurity risk for Bt alleles & RMP implication

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Project code:

RRDP2108 – (HIA reference ST16010 (CON-002037))

Date:

3 May 2022

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Funding statement:

This project is part of iMapPESTS, which is led by Hort Innovation, through funding from the Australian Government Department of Agriculture, Water and the Environment as part of its Rural R&D for Profit program, with contributions from 17 partner organisations, including the Cotton Research and Development Corporation.

Publishing details:

ISBN <Hort Innovation to add>

Published and distributed by: Horticulture Innovation Australia Limited
ABN 71 602100149

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North Sydney NSW 2060

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Public summary

International trade represents an important pathway for the accidental introductions of alien species that threaten primary industries' (e.g., Australia's cotton industry's) resistance management program (RMP). This is especially important when the target pest is also a cosmopolitan species, and resistant genotypes selected elsewhere could rapidly spread across new geographic ranges. Recent high-profile introductions of noctuid pests into the Americas (i.e., *Helicoverpa armigera*) and the Old World/Oceania (i.e., *Spodoptera frugiperda*), are examples highlighting the importance of trade-assisted pest spread. *Helicoverpa armigera* also represents a significant biosecurity threat to Australia's cotton industry because of endemic Australian populations, and of known resistance to different *Bacillus thuringiensis* (Bt) toxins, including dominant resistances to the Cry1Ac toxin reported from northern Chinese populations.

To understand threats posed by foreign *H. armigera* via global trade pathways, it is necessary to first assess the frequency and species status of specimens from Australia's pre-border inspections of imported agricultural/live-plant commodities, and to develop the best practice for detecting known resistance alleles. Various scenarios addressing the implications to industry of accidental introductions of a dominant resistant allele and appropriate management strategies can be assessed by modelling and computer simulations. Finally, the relevant RMP should be reviewed and compared with other countries' RMP, especially from where the dominant resistant genes originated from. To date, these aspects remained unexplored by Australia's cotton industry.

We address these issues through: **(i)** analysis of historical pre-border pest interception data to identify patterns and species status, and to identify potential factors that limited the use of interception data to bolster our primary industry's biosecurity plans; **(ii)** apply molecular approaches to confirm the species status, and to characterise known Cry1Ac dominant resistance genes; **(iii)** using a computer simulation approach to provide a preliminary understanding of the speed of resistance allele fixation in the Australian cropping landscape with different refugia and dominance scenarios, thereby enabling policy makers to better comprehend and identify potential difficulties associated with the current RMP, and **(iv)** undertaking a comprehensive review comparing Australia's and China's cotton industries' Bt RMP to enable recommendations to be made to prepare for the accidental introduction of dominant Cry1Ac resistance genes. This work will contribute to Australia's cotton industry biosecurity preparedness, and protect growers' income and the transgene Bt technology.

Analyses of historical interceptions and trade data identified challenges relating to species identification (Appendix I). Molecular diagnostics via DNA-barcoding (Appendix II) delivered a comprehensive DNA database for global *H. armigera* populations (Appendix III) to accurately identify and assist with differentiating between endemic and non-native individuals of this high priority agricultural pest including from imported live plant-related commodities (Appendix IV). The whole genome sequencing approach represents a valuable tool-set to obtain large volume genome data and enabled surveys of the Tetraspanin and E-cadherin genes of intercepted *H. armigera* for known dominant Cry1Ac resistance-associated mutations (Appendix V). A review of current Bt RMP practice and simulation modelling assessments enabled six recommendations to prepare the cotton industry to the dominant Cry1Ac resistant genes (Appendix VI).