CRDC ID: CSE1801



CRDC ID: CSE1801 Summary Only

**Project Title:** Application of molecular tools to monitoring for resistance alleles in

Helicoverpa spp.

## Confidential or for public release?

**Recognition of support:** The Research Provider CSIRO acknowledges the financial assistance of the Cotton Research and Development Corporation Bayer in order to undertake this project.

## Part 1 – Contact Details & Submission Checklist

Principal Researcher: Dr. Amanda Padovan

**Organisation:** CSIRO **Ph:** 02 62464156

**E-mail:** Amanda.padovan@csiro.au

Supervisor: Dr Tom Walsh, Principal Research Scientist

**Organisation:** CSIRO **Ph:** 02 62464083

**E-mail:** tom.walsh@csiro.au

Researcher 2: Dr Sharon Downes, Senior Principal Research Scientist

**Organisation:** CSIRO **Ph:** 02 6799 1576

**E-mail:** Sharon.downes@csiro.au

#### Submission checklist.

Please ensure all documentation has been completed and included with this final report:

□ Final report template (this document)

☐ Final financial report

□ PDF of all journal articles (for CRDC's records)

**Signature of Research Provider Representative** 

**Date submitted:** 07/09/2021

Apr2021 template 1 of 8

# Part 4 — Summary for public release

This summary is designed to provide a short overview of the project for all interested parties. It will be published on Inside Cotton, CRDC's digital repository, along with the full final report (if suitable for public release). The summary may also be published on grow<sup>AG.</sup>, a collaborative platform that showcases Australian agrifood research, development, and extension projects that are current or have been completed since 1 July 2018. Please complete all fields, ensuring that this exceeds no more than two pages.

Project title:	Error! Reference source not found.	
Project details:	CRDC project ID:	Error! Reference source not found.
	CRDC goal:	Increase productivity and profitability on cotton farms
	CRDC key focus area:	1.3 Protection from biotic threats and environmental stresses
	Principal researcher:	Dr Amanda Padovan and Dr Tom Walsh. CSIRO
	Organisation:	Error! Reference source not found.
	Start date:	July 2017
	End date:	Aug 2021
Objectives	<ul> <li>To develop and test a suite of molecular tools to test for known Bt resistance alleles</li> <li>To use molecular approaches to predict the impact of DNA variations on Bt resistance in sequenced individuals</li> </ul>	
Background	Insecticidal cotton expressing Bt toxins is highly valued by growers. The introduction of insecticidal transgenic varieties into the Australian cotton market by Monsanto (now Bayer) has allowed the industry to reduce its pesticide use by more than 89 percent and is arguably the most important technology the industry uses. However, resistance in the targets Helicoverpa spp. is a great threat to the continued availability and efficacy of Bollgard III cotton, an issue recognised by both the industry and Bayer which supplies all the Bt cotton in Australia.	
	to use molecular methods to identify of relevant Bt resistance alleles in <i>H.</i> view to developing a cost effective h monitoring. The primary aim is to primonitoring of the success of Bt resis Molecular tools do not require live in a faster, more efficient manner and The assays can also be performed or	igh throughout technique for ovide knowledge that will allow a closer tance management in Australia. Insect bioassays and can be performed in do not require any rearing of insects. It will be known resistance mechanisms as well

Apr2021 template 6 of 8

## Confidential

Research	In this project we undertook molecular analysis of laboratory and field	
activities	collected Helicoverpa sp. to specifically examine their Bt resistance alleles.	
	This involved a number of different molecular approaches from individual	
	amplification of specific genes and alleles to whole genome sequencing.	
0		
Outputs	In this work we have developed several different methods for identifying Bt resistant alleles.	
	1. We can identify known resistant alleles by allele specific PCR. This can be on an individual insect basis or this approach has been demonstrated in pooled DNA.	
	2. We can deploy sophisticated capture tools to identify known resistance	
	alleles and potentially predict unknown resistance alleles in known genes.	
	We can use whole genome sequencing to capture all the variation and	
	map this back to our reference genome. This not only identifies all the	
	known resistance alleles and allows the prediction of potential resistance	
	alleles in known genes, it also captures all the available information in the	
	genome.	
Impacts	The advantages of a molecular approach are:	
-		
	1. It can dramatically reduce the cost per individual for a resistance allele	
	detection.	
	It does not rely on live insects and can be performed on trap caught	
	material as well as parallel and validate bioassay results.	
	· · · · · · · · · · · · · · · · · · ·	
	3. The whole genome approach also offers the possibility of building a	
	database of samples with genomics information fixed in both time and space	
	which allows the interrogation of these data at any point into the future.	
	While a molecular approach offers an extremely powerful set of methods	
	for identifying and quantifying resistance alleles, it remains the case that	
	phenotypes to validate molecular results are vitally important. The	
	molecular tools described herein are a tool that can be used to shed more	
	light on the resistance situation in Australia can complement a phenotype	
	based resistance monitoring program.	
War.	0. 0	
Key	A number of publications are ongoing but through the course of the pdf we	
publications	have developed associated publications with collaborators extending the	
	same approach to the newly invaded Fall Armyworm, Spodoptera	
	frugiperda.	
	Guan, F., Zhang, J., Shen, H., Wang, X., <b>Padovan, A., Walsh, T.K.,</b> Tay, W.T.,	
	Gordon, K.H.J., James, W., Czepak, C., Otim, M.H., Kachigamba, D. and Wu,	
	Y. (2021), Whole-genome sequencing to detect mutations associated with	
	resistance to insecticides and Bt proteins in Spodoptera frugiperda. Insect	
	Science, 28: 627-638. https://doi.org/10.1111/1744-7917.12838	
	Science, 20. 027-030. https://doi.018/10.1111/1/44-7917.12636	
	WT Tay, R Rane, <b>A Padovan, T Walsh</b> , S Elfekih, S Downes, K Nam, E	
	· · · · · · · · · · · · · · · · · · ·	
	d'Alençon, J Zhang, Y Wu, N Nègre, D Kunz, DJ Kriticos, C Czepak, M Otim,	

Apr2021 template 7 of 8

### Confidential

KHJ Gordon. Global FAW population genomic signature supports complex introduction events across the Old World. bioRxiv 2020.06.12.147660;

Molecular resistance monitoring in Helicoverpa armigera and Helicoverpa punctigera in Australian cotton fields. Amanda Padovan. Australia Cotton Grower 2020. <a href="https://www.cottongrower.com.au/read/17#42">https://www.cottongrower.com.au/read/17#42</a>

Apr2021 template 8 of 8