Posters from Centre Forum 2026

Page	Presenter	Project Title	Project Summary
3	Dr Mohammad Jahanbakht 	Remote sensing of priority weeds in sugarcane	A pilot study that will focus on remote sensing in one cane district and up to five troublesome weed species. The first part of the project will require ground truthing and AI training.
4	Dr Elle Saber 	Developing robust proof-of-freedom surveillance systems for Australia	Seeks to refine statistical models that can be incorporated into surveillance guidelines for governments and industry to plan area freedom surveillance.
5	Dr Matt Nurse 	Reducing harm from misinformation in plant biosecurity	Projects in the areas of 1. Misinformation in plant biosecurity, 2. Adoption within the sector, 3. Adoption outside the sector, and 4. Cultural infrastructure for mission science.
6	Charlie Morgan on behalf of Dr Rachel Tulloch	Determining provenance of biosecurity pests using new genomic technologies	Aims to use undertake genome profiling of a high priority pest species and determine the provenance of current and future pest species of importance to Australia.
7	Sylvia Jepkemboi 	Transformational molecular approaches for forest pests and pathogens	Studies invasion biology of established exotic forestry pests to investigate how populations have changed over time.
8	Shiron Thalagala 	Smart plant biosecurity surveillance of airborne fungal pathogens using machine learning	Focuses on a smart biosecurity surveillance network composed of novel rotating-arm impaction samplers and implements computer vision to detect known plant pathogens and unknown exotic threats.
9	Guillia de Freitas Rossi 	Taxonomy and biology of Euwallacea shot hole borer beetles	Takes an integrative taxonomic approach to test hypotheses for seven species of Euwallacea, including the E. fornicatus complex, for an Australian context.
10	Shimi Jose 	Natural and synthetic antibodies to identify spider mite eggs during import	Aims to develop a new and novel method for identifying whether eggs found on fresh produce belong to the Tetranychidae family.
11	Jowell El-Darwiche 	Identifying fruit fly biomarkers using mass spectrometry	Explores the use of MALDI-ToF mass spectrometry to differentiate species and populations of fruit fly.
12	Lavi Singh 	Molecular characterisation of rust pathogens	Aims to gain insights into the infection mechanisms of sugarcane brown rust pathogen by developing complementary genomic and transcriptomic resources.
13	Vida Burger 	Epidemiology of Botryosphaeriaceae associated with mango dieback	Explores infection biology of Lasiodiplodia species and resulting disease expression in mango.
14	Yilin Bai 	Investigating scale and mealybug control in Australian viticulture	Addresses key knowledge gaps through a fundamental investigation of scale and mealybug biology in the context of viticulture.

Page	Presenter	Project Title	Project Summary
15	Jessica Kriticos 	Ranking priority plant pest and diseases and their preparedness activities	Supports Australia's preparedness for an emergency response to exotic plant pests and diseases by developing robust and scientifically valid models for ranking priority pest lists and preparedness activities.
16	Yufan Zheng 	Data driven decision models for forest biosecurity	Catalogues the breadth of forest pest surveillance and diagnostic data being collected through targeted and general biosecurity activities at regional and national levels.
17	Viviana Aya Vargas 	Exotic moth borers – Conservation biocontrol	Targets three high-risk exotic Lepidopteran moth borer genera (*Chilo*, *Sesamia* and *Scirpophaga*) along with the only known endemic moth borer (*Bathytricha truncata*) of sugarcane.
18	Alphonsa Baby 	Target gene discovery for locust control	Investigates the transcriptional profile divergences between solitary and gregarious phases of Australian Plague Locust and identifies key genes and pathways for the development of control strategies.
19	Aphrika Gregson 	Strategies for building and maintaining social licence during a biosecurity outbreak	Aims to identify strategies against misinformation in plant biosecurity.
20	Esteve Mesen Porras 	Fall armyworm population genomics and biocontrol options	Aims to apply population genomics to identify and compare establishment dynamics of fall armyworm and the likely next emerging pest threat in the related species: African cotton leafworm.
21	Bethany Perry 	Invasive snails as vectors of pathogens and parasites	Focuses on different snail species that are commonly intercepted at the borders and that have at least one current incursion to determine their parasite and pathogen loads in their country of origin, when intercepted and once introduced in Australia.
22	Xin Zhu 	Absence-aware generalised referring expression comprehension for agriculture	Aims to train an absence-aware head using a dataset with hard negatives leading to stronger rejection ability that could be applied to fruit counting, weed mapping and plant disease surveillance.
23	Addam Corallo 	Water sampling for detection of vegetable pathogens	Aims to develop surveillance methodology to detect and diagnose pathogen(s) of vegetable crops in drain water and irrigation systems on farm to inform day to day management options and biosecurity response strategies.
24	Stephanie Morgan 	Plant disease diagnostics in tissue culture	Aims to develop a reliable plant disease assay that is directly applicable to tissue culture material. The focus will be on viruses and bacteria that are non-culturable or very challenging to culture.
25	Claudio Cipriani 	Resolving the pumpkin fruit fly complex	Provides a new taxonomic hypothesis for the 21 species-strong *Zeugodacus tau* complex using molecular, morphological, and biological evidence, allowing for improved species delimitation.
26	Samantha Whitling 	Molecular characterisation of rust pathogens	Investigates the infection biology, genome biology, and population genetics of *Puccinia kuehnii,* the causative agent of sugarcane orange rust, to address fundamental questions around pathogen biology.

Remote sensing of priority weeds in sugarcane

Mohammad Jahanbakht[1,2,3] and Mostafa Rahimiazghadi[1,2,3]

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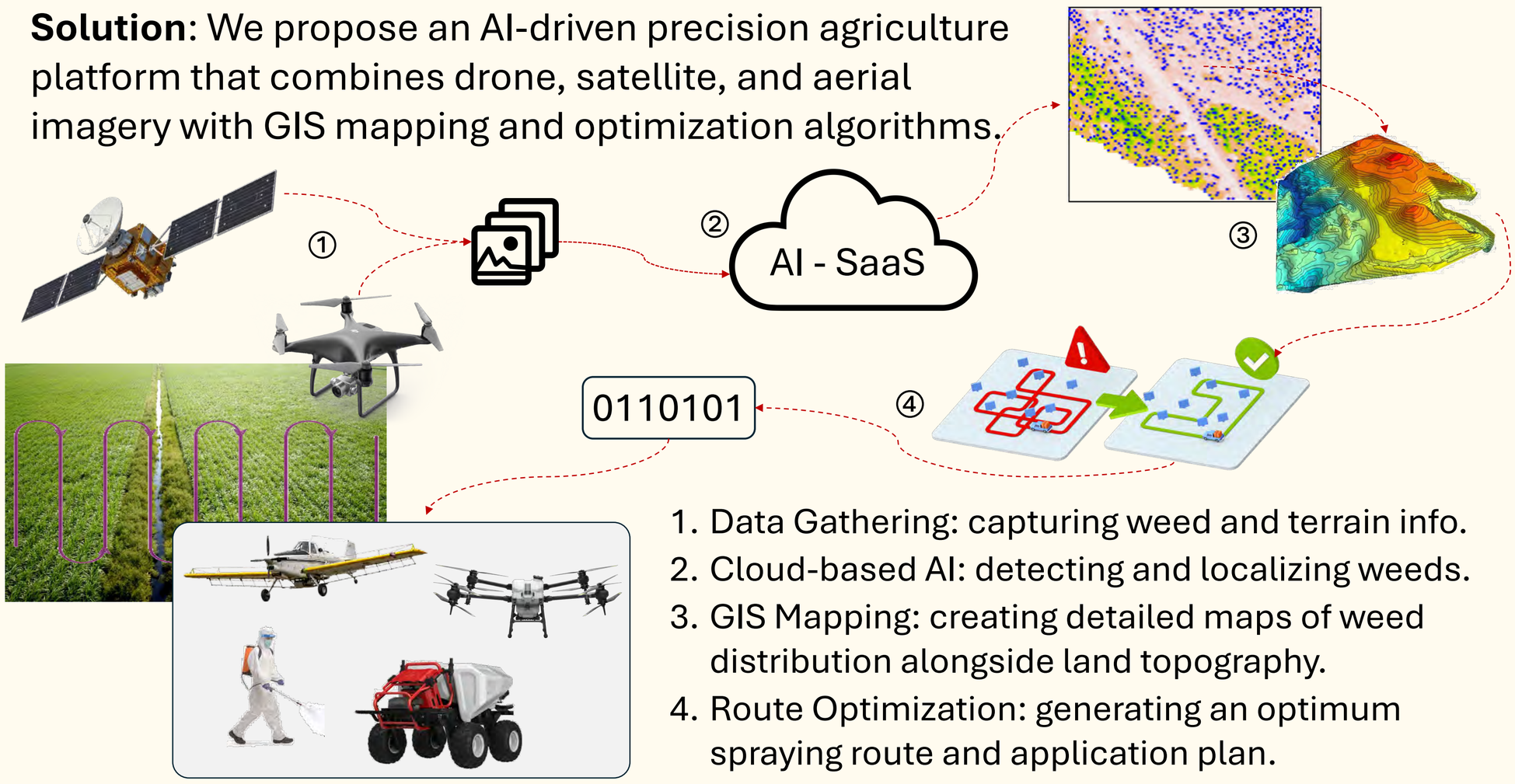
[2] Centre for AI and Data Science Innovation, James Cook University, Townsville, QLD, Australia
[3] Australian Research Council Training Centre in Plant Biosecurity, Australia

Problem: Traditional weed spraying on large sugar farms is inefficient, costly, and environmentally damaging because it applies chemicals broadly.

- Blanket spraying wastes herbicides and increases chemical use.
- Labor, fuel, and operational costs are unnecessarily high.
- Non-target vegetation and waterways can be harmed by overspray.
- Manual surveying and spraying are slow and prone to human error.

Solution: We propose an AI-driven precision agriculture platform that combines drone, satellite, and aerial imagery with GIS mapping and optimization algorithms.

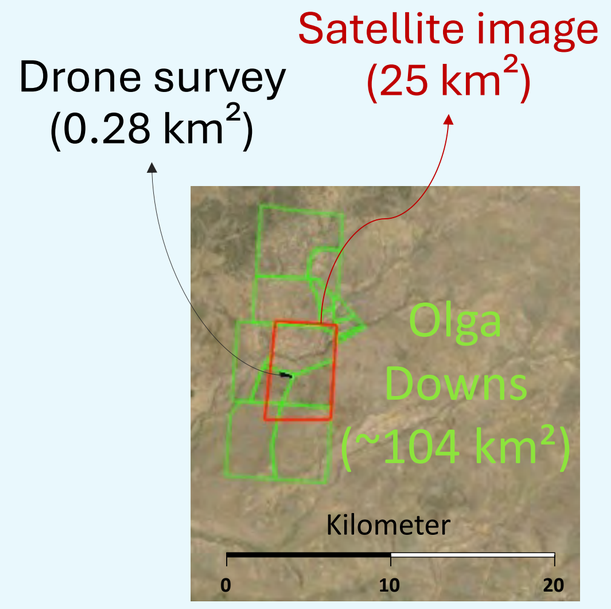


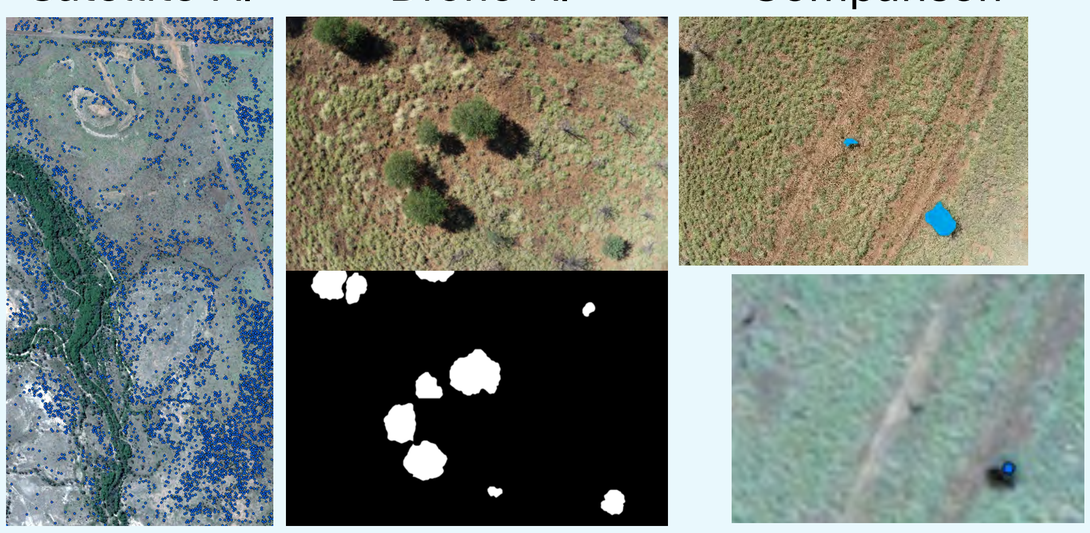
1. Data Gathering: capturing weed and terrain info.
2. Cloud-based AI: detecting and localizing weeds.
3. GIS Mapping: creating detailed maps of weed distribution alongside land topography.
4. Route Optimization: generating an optimum spraying route and application plan.

By focusing treatment only where needed, this solution reduces chemical use, operational costs, and environmental impact while improving efficiency and scalability for large landholders.

Case Study: At Olga Downs, our AI system successfully mapped Prickly Acacia across a 25 km^2 study area.

- More than 83,500 Prickly Acacia trees were detected.
- Optimized treatment routes were generated.





Parameter	Scenario A (car)	Scenario B (drone)
Workdays count	34	21
Travelled distance	1,275.4 km	1,275.4 km
CO_2 emission	390.79 kg	292.22 kg
Total cost	$14,759.3	$12,208.2
• Labour cost	$8,148.9	$6,945.8
• Chemical cost	$2,943.9	$2,943.9
• Power/fuel cost	$266.4	$218.5
• admin cost	$3,400.0	$2,100.0

It showed that a drone-based spreading could reduce project duration by 38% and lower operational costs by 18% compared with traditional vehicle-based methods.

ARC Training Centre in Plant Biosecurity

Confidence in what?
The statistical foundations of pest freedom surveys

Elle Saber[1]
Advised by Eric Stone[1]**, Mark Stanaway**[2]
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Acknowledgement: This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

What is the confidence level for pest surveillance?

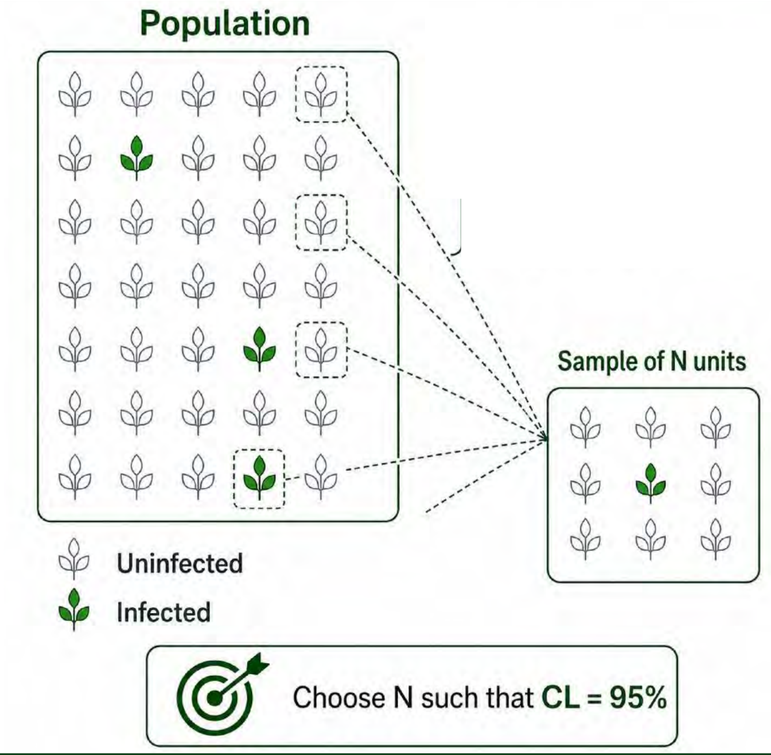
The confidence level (CL) for a surveillance system is:

$$CL = 1 - (1 - \mathrm{DP} \times \mathrm{MeSe})^{N}$$

Where:
$MeSe$ = method sensitivity
DP = design prevalence
N = sample size

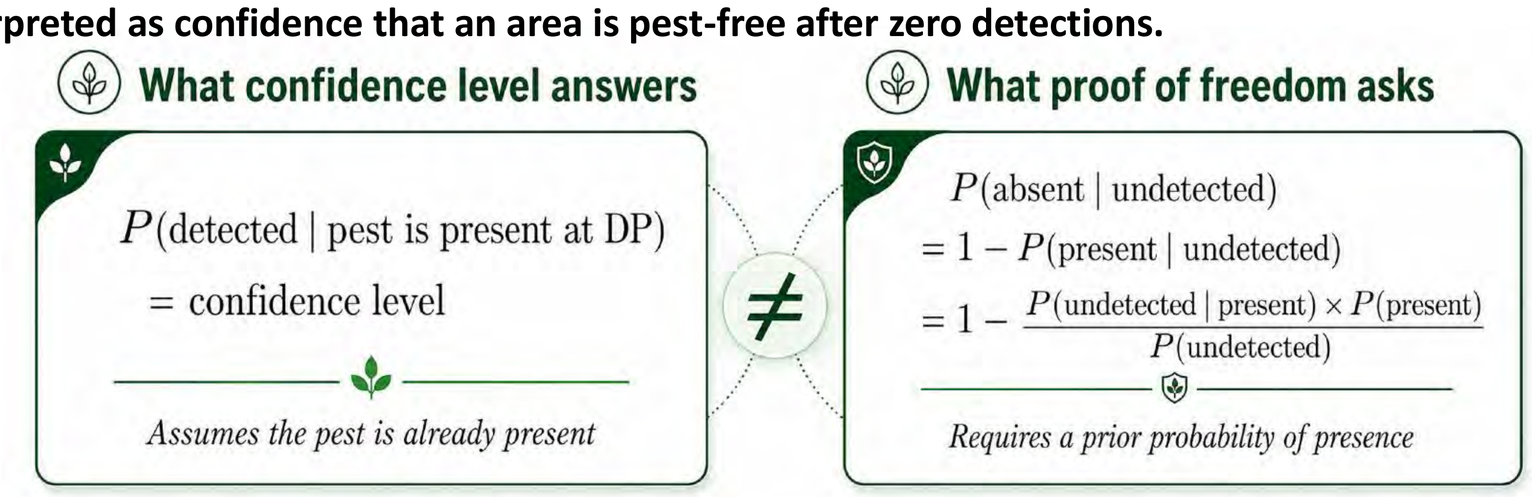
CL is the probability of detecting the pest at least once, if it is present at the design prevalence.

In practice, surveillance is often designed by choosing **N** so that **CL reaches a target such as 95%**.



The common error in interpreting this confidence level:

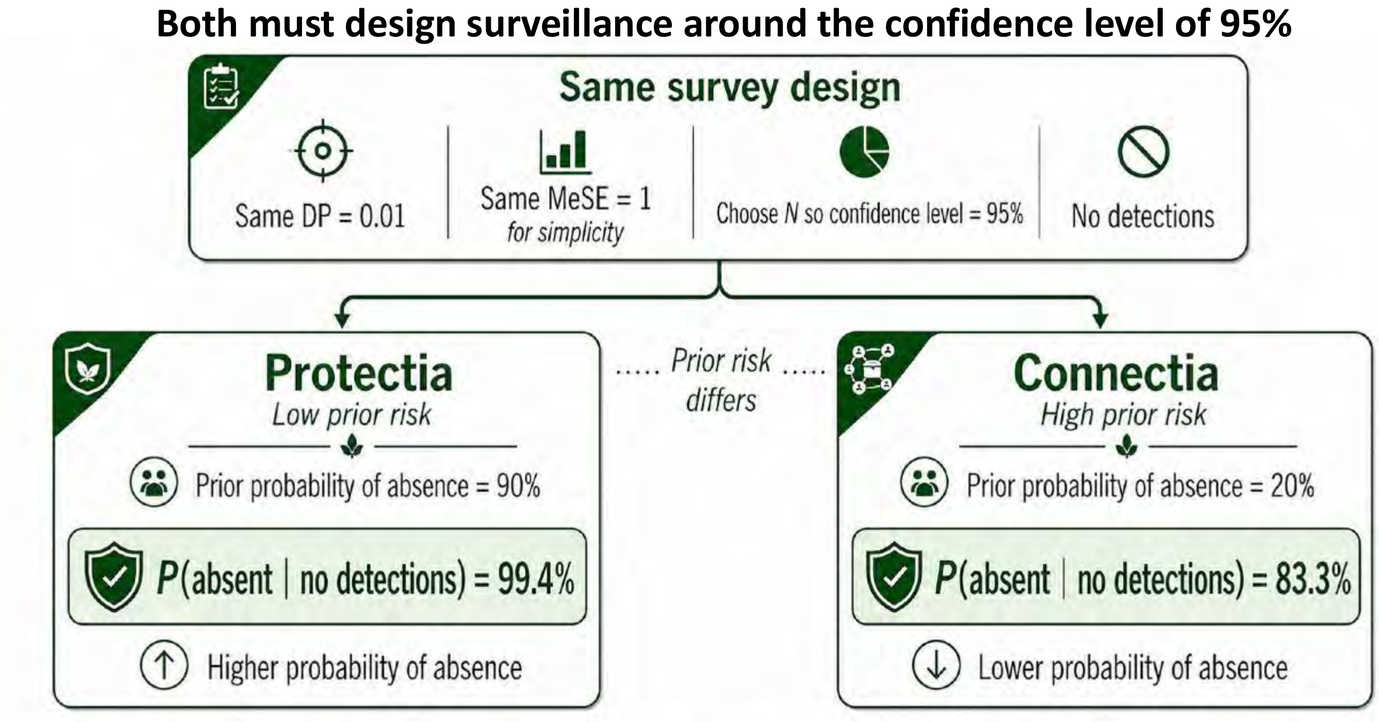
The confidence level is widely used to design surveys intended to support claims of pest absence. This quantity is often interpreted as confidence that an area is pest-free after zero detections.



Confidence level assumes the pest is present and asks whether surveillance would detect it.
Proof of freedom asks what the surveillance result implies about absence.

Why does this matter?

Imagine two countries: *Protectia* low prior probability of presence and *Connectia* a much higher prior probability. Both must design surveillance around the confidence level of 95%



A fixed confidence level standardises detection probability, not confidence in pest absence

What should we do instead?

Clear language

Call confidence level what it is:
detection probability

Better inference

Estimate what matters:
$P(\text{absent} \mid \text{surveillance data, prior risk, space, spread})$

The problem is not the formula. The problem is what we say the formula means

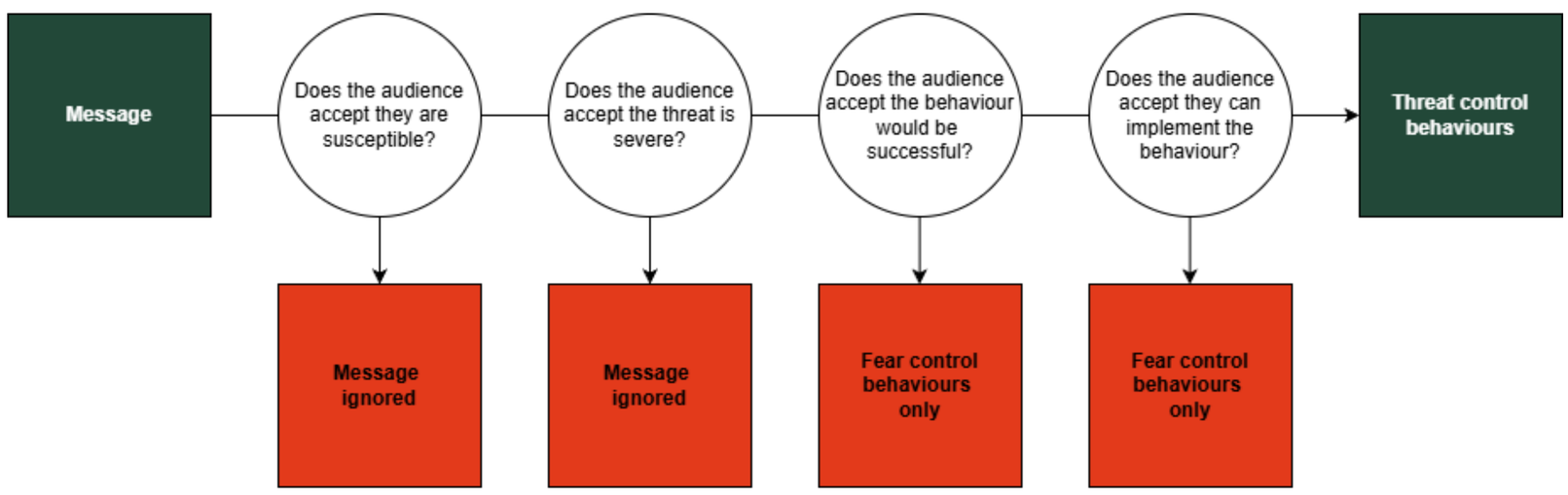
Fear appeals in biosecurity communication

Dr Matthew Nurse

The project

Public health campaigns often use a structured approach to fear appeals. They use messages that highlight the audience's susceptibility to a threat and the consequences it may cause, before convincing them that a recommended action will work and that they are capable of carrying it out. This theory-based approach is designed to make sure people are guided into useful behaviours, rather than simply dismissing the warning to manage their own anxiety.

Simplified model of the extended parallel process model (Witte, 1992)



Two research questions

- RQ1 (practical): Do fear appeals work in biosecurity contexts?
- RQ2 (theory): Does it matter what type of action is being recommended?

Risk control	Risk mitigation
Stopping the threat before it takes hold	Reducing harm once the threat is already present
Example: Reporting a suspected exotic plant pathogen to authorities	Example: Applying treatment or hygiene measures on an affected property

I need your help

I'm designing realistic scenarios for study participants to respond to. I need examples from Australian plant biosecurity where people are asked to take a control or a mitigation action.

- Can you give me an example of a **control action scenario**
- Can you give me an example of a **mitigation action scenario**.
- Are there cases where it's genuinely hard to classify or where the required action shifts as a situation develops?

Witte, K. (1992). Putting the fear back into fear appeals: The extended parallel process model. *Communication Monographs*, *59*(4), 329–349. https://doi.org/10.1080/03637759209376276

Email me via this QR code. I'd love to know what you think.

Australian National University

ARC Training Centre in Plant Biosecurity

Tracing invasive pests using genomics to strengthen Australia's biosecurity

Understanding where pests come from. Supporting smarter, faster responses.

Rachel Tulloch[1],[2], **Dianne Gleeson**[1], **Alejandro Trujillo Gonzalez**[1], **Mike Elias**[3]

[1] University of Canberra, Australia
[2] ARC Training Centre for Plant Biosecurity, Australia
[3] Department of Agriculture, Fisheries and Forestry (DAFF), Australia

THE PROBLEM

Invasive pests cost Australia billions each year and threaten our environment, agriculture and economy.

Limited resolution of provenance using current approaches
Restricts accurate assignment of incursions and informed response strategies

Lack of standardised detection thresholds across laboratories.
Limits comparability and confidence in results

Delayed or ineffective responses increase spread and costs

PROJECT GOALS

Use genomics to map origin, inform decisions, and standardise detection.

Build genomic reference datasets
To map pest distributions across native and invaded ranges

Develop decision-support frameworks
To translate genomic data into origin assignment and response decisions

Enable cross-laboratory reproducibility
Through collaboration with DAFF and state agencies to standardise detection methods

DETERMINING PROVENANCE

Sampling & DNA Extraction
Field or historical samples

qPCR
Species Confirmation

Sequencing
Mitochondrial and genome-wide SNPs

SNP Panel
Cost-effective genotyping for assignment

Origin & Spread
Reconstruct population structure and source

PROOF OF CONCEPT

Green Vegetable Bug (*Nezara viridula*)
Invasive sap-sucking pest impacting multiple Australian agricultural systems, including tomatoes, beans and macadamias

PILOT STUDY

40 historical *N. viridula* and
40 closely related species from local and international collections

APPLIED OUTCOMES AND EXPERT INPUT

Targeted Surveillance & Response
Using provenance to identify source pathways and guide action

Confidence to act on results
What level of evidence is needed to support decisions?

Validation across laboratories
Interest in participating in species identification ring trial

INTERESTED IN COLLABORATING?
SCAN THE QR CODE TO *express your interest!*

Dr Rachel Tulloch
Rachel.Tulloch@canberra.edu.au
University of Canberra
ARC Training Centre for Plant Biosecurity

SPECIES DETECTION RING TRIAL

WHAT IS PROVIDED

qPCR Assay
Primer & Probe for species detection

Concentration Series
A range of DNA concentrations

Calibrated Reference Materials
Prediluted standard curves

WHAT IS ASSESSED

Detection Sensitivity
Limits of detection & ability to detect low levels of target DNA

Consistency Across Laboratories

Reproducibility of Results

Australian Government
Department of Agriculture, Fisheries and Forestry

Australian Government
Australian Research Council

UNIVERSITY OF CANBERRA

ARC Training Centre in Plant Biosecurity

Transformational molecular approaches for forest pests and pathogens

Sylvia Jepkemboi[1,2], Supervisors: Dianne Gleeson[1,2], Alejandro Trujillo-González[1,2] , Angus Carnegie[3], Conrad Trollip[3]

1. Institute of Applied Ecology, University of Canberra
2. ARC Training Centre in Plant Biosecurity
3. NSW Department of Primary Industries and Regional Development

Background

- Forest pests and pathogens are a threat to forest health, particularly under increasing environmental stress
- Study system: Five spined bark beetle- *Ips grandicollis* (Eichoff)
- *I. grandicollis* is an invasive bark beetle of pine trees, established in Australia for over 80 years
- It is widespread across Australian plantations, dominated by *Pinus radiata*
- It causes tree mortality in presence of stressors like drought and fire, and transmits blue-stain fungi

Problem

Current surveillance detects but cannot distinguish between:

- New incursions: Potentially introducing new fungal strains
- Domestic Spread: Local expansion from long-established populations

Uncertainty delays biosecurity decisions and management, leaving plantations vulnerable to undetected fungi that reduce timber value

Aim

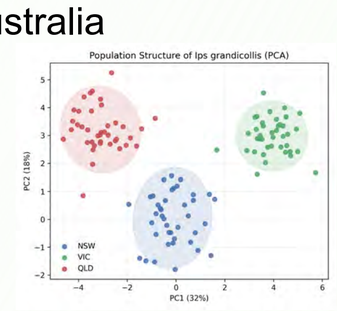
Assess molecular approaches and infer population dynamics and incursion history of forest pests and pathogens using *Ips grandicollis* and associated fungi as the study system

Objectives

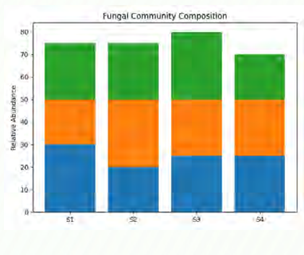
1. Compare genomic methods for analysing *Ips grandicollis*

Short-read (whole genome)	Long-read (whole genome)	DArT-Seq (reduced representation)
High coverage	Long contigs	SNP panel
Moderate cost	Expensive	Lower cost
Fragmented reads	Long reads (better assembly)	Reduced genome

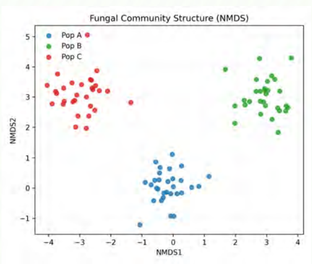
2. Assess population dynamics of *I. grandicollis* across Australia



3. Identify fungal associates from beetle genomic data



4. Analyse fungal community dynamics across populations



Research framework

Beetle samples (from Australian *Pinus* plantations)

↓

DNA extraction

↓

Compare molecular methods

↓

Select a suitable molecular approach

↓

Population dynamics of beetle

↓

Metagenomic recovery of fungi

↓

Population dynamics of fungi

↓

Integration of beetle-fungi genomics for invasion inference

Expected outcomes & significance

- Improve understanding of established pests
- Distinguish new incursions from spread
- Identify potential introduction of new fungal risks
- Improve interpretation of surveillance data
- Provide informed forest biosecurity decisions and management (e.g resource allocation, diagnostic efforts and threat ranking)

Acknowledgements:
This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

References

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2. Kilian et al,. (2012). Diversity Arrays Technology: A Generic Genome Profiling Technology on Open Platforms. In F. Pompanon & A. Bonin (Eds), *Data Production and Analysis in Population Genomics: Methods and Protocols* (pp. 67–89). Humana Press.
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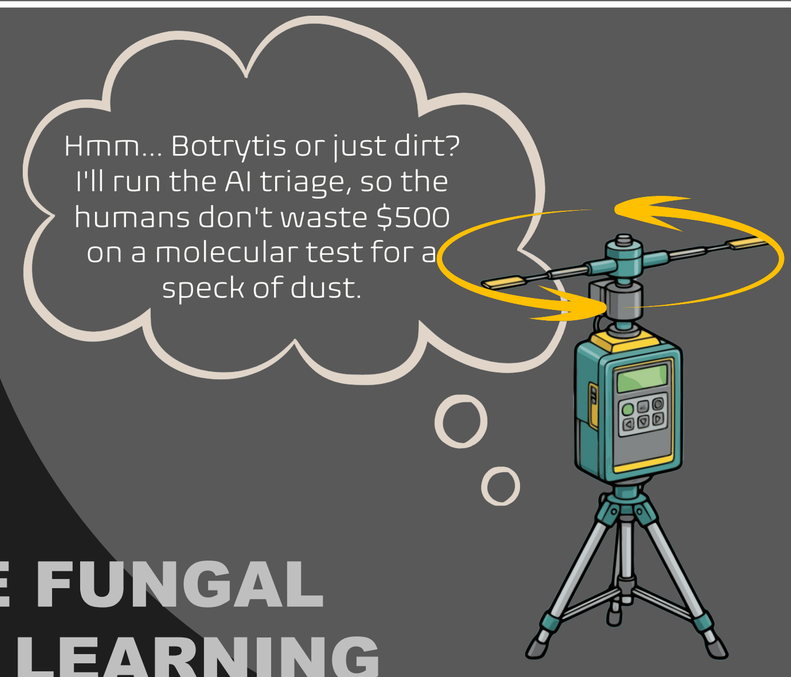
4. Yousuf et al., (2014). Biology of the bark beetle *Ips grandicollis* Eichhoff (Coleoptera: Scolytinae) and its arthropod, nematode and microbial associates: A review of management opportunities for Australia. Austral Entomology, 53(3), 298–316

What if a SPORE TRAP Could Think?



SMART PLANT BIOSECURITY SURVEILLANCE OF AIRBORNE FUNGAL PATHOGENS USING MACHINE LEARNING

Shiron Thalagala[1,3], Rohan Kimber[2,3] and Bronson Philippa[1,3]

[1] James Cook University, Townsville, QLD, Australia, [2] South Australian Research & Development Institute, Adelaide, SA, Australia, [3] ARC Training Centre in Plant Biosecurity, Australia

DID YOU KNOW?

$220 billion in global crop losses annually due to plant pests and diseases[1]

62% of all plant pathogens in Australia are airborne[2]

29% of all airborne plant pathogens in Australia are fungi[2]

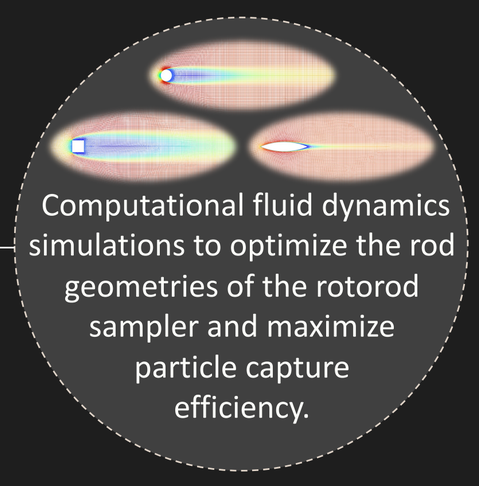
Fungal spores can travel between continents using “aerial superhighways”[3]

We propose a smart spore trap that can be deployed within a surveillance network. AI will be used not only to detect known pathogens (supervised learning) but also to identify unknown exotic species (unsupervised learning).

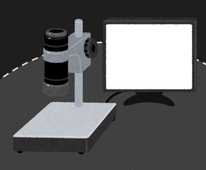
Additionally, AI will triage spore samples so that not every sample needs to undergo resource-intensive molecular diagnostics.

DON'T LAB-TEST EVERYTHING. TEST WHAT MATTERS.

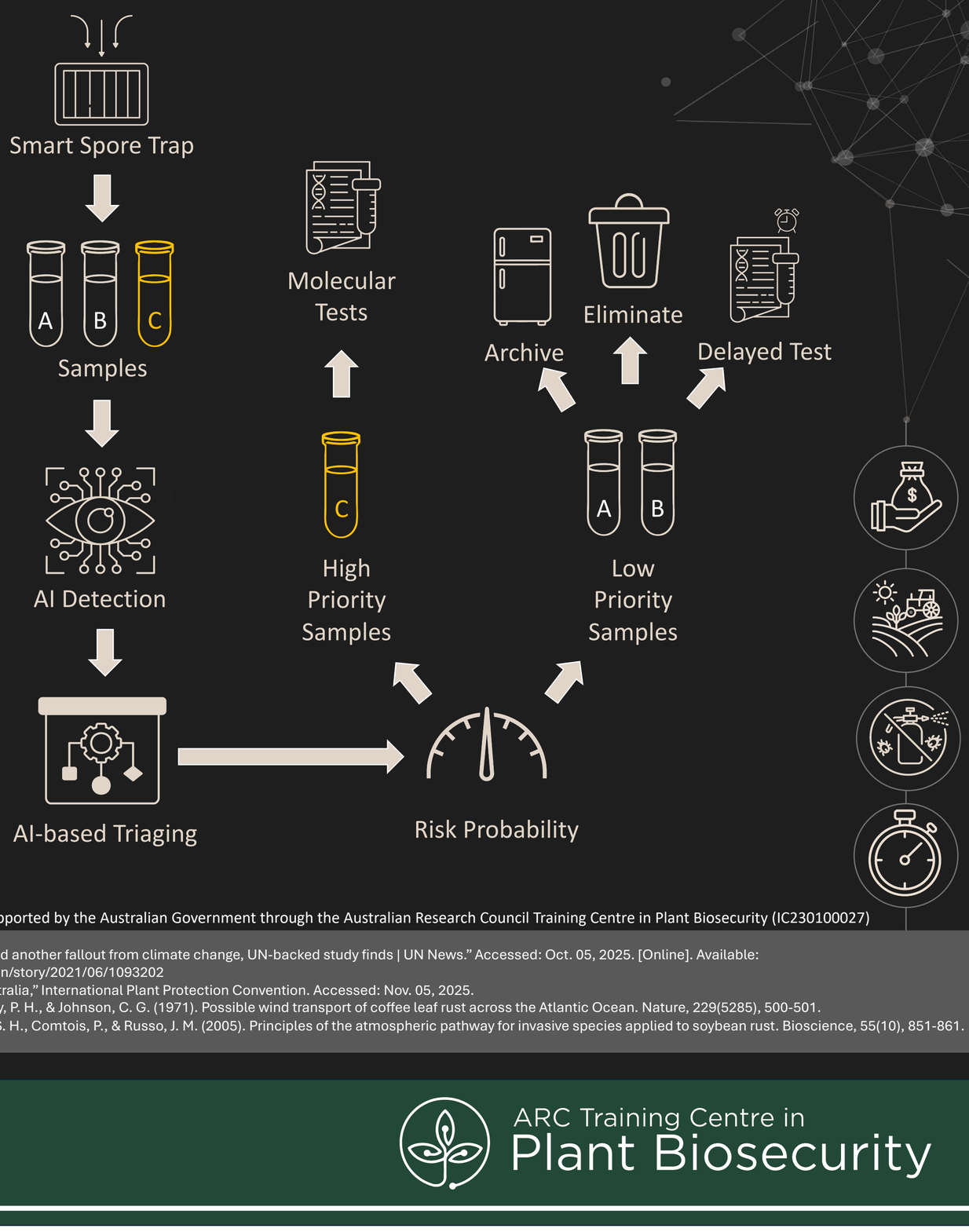
A modified rotorod sampler for high-volume sampling.



Computational fluid dynamics simulations to optimize the rod geometries of the rotorod sampler and maximize particle capture efficiency.



A custom microscopic imaging device captures images from the rotorod and uses computer vision for detection.



This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)

1. Invasive pest spread another fallout from climate change, UN-backed study finds | UN News.” Accessed: Oct. 05, 2025. [Online]. Available: https://news.un.org/en/story/2021/06/1093202
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SCAN ME TO LEARN MORE!

ARC Training Centre in Plant Biosecurity

Resolving Australian *Euwallacea* (Curculionidae): the other shot hole borers

de Freitas Rossi, G[1,2].; Schutze, M.K[2].; Bartlett, J[2].; Edward Gilding[2]; Head, M[1]
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Australian National University
Queensland Government
ARC Training Centre in Plant Biosecurity

BACKGROUND

Seven species of *Euwallacea* are known to occur in Australia, among which *Euwallacea fornicatus* (Polyphagous Shot Hole Borer 'PSHB') and *Euwallacea perbrevis* (Tea Shot Hole Borer 'TSHBa'); are the most significant (Fig.1). Both species belong to the *Euwallacea fornicatus* species complex, a complex of four **morphologically similar species**. The other species of the complex are *Euwallacea kuroshio* (Kuroshio Shot Hole Borer 'KSHB') and *Euwallacea fornicatior* (Tea Shot Hole Borer 'TSHBb') which do not occur in Australia. PSHB is currently recorded in Perth, whereas TSHBa is distributed from Far North Queensland to Sydney (Fig.2).

These beetles are associated with symbiotic fungi, including *Fusarium* spp (Fig.7)., which can cause plant dieback (Fig.3).

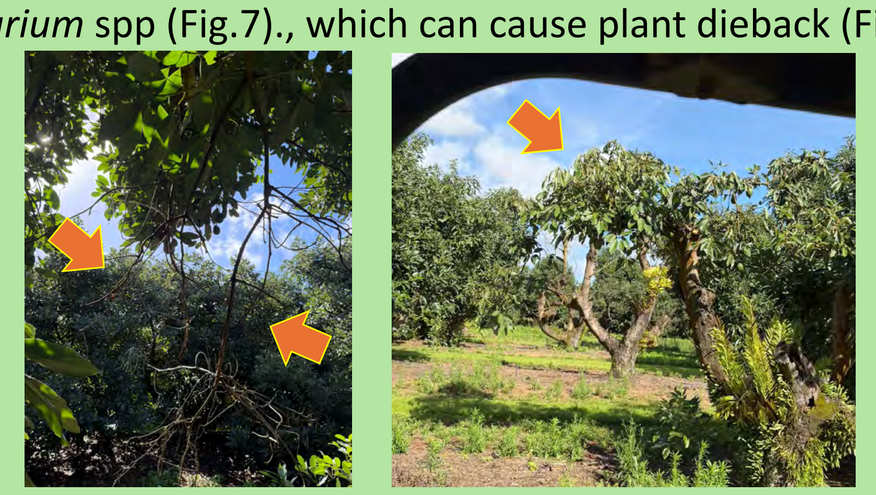


Figure 3: Plant dieback observed in a fig tree from Stradbroke Island (QLD), and in an avocado tree from Tolga (FNQ), respectively.

OBJECTIVES

Resolving taxonomic/ecological questions within the *Euwallacea fornicatus* species complex in Australia:

- Are TSHBa individuals along Australia's east coast one species or a complex of cryptic species?
- Are geometric morphometric methods effective for species delimitation in the *Euwallacea fornicatus* complex in Australia? Specifically in distinguishing PSHB and TSHBa?
- Is TSHBa associated with a single *Fusarium* spp. in Australia?
- Does the life cycle of TSHBa in Australia differ from elsewhere?

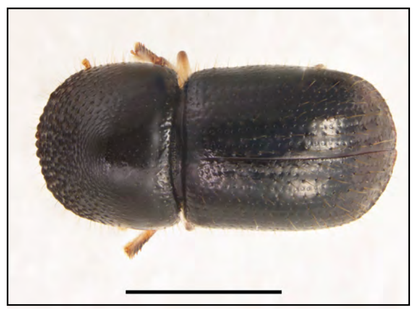
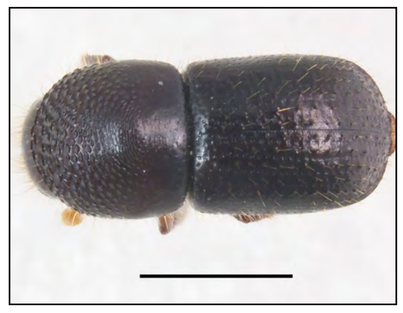


Figure 1: TSHBa (female).



PSHB (female). Scale bar: 1mm.

PLANT HOSTS

TSHBa hosts plants in Australia include: *Persea americana* (avocado), *Cupaniopsis anacardioides* (tuckeroo), *Acer negundo* (box elder), *Macadamia* sp., and *Ficus* sp.

RESULTS SO FAR...

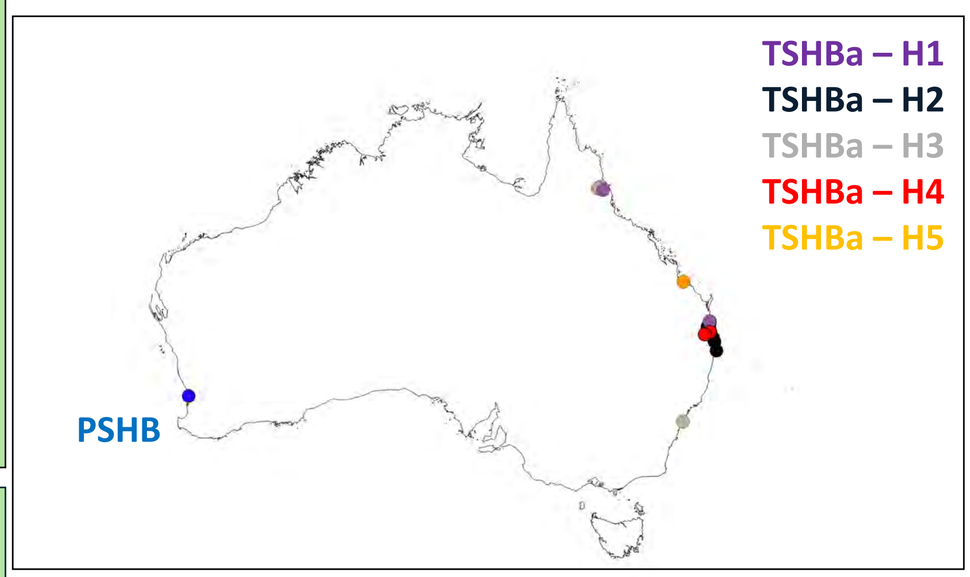


Figure 2: Map showing the distribution of PSHB and TSHBa in Australia. "H" represents different haplotypes, and their respective given number.

To date, five different COI haplotypes have been identified in TSHBa, differing by approximately 4% between them. These haplotypes clustered in two distinct groups: Group 1 (H1 to H3) and Group 2 (H4 and H5), which sequences from each group differing less than 3% from one another and differing more than 3% from haplotypes in the other group.

METHODS

Figure 4. Sample collection using sticky traps (A) and manual field collection method (B).

Figure 5. Standardised anatomical views for geometric morphometric analysis. Representative dorsal, lateral and ventral views, respectively, of the specimen.

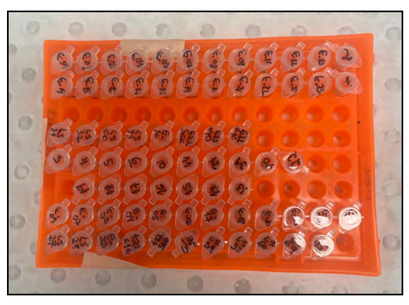


Figure 6. DNA extracted from various TSHBa specimens.

Figure 7. *Fusarium* growth on potato dextrose agar (PDA) supplemented with tetracycline.

BIOSECURITY IMPORTANCE

Developing an integrative diagnostic framework for the *Euwallacea fornicatus* species complex is essential for early detection enabling rapid and reliable identification of the Polyphagous Shot Hole Borer versus the Tea Shot Hole Borer(a).

Key contribution to the biosecurity sector include:

- Improving species level identification to prevent the misidentification of PSHB and TSHBa.
- Generating a comprehensive dataset of publicly DNA sequences of TSHBa from Australia to facilitate rapid and accurate identification in cases of this species colonizing other Australian states.
- Identify the *Fusarium* spp. associated with TSHBa and investigate their pathogenicity.
- To compared the reproductive fitness and life cycle of TSHBa across diverse host tress to establish scientific baselines for targeted surveillance.

Acknowledgement: This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027). We would like to thank Angus Carnegie, Bridie Carr, Chris Reid, Conrad Trollip, Dalton Baker, David Bin, Donna Chambers, Emily Lancaster, Giovanni Ramon, Helen Nahrung, Lauren Mather, James Bickerstaff, Janet McDonald, Louise Shuey, Madaline Healey, Matt Shaw, Melinda Moir, Nico Badenhorst, Peter Gillespie, Simon Lawson, for all the samples and shared knowledge about *Euwallacea*. Also, Iain Jamieson, Anthony Allan (Gold Coast Council), Rex Kelly, Ian Dawes (Moreton Bay Council), Russel Tomlin (Brisbane Council) for all the support regarding installing traps. We would like to thank the avocado growers in the Atherton (Far North Queensland) for their collaboration, and access to field sites.

Natural and synthetic antibodies for detection of spider mite eggs during import

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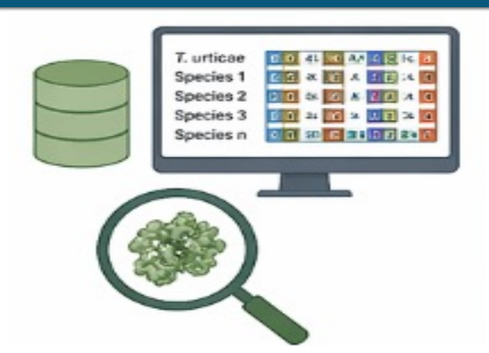
Background

At Australia's borders, imported plant consignments are frequently detained due to the detection of insect eggs, necessitating precautionary delays for laboratory-based molecular diagnostics. These eggs are often identified as spider mites (Acari: Tetranychidae), which are endemic to Australia. However, their minute size and lack of distinguishing morphological features prevent rapid assessment of viability, identity, or potential exclusion of higher-risk species. Consequently, consignments are subjected to precautionary treatments such as methyl bromide fumigation, incurring unnecessary costs and trade delays.

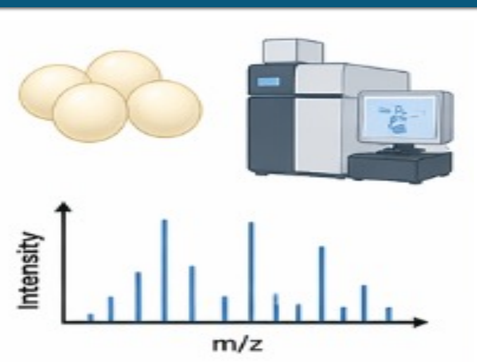
Decision Gap?

"Lack of rapid tools prevents real-time decision-making on egg viability and identity at the borders."

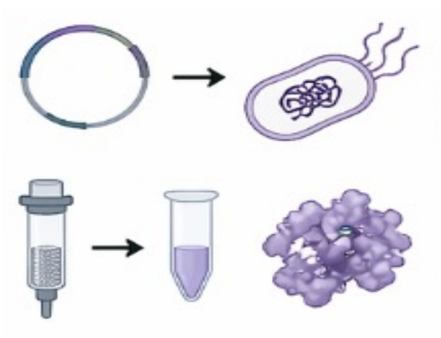
Developing specific and selective mite binders



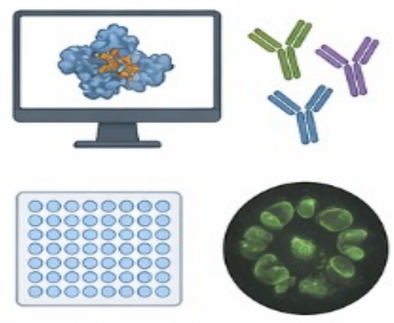
1. Identify suitable mite egg proteins (targets) using genomic and protein datasets



2. Confirm and validate egg proteome targets using proteomics



3. Express and purify candidate targets for developing molecular binders



4. AI-driven protein design, screen candidate binders and characterise specificity and selectivity

Project outcomes

- Egg targets
- High affinity binders
- Informed border surveillance practices for spider mites

Future Applications

- Binders can be used for lateral flow assay platforms (e.g. COVID-19)
- Laboratory diagnostics (ELISA, immunoassays)
- Biosensors

Acknowledgement: This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)

Australian National University

Australian Government
Australian Research Council

Australian Government
Department of Agriculture, Fisheries and Forestry

ARC Training Centre in Plant Biosecurity

Identifying Fruit Fly Biomarkers via MALDI-ToF Mass Spectrometry

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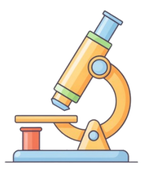
This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)

Invasive fruit flies cost Australia $300-million every year, in management, crop damage & trade restrictions! To stop the spread, **pest diagnostics are vital to protect Australian biosecurity** by supporting in-field & at-border pest control

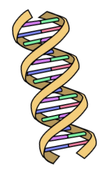
How Do We Identify Flies?



Morphological Identification

Primary Choice - based on **physical features**

Limited by – subjectiveness & sample quality



Genetic Diagnostics

Secondary Choice - based on **DNA regions**

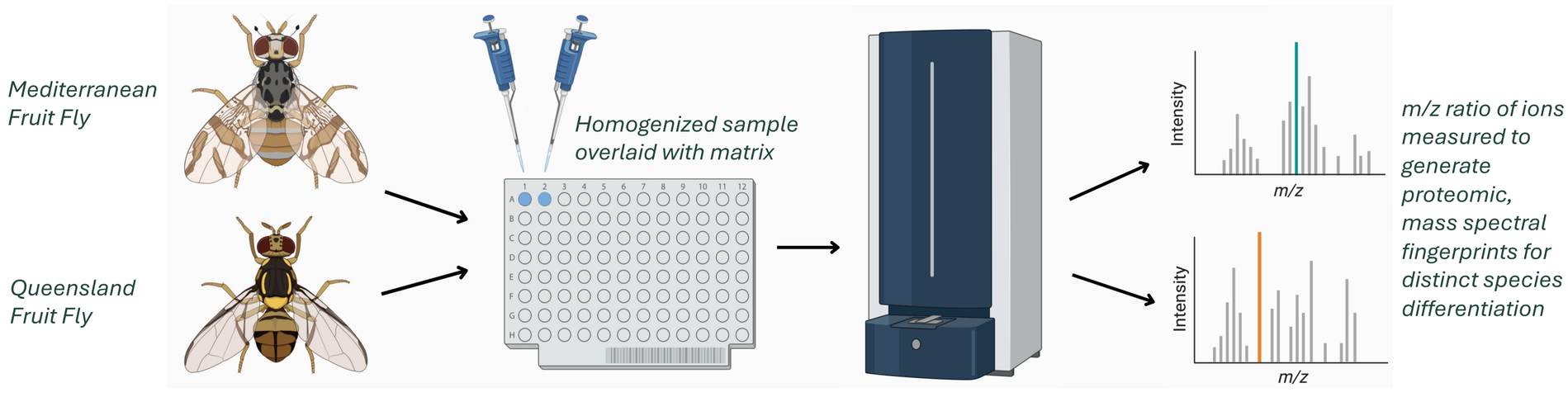
Limited by – resources, labor, cost & time

To address limitations & fill the gap between these techniques:

***M**atrix **A**ssisted **L**aser **D**esorption/**I**onization - **T**ime of **F**light*

MALDI-ToF Mass Spectrometry - Advancing Pest Diagnostics!

Mass spectrometry can create molecular **'fingerprints'** to identify fruit flies



Advantages:

- Rapid (less than 60 seconds per spot)
- Cost-effective (less than $1 per test-spot)
- Efficient & simple sample preparation
- Can detect specific characteristic traits

PhD Project Goals – Use MALDI-ToF To:

- Assess **species identification across tissues, life stages & matrix choice** → *to improve pest detection, surveillance & border interception*
- Determine **biological status (sex, fertility, mating status)** → *to evaluate pest control success & better target responses*
- Identify **lab-reared & wild flies** → *to support sterile insect & male annihilation tactics*
- Detect **pesticide resistance & radiation exposure biomarkers** → *to monitor pesticide resistance & confirm phytosanitary irradiation of imports*

ARC Training Centre in Plant Biosecurity | Australian National University | Australian Government, Department of Agriculture, Fisheries and Forestry

Insights into the infection and genome biology of the sugarcane brown rust pathogen

Lavi Singh[1], Samantha Whitling[1], Seona Casonato[2], Celeste Linde[1], Benjamin Schwessinger[1]

[1]Research School of Biology, Australian National University, [2]Sugar Research Australia

Why should we care about sugarcane brown rust?

Sugarcane brown rust disease can cause yield losses around 25% in susceptible varieties.[1]

Caused by the fungal rust pathogen *Puccinia melanocephala*.

Symptoms are brown pustules (urediniospores) erupting from leaf surfaces.

Erupting pustules reduce photosynthetic capacity of the plant, driving yield loss.

Managed through breeding resistant varieties but there is constant threat of new pathogen isolates that can break down existing resistance.[1,2]

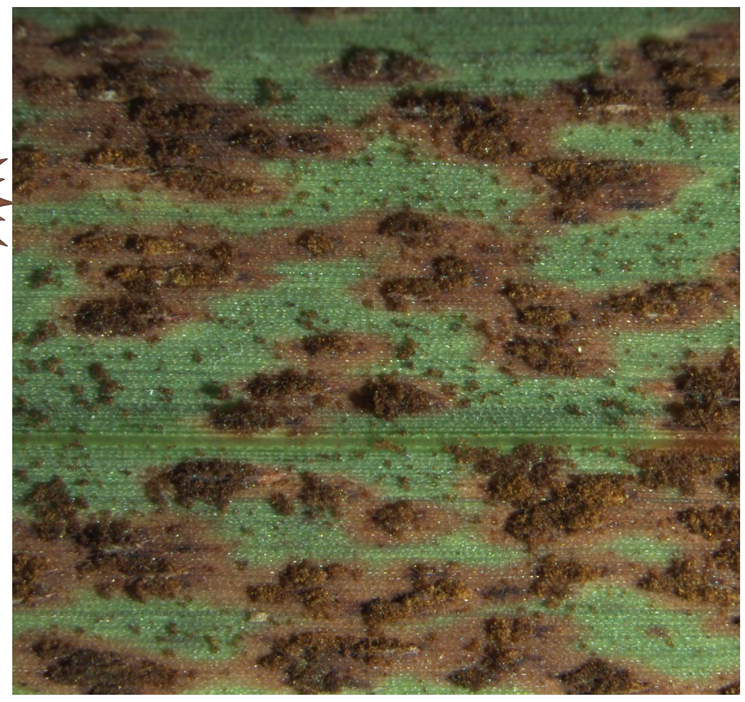


Image of a sugarcane leaf infected with brown rust 14 days post infection under controlled conditions.

What are the gaps in our current understanding?

- **Infection process remains poorly characterized**
- **Limited molecular understanding during infection**
- **Lack of high-quality reference genome**
- **Limited knowledge of genome architecture and its role in pathogen evolution**

Pearson Scott Foresman, Public domain, via Wikimedia Commons

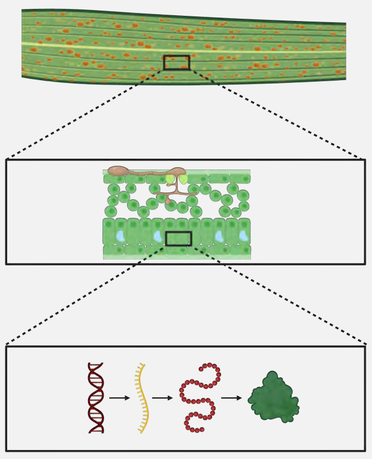
Progress to date

Setup infection assays in controlled conditions to harvest sugarcane brown rust urediniospores.

Carried out DNA extraction and sequencing using Nanopore long-read and Hi-C. Genome assembly in progress.

Current Aims and Approaches

Aim 1: To characterize the infection process across different scales and time.

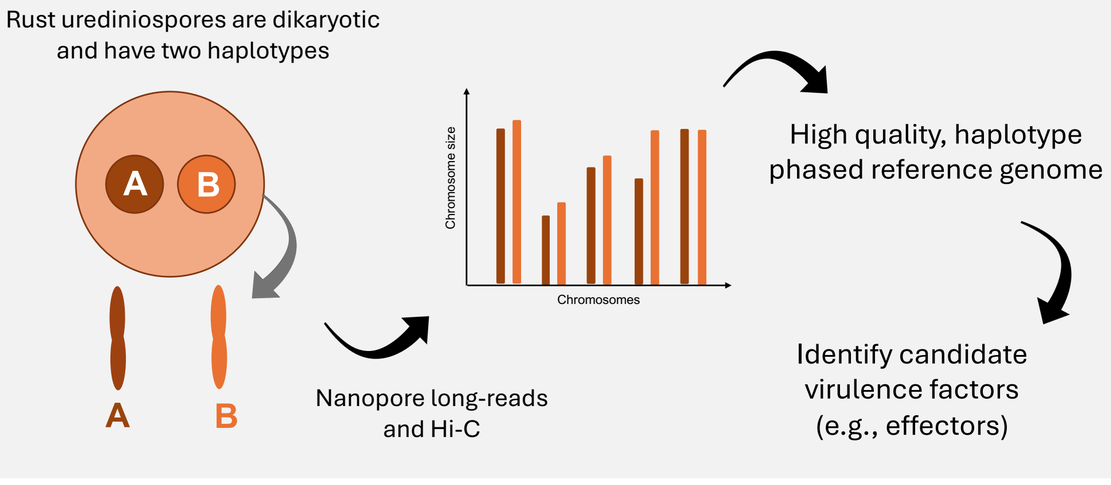


Infection Phenotyping in controlled environment (Macro).

Microscopic characterization of infection using confocal microscopy.

Gene expression analysis of the pathogen during infection (Molecular).

Aim 2: To generate a high-quality reference genome and identify candidate virulence factors.



Impact and Outcomes

Establish a reliable infection protocol under controlled conditions.

Identify candidate virulence factors.

Develop the first genomic resource to support future diagnostics and surveillance.

Acknowledgements

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027). The authors also acknowledge the facilities, as well as the scientific and technical support provided by the Bioplatforms Australia network, which is supported through NCRIS.

References

[1]Braithwaite, K.S., 2005. Assessing the impact that pathogen variation has on the sugarcane breeding program : SRDC final report BSS258.

[2]Sugar Research Australia, 2022. Do you know your rusts?

Images created with BioRender

Sugar Research Australia

Australian National University

ARC Training Centre in Plant Biosecurity

From endophyte to pathogen: epidemiological and molecular drivers of mango dieback

Vida Burger[1]; Sonu Yadav[2]; Sharl Mintov[2]; Ayomide Fadiji[2] ; Celeste Linde [1]; Benjamin Schwessinger [1]
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Background

- Mango is an important tropical fruit
  - 4.3 million trays in 2025/26 season (7.5% annual increase)
  - >$128M to the economy
  - 50% is supplied by the NT
  - 90% are sold fresh
  - Therefore disease-free fruit is critical
- Select Botryosphaeriaceae fungi cause stress-associated dieback in woody hosts e.g. grapevine, pine, mango
- *Lasidiplodia theobromae* is a causal agent of mango dieback
- Soil-borne, dispersal of conidia via wind & rain
- Can persist as latent pathogen
- Environmental stress can trigger pathogenicity

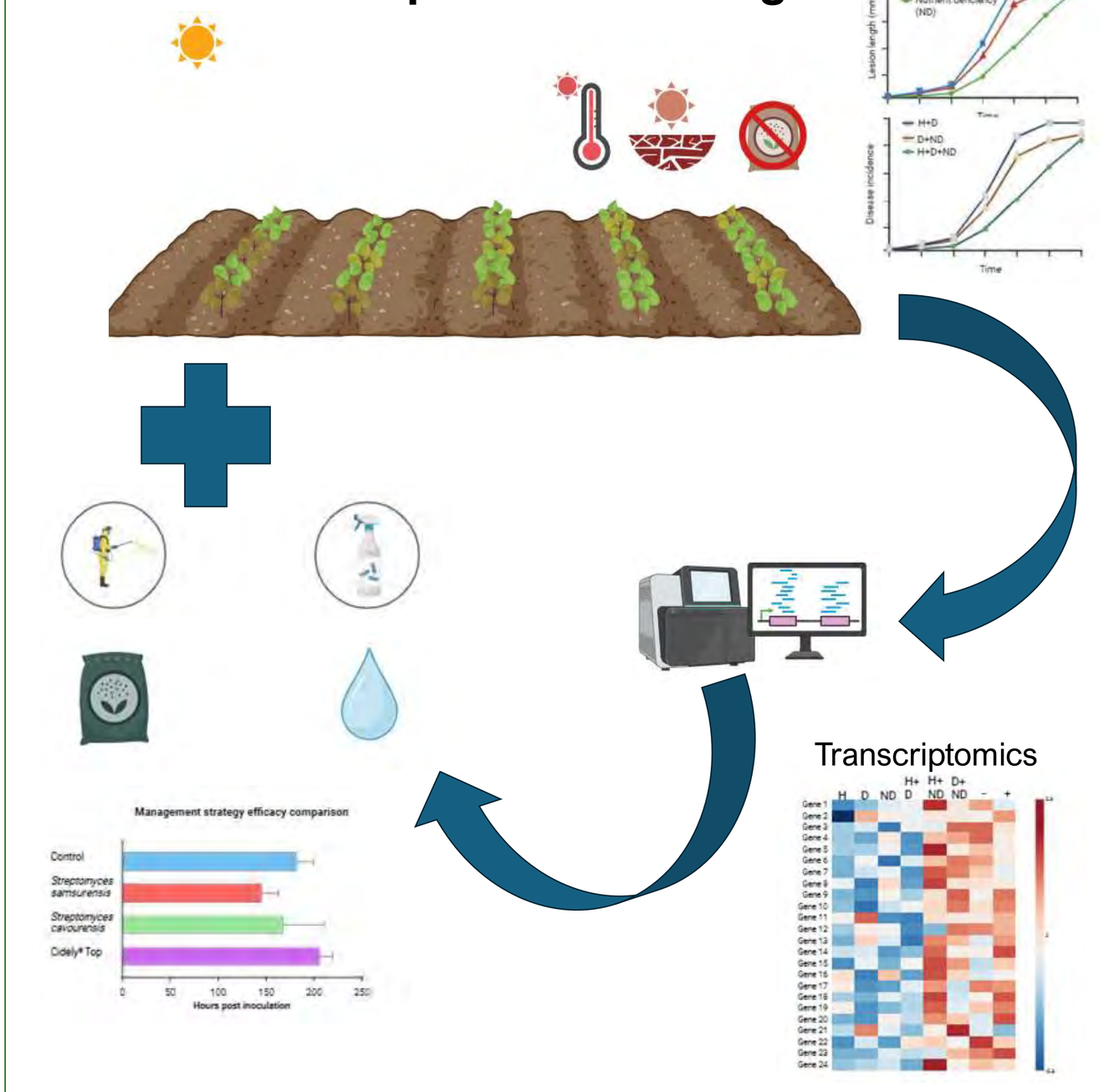
Aim and objectives

- To investigate the infection biology of *Lasiodiplodia* species & the resulting disease expression in mango

Objectives

- Determine infection timing & colonisation pathways in mango
- Determine which *in planta* inoculation method most closely mimics natural infection pathways
- Assess the role of environmental stress in disease expression
- Inform future disease management strategies

Experimental design



Mock data. IC: Biorender

Infection symptoms

- **Early symptoms**
- General wilting appearance
- Twig dieback
- **Late-stage symptoms**
- Leaf curling & drying → defoliation
- Vascular discoloration on stems & branches

Why this matters

- Mango dieback causes significant economic losses
- Better understand disease epidemiology – improve understanding of the shift from latent to pathogen
- Enables farmers to improve management strategies
- Understanding stress-driven disease emergence is critical for sustainable mango production under climate change

References consulted

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- NT Farmers (2024) *Mangoes*. Available at: https://ntfarmers.org.au/commodities/mangoes/ (Accessed: 12 April 2026).
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Australian National University
NORTHERN TERRITORY GOVERNMENT
ARC Training Centre in Plant Biosecurity

Uncovering Hidden Diversity in Vineyard Scale Insects:

Population genomics of Parthenolecanium corni across South Australian wine regions

Yilin Bai

Australian National University | Australian Wine Research Institute

ARC Training Centre in Plant Biosecurity

Supervisors: Megan Head (ANU), Chris Ward, Anthony Borneman, Markus Herderich (AWRI)

Background

- **Scale insects are a widespread and economically important pest of grapevines, with populations recently increasing to levels requiring intervention**
- **They feed by extracting nutrients from the vine's phloem and act as vectors for multiple grapevine viruses (eg. Grape leafroll-associated virus)**
- **During feeding, scale insects excrete sugar rich honeydew as a waste product, promoting fungal growth that reduces grape and wine quality.**
- **Effective management has been hindered by species misidentification: *P. corni*, previously thought to be absent from Australian vineyards, has recently been identified as the dominant coccoid species across multiple wine regions**
- **However, population-level genetic diversity and structure of *P. corni* in Australia remain poorly understood**

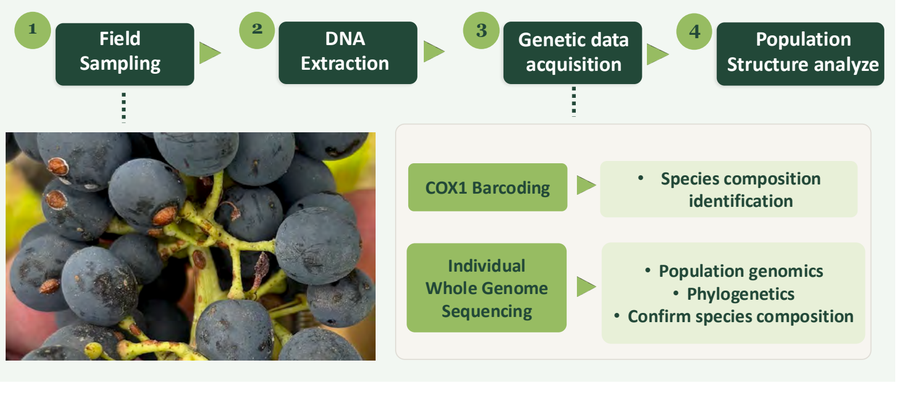
Overall PhD Project Aims

- **Identify the species of scale insects and mealybugs present in Australian vineyards**
- **Investigate population dynamics, including population structure, connectivity, invasion dynamics, and landscape-level impacts.**
- **Characterize the natural enemy communities associated with scale insects and mealybugs, and examine their population dynamics in relation to pest abundance.**
- **Develop biological control-based management strategies**

Pilot Study

A pilot study is currently being conducted to develop and validate core methodologies prior to the formal experiment, focusing on:

- **Establish field sampling methodology**
- **Determine a fit-for-purpose DNA extraction protocol**
- **Develop an automated pipeline for bioinformatic analysis**
- **Understand broad population dynamics to drive decisions in the main project**



1 Pilot study – Sampling

- **Three vineyards selected for sampling**
- **Rows selected at regular intervals (e.g., every 2nd row) across vineyard block**
- **Scale insects collected by tissue type (leaf, stem, trunk)**

	Barmera V1	McLaren Vale V1	McLaren Vale V2
Expected species	*P.corni*	*C.Hesperidum*, soft brown scale	*P.corni*
Life stage	2nd instar, Adult	3rd instar	Adult
Sampling Vine number	9	11	16
Sample number	19	25	35

2 Pilot study – DNA extraction

- **Compared three extraction methods (DNeasy Kit, Mag-Bind, Phenol-Chloroform) on 2nd instar and adult female *P. corni***
- **Mag-Bind kit selected as optimal method for subsequent extractions**

Extraction Method	Life Stage	Total DNA (ng)
Phenol-Chloroform	2nd instar	1.068
	2nd instar	/
DNeasy mini kit	2nd instar	/
	2nd instar	/
Mag-Bind	2nd instar	5.85
	2nd instar	1.42
	2nd instar	6.8
	2nd instar	1.44
	Adult	9.1
	Adult	59
	Adult	1.3
	Adult	48.2

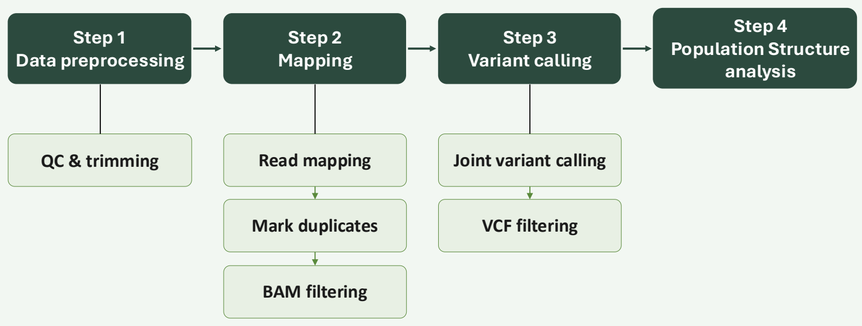
2nd instar *P.corni*

2nd instar *P.corni* in 1.5ml tube

Adult female *P.corni* in 1.5ml tube

Preliminary analysis — Pipeline development

- **An existing pool-seq dataset was used to develop and test the bioinformatics pipeline prior to formal sampling**
- **Dataset: 78 samples (26 NSW + 52 SA), species using metagenomicspre-identified**
- **20 samples selected to build and validate the pipeline: 9 confirmed P. corni pools across 5 SA wine regions, 6 pure non-target species, and 5 mixed samples with known composition gradients (0.2%–50%)**



Future Directions

- **Extract DNA from all collected samples using the Mag-Bind kit and conduct COX1 barcoding followed by individual whole genome sequencing on selected samples**
- **Apply the pipeline to all 78 pool-seq samples to complete the dataset analysis**
- **Begin formal field sampling across Australian wine regions (from September 2026)**

References

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Wührl, L., Pylatiuk, C., Giersch, M., Lapp, F., von Rintelen, T., Balke, M., Schmidt, S., Cerretti, P., & Meier, R. (2022). DiversityScanner: Robotic handling of small invertebrates with machine learning methods. Molecular Ecology Resources, 22(4), 1626–1638. https://doi.org/10.1111/1755-0998.13567

Acknowledgement

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)

AWRI | Australian National University | Wine Australia | ARC Training Centre in Plant Biosecurity

Ranking priority plant pests and diseases

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3: Department of Agriculture, Fisheries, and Forestry,

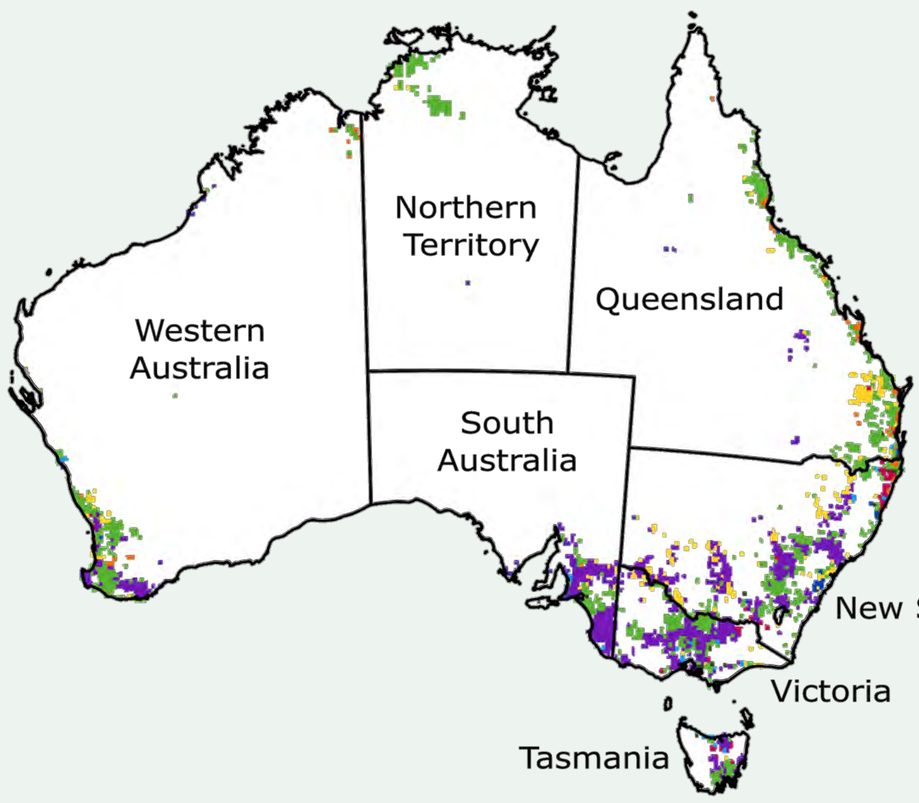
Current qualitative and semi-quantitative approaches lack an objective means to rank National Priority Plant Pests (NPPPs). To address this, we aim to develop a framework that quantitatively ranks plant pests and diseases based on NPPP criteria.

Proposed framework approach

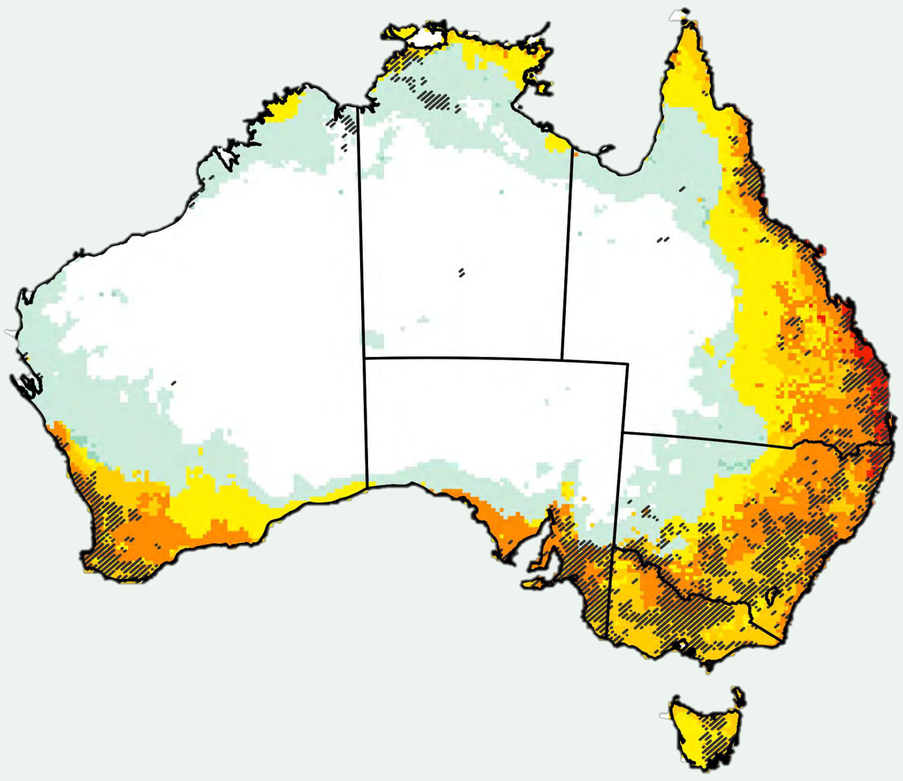
Current NPPP criteria	Quantitative models and data
Harmful to plants	On a list of invasive species elsewhere
Absent from Australia	Not recorded in the last 5 years
Could enter Australia	Arrival probability model
Could establish and spread in Australia	1. Similar climatic niche to Australia
	2. At-risk area (climate and hosts)
	3. Spread models
May impact the economy, environment, or people	Bioeconomic damage model to prioritise pests based on potential costs

Case study: hosts and climate suitability for *Drosophila suzukii*

We mapped the presence (per 0.1667°) of *D. suzukii* host land use types in Australia using ABARES NLUM data. We then fit a CLIMEX model to the global distribution of *D.* suzukii, including the effects of irrigation on climatic suitability.



Host presence
- Perennial horticulture
- Tree fruits
- Shrub berries and fruits
- Citrus
- Grapes
- Intensive horticulture
- Shadehouses
- Glasshouses



CLIMEX model of suitable climate (including irrigation) and host presence

Permanent climate suitability (1-100)
- 1 – 20
- 20 – 40
- 40 – 60
- 60 – 80
- 80 – 100

Seasonal climate suitability (1-100)
- 1 – 20
- 20 – 40
- 40 – 60
- 60 – 80
- 80 – 100

Host presence
- Commercial hosts

All host commodities in Australia are found in climatically suitable areas for the establishment of the NPPP fruit fly *D. suzukii* = large potential impact!
We can then model potential economic impacts in the at-risk area.

ARC Training Centre in Plant Biosecurity

Plant Biosecurity Research Symposium 2026

This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

PLANT BIOSECURITY RESEARCH INITIATIVE

Modelling Invasive Spread with Citizen-Science Data: A Dynamic Occupancy-Detection Model

YufanZheng[1,2], Elle Saber[2,3], Bernd Gruber[1], Helen Nahrung[4], Angus Carnegie[5], Richard P. Duncan[1]

[1]University of Canberra; [2]ARC Training Centre in Plant Biosecurity; [3]Australian National University;

[4]University of the Sunshine Coast; [5]NSW Department of Primary Industries and Regional Development

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

UNIVERSITY OF CANBERRA

Background

- Biological invasions are increasing worldwide[1].
- Abundant presence-only data lack "true absence" records, making it hard to distinguish non-detection from absence[2,3].

Motivation & Aim

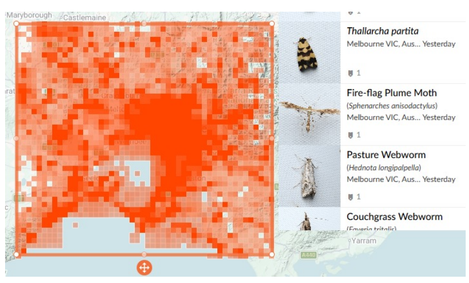
- **Gap:** A few frameworks to use presence-only data for occupancy dynamics estimation.
- **Aim:** To infer invasion dynamics from opportunistic presence-only data.

Methodology

Input

Presence-only Data

- Target Species Record
- Target Area Sample Effort



Dynamic Occupancy-Detection Model

Occupancy Model

- Temporal Effect
- Neighbourhood Occupancy Effect

Detection Model based on Background Sampling Effort

Output

- Relationship between Effort and Detection
- Invasive Species Spread Reconstruction
- Dynamic in Extinction and Colonisation

Conclusion

- A well-structured occupancy model can unlock invasion dynamics from presence-only data and support risk mapping.
- Incorporating the neighbourhood occupancy effect captures the species occupancy dynamics and trends better.

Study Area & Species

Hemlock Woolly Adelgid

Emerald Ash Borer

Mediterranean Fruit Fly

Box Tree Moth

Brown Marmorated Stink Bug

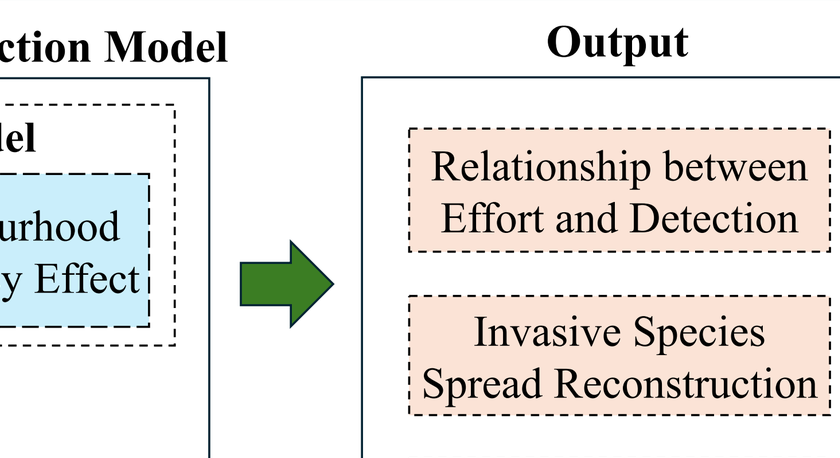
African Big-headed Ant

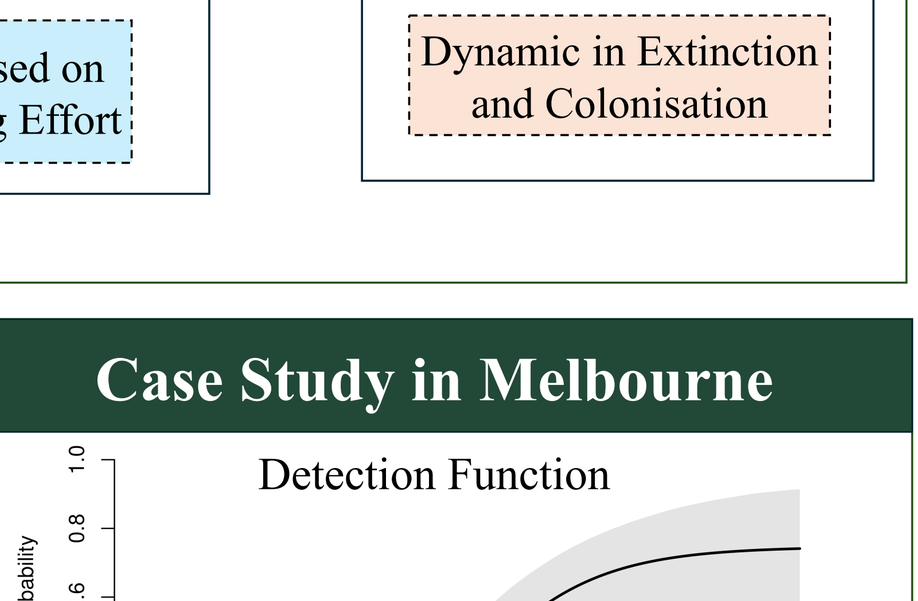
Red Imported Fire Ant

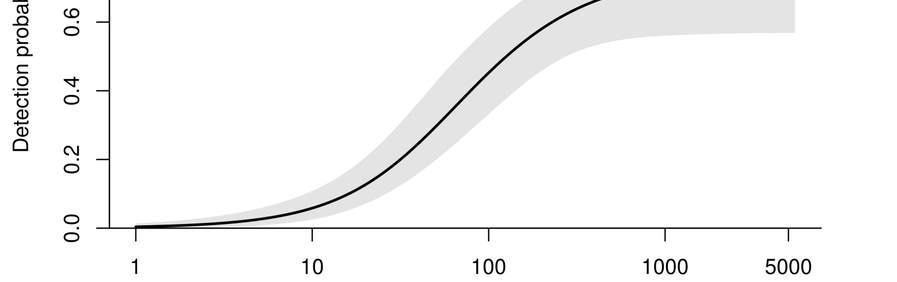
European Firebug

- Record data, 2018/06 – 2025/06 iNaturalist
- Sixteen species-location pairs (with two locations for each species)

Case Study in Melbourne







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[4] Insect images from iNaturalist are used under the following licenses: CC BY-NC 4.0 (Harsi S. Parker, Jessee J. Smith, dbeadle, ildikorab, Sergio Ibarra, Riki Miller), CC BY 4.0 (Michael Knapp), and CC0 1.0 (Katja Schulz).

ARC Training Centre in Plant Biosecurity

CONSERVATION BIOLOGICAL CONTROL
strategies for exotic sugarcane moth borers

Viviana Marcela Aya [1,2,3], Myles Menz [1], Lori Lach[1,2], Emtia Chandrima[3], Kevin Powell[4]

[1] James Cook University, QLD, Australia; [2]ARC Training Centre for Plant Biosecurity, Canberra ACT, Australia;

[3]Sugar Research Australia (SRA), Meringa QLD, [4] Sugar Research Australia (SRA), Brisbane QLD.

MAIN GOAL

Develop a Conservation Biological Control strategy for long term post-incursion management of moth borers

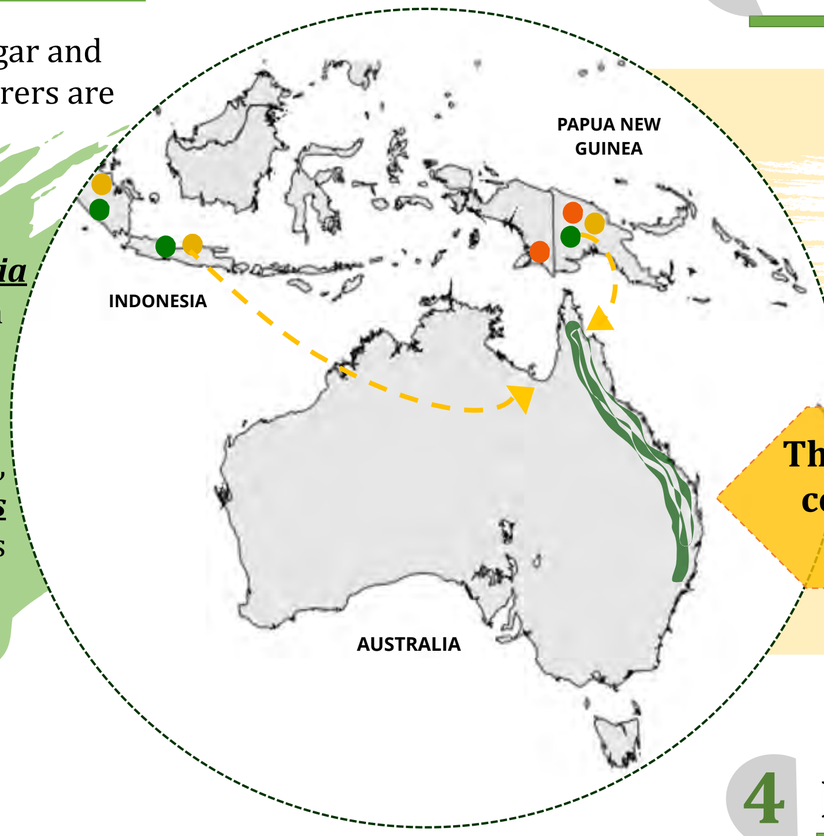
1 WHY THIS MATTERS?

Sugarcane is a major crop for sugar and ethanol production, but moth borers are serious pests.

70% yield loss due to ***Sesamia grisescens*** in PNG.

In Indonesia, ***C. sacchariphagus*** causes **19% yield loss**

Chilo sacchariphagus



2 BIOSECURITY CHALLENGE

7 extreme risk species

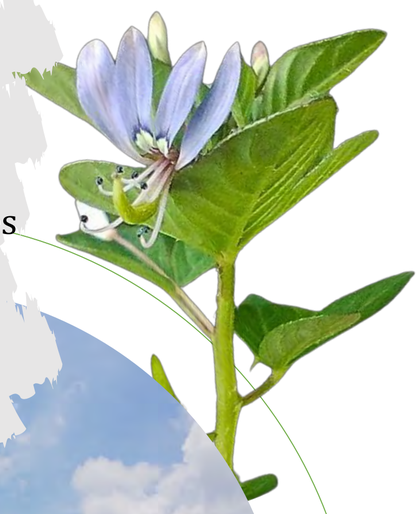
3 GENERA
- *Sesamia* (2 species)
- *Chilo* (4 species)
- *Scirpophaga* (1 species)

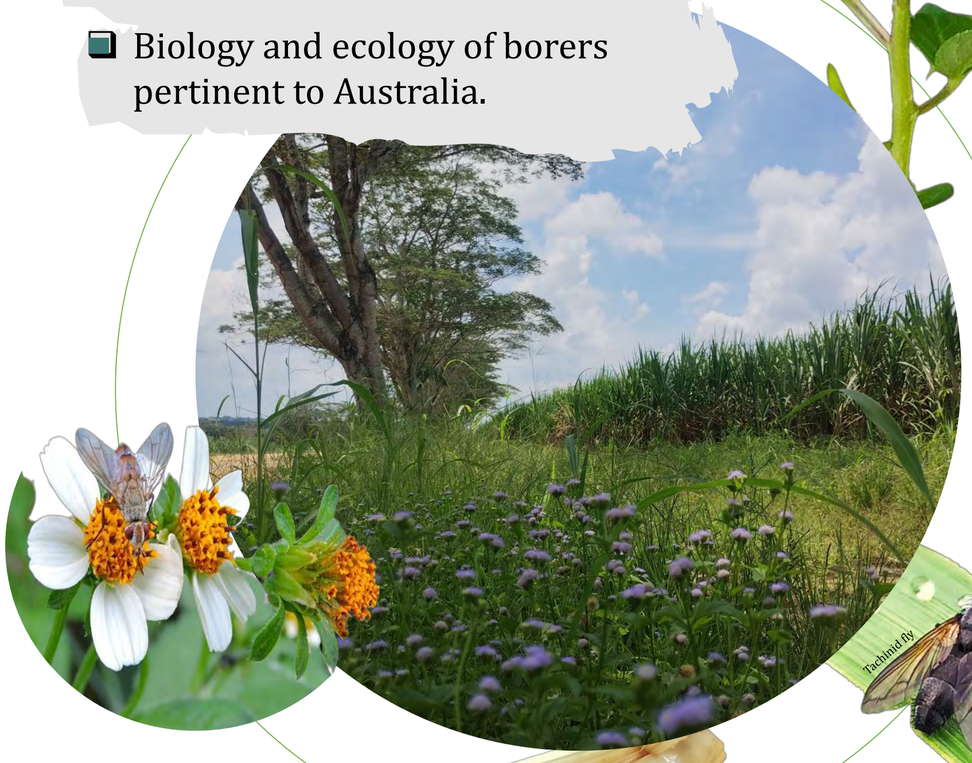
Their presence in neighboring countries pose a high risk to Australian canegrowers.

Scirpophaga excerptalis

3 WHAT DO WE NEED TO KNOW?

- How landscape complexity shapes natural enemy communities.
- Native parasitoid associations in case of an incursion.
- Role of refugia and floral resources for biological control.
- Biology and ecology of borers pertinent to Australia.





4 RESEARCH APPROACHES

Field surveys

Conduct overseas field studies to examine population dynamics and refuge use by borer populations.

Enemy interactions

Measure parasitism rates and document associated natural parasitoids.

Surveillance and monitoring strategies

Identify the most effective early detection methods for the borers (e.g., pheromone traps, light traps, and sticky traps).

Field experiments

Manipulate floral resources and habitat features to see if they affect for natural enemy populations.

5 RESEARCH OUTCOME

This research aims to improve preparedness for a potential exotic moth borer incursion in Australian sugarcane systems.

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This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)

SCAN Me to view the poster

ARC Training Centre in Plant Biosecurity · James Cook University Australia · Sugar Research Australia · New Britain Palm Oil, An SD Guthrie Company

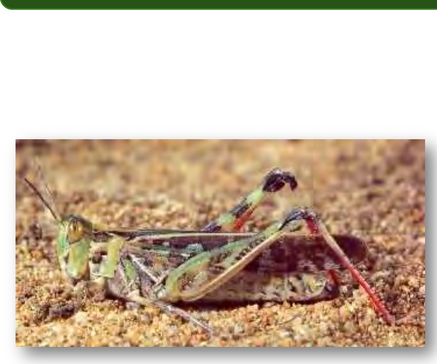
Target gene discovery for the control of Australian Plague Locust (APL)

Alphonsa Baby[1,2]; Con Goletsos[3]; Raj Karunanithi[3]; Shamila Abeynayake[4]; Myles Menz[1]; Dena Francis[1]

1. James Cook University, Townsville, Queensland, Australia.
2. Australian Research Council Training Centre in Plant Biosecurity, Australia.
3. Australian Plague Locust Commission, Department of Agriculture, Fisheries and Forestry, Canberra, Australia.
4. Plant Innovation Centre, Department of Agriculture, Fisheries and Forestry, Mickleham, Victoria, Australia

✉ alphonsa.baby@my.jcu.edu.au

Background



Solitary APL

Gregarious APL

Aerial photo of damage to a wheat crop caused by bands of APL nymphs

- The Australian Plague Locust (APL), *Chortoicetes terminifera,* is a significant agricultural pest in Australia[1].
- APL forms dense hopper bands and adult swarms that cause severe economic damage to crops and pastures, threatening food security[1].
- The APL exhibit density-dependent polyphenism, transitioning from a solitarious phase at low densities, where they avoid other locusts, to a gregarious phase at high densities, where they form large, devastating migratory bands and swarms[2].
- The transcriptional mechanism underlying the solitarious-to-gregarious phase transition in APL remains unknown.

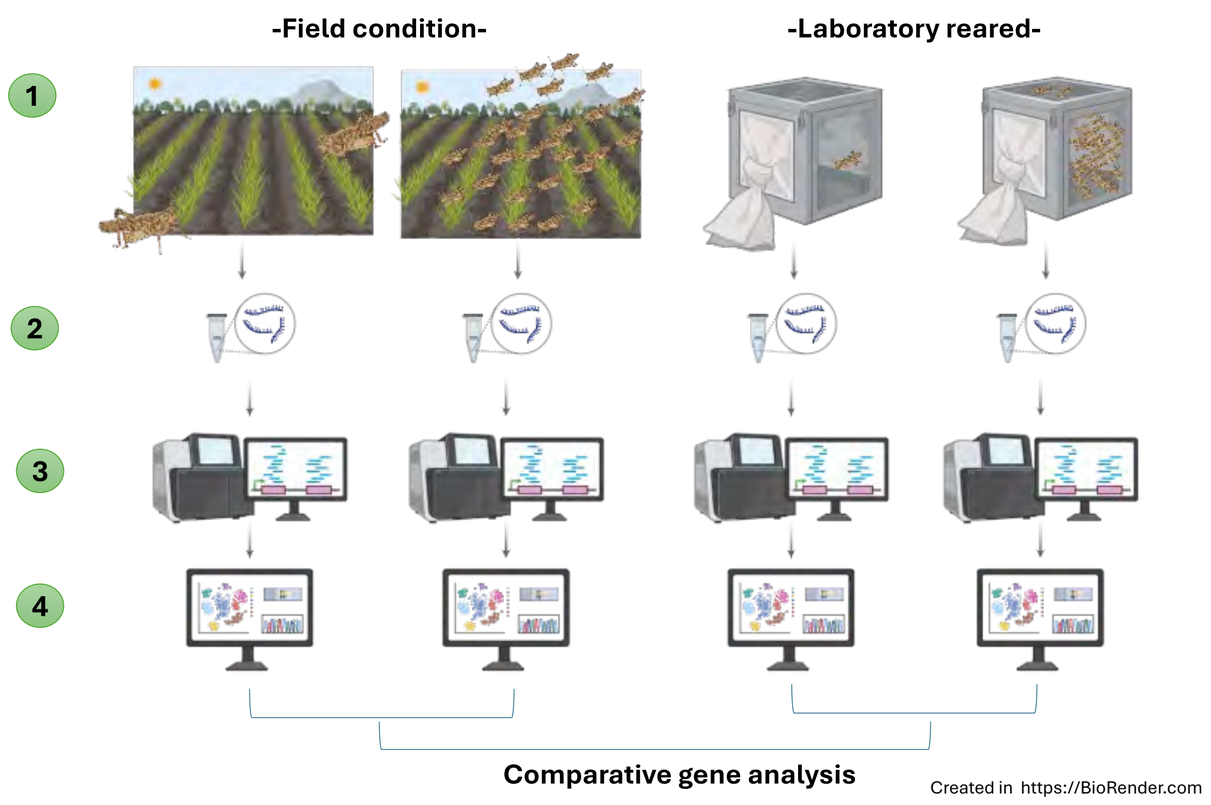
Photo credit: https://www.agriculture.gov.au/biosecurity-trade/pests-diseases-weeds/locusts/about/australia

Aims

- Develop the first transcriptomic database of APL.
- Identify the Differentially Expressed Genes(DEG) in the solitary and gregarious phases of APL collected from the field.
- Identify the DEGs in the solitary and gregarious phases of APL reared in the laboratory.
- Comparative analysis between field-collected and lab-reared APL to validate the findings.

Methodology

1. Collection of solitary and gregarious APLs from both field populations and laboratory-reared colonies.
2. RNA extraction and quality assessment.
3. RNA-seq library preparation and sequencing.
4. Bioinformatic analysis to identify the DEGs between the solitary and gregarious phases.



Future implications

- Improved understanding of the genetic mechanisms responsible for phase changes in APL.
- Opportunities for comparative gene expression studies with other locust species, which can serve as a foundation for broader phylogenetic research, offering insights into the evolution of phenotypic plasticity.
- Critical foundation for the development of novel RNA interference-based genetic control strategies, offering targeted and sustainable management of APL.

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1. Story, P.G., Walker, P.W., McRae, H. and Hamilton, J.G. (2005), A case study of the Australian plague locust commission and environmental due diligence: Why mere legislative compliance is no longer sufficient for environmentally responsible locust control in Australia. Integr Environ Assess Manag, 1: 245-251. https://doi.org/10.1897/2004-028.1
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Acknowledgement: This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

JAMES COOK UNIVERSITY AUSTRALIA

ARC Training Centre in Plant Biosecurity

Australian Government
Department of Agriculture, Fisheries and Forestry

Building and maintaining social licence in Biosecurity Response: Varroa Case Study

Biosecurity only works when people participate. Social licence is the ongoing acceptance of a response by those it affects. It cannot be mandated, only earned. When people disengage or withdraw support, even well-resourced and technically sound responses can fail. This research investigates what builds and weakens the relationship between governments and people during biosecurity emergencies, and how governance can be designed to gain and maintain social licence to operate.

Science communication · Behavioural Psychology · Regulatory Design · Trust· Passing the Pub Test

Document Analysis

What happened to social licence during the Varroa response?

Surveys and Interviews

What did affected beekeepers experience?

Media Analysis

What role did misinformation play; cause or consequence?

Biosecurity Wargaming

How do we put social licence into practice?

If you could "fix" one thing to improve public support in biosecurity response, what would it be?

Contact me:
Aphrika Gregson, PhD candidate

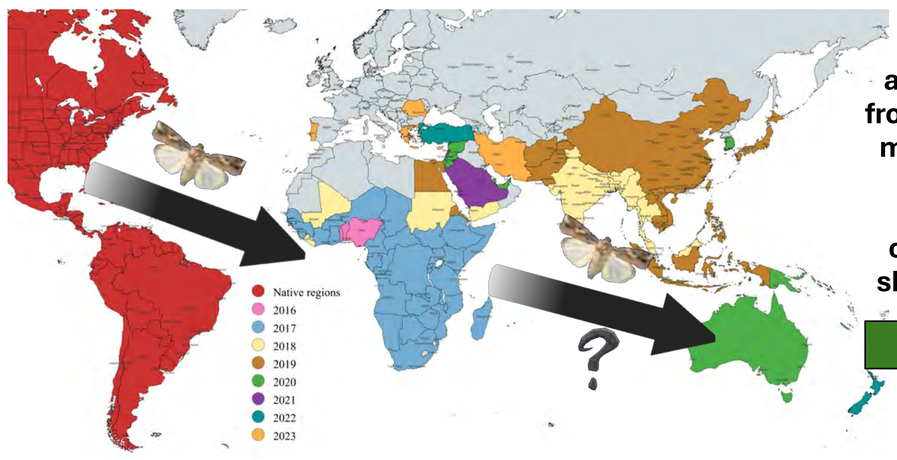
Partner Organisation: NSW DPIRD
Australian National University
James Cook University

ARC Training Centre in Plant Biosecurity

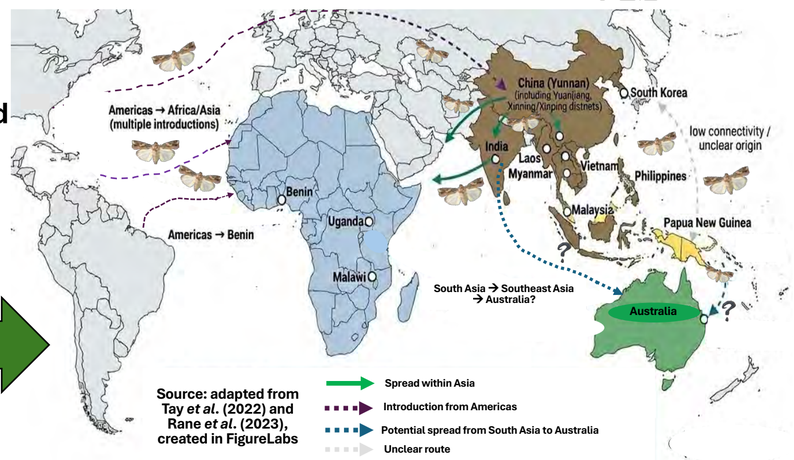
Global invasion multi-omics and microbial control agents immune profiling of *Spodoptera frugiperda*, and population genomics *Spodoptera littoralis*

Esteve Mesén-Porras[1,2,3], Heng Lin Yeap[3], Andreas Bachler[3], Rahul Rane[3,4], Tom Walsh[3.4], Karl Gordon[3], Megan Head[2], Peter Solomon[1,2], and Wee Tek Tay[2,3,4]

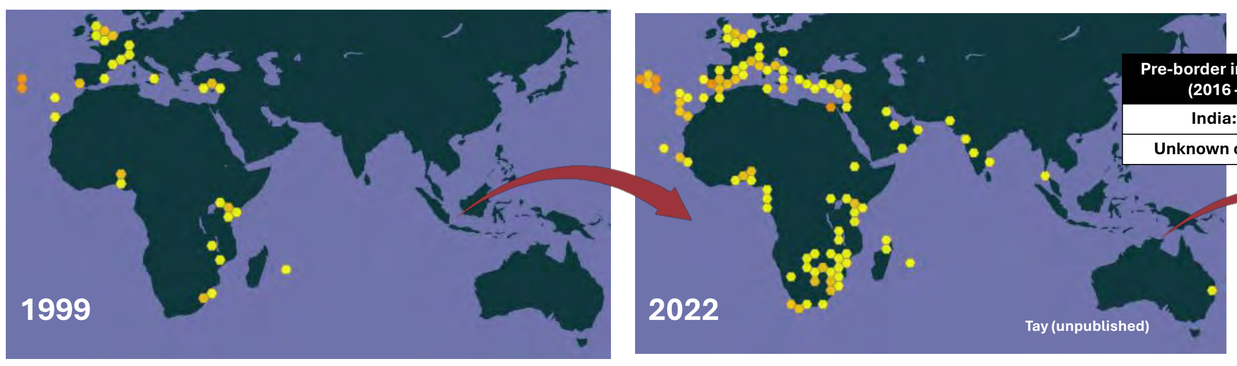
[1] ARC Training Centre in Plant Biosecurity, [2] Australian National University (ANU), [3] CSIRO, [4] Applied Biosciences, Macquarie University



Hypothesis: Fall armyworm invasions from Americas involved multiple independent introductions and adaptive genomic changes continue to shape biosecurity risk



Emerging threat: *Spodoptera littoralis*



Pre-border interceptions (2016 – 2018)

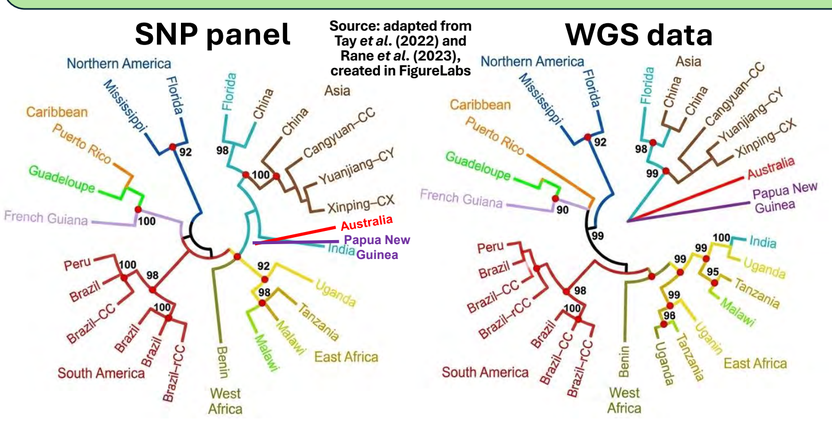
India: *n* = 17
Unknown origin: *n* = 8

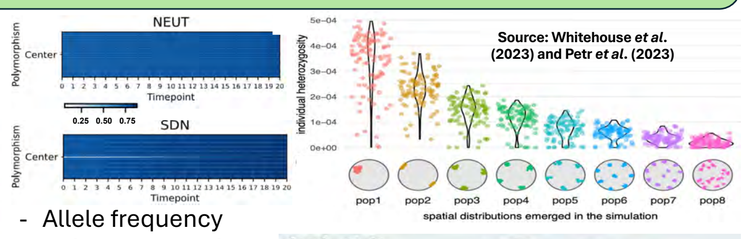
Distribution model based on suitability

Eduardo Parra

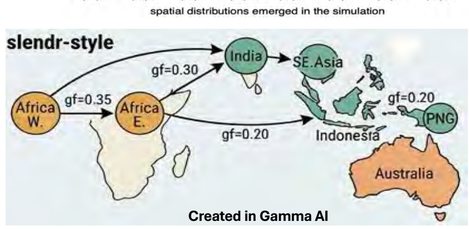
Aim 1: Reconstruction of FAW global invasion and establishment: Population and spatial-temporal genomics from WGS data

Comparison of selected SNP panel vs. WGS population genomics analysis / Identifying signatures of selective sweeps through WGS and temporal genomic data





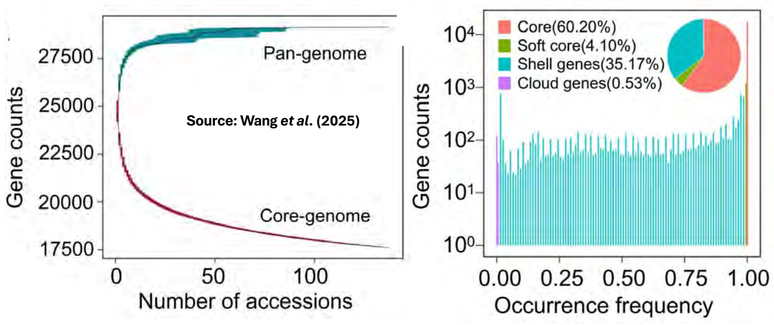
- Allele frequency trajectory over time
- Heterozygosity distribution
- Spatio-temporal model based on selection sweeps

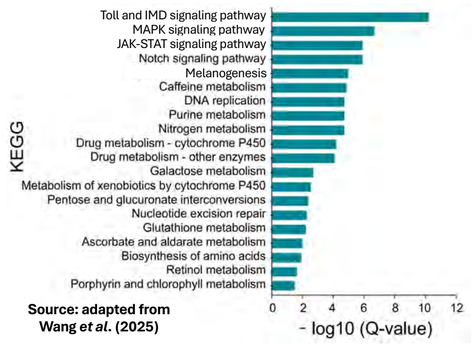


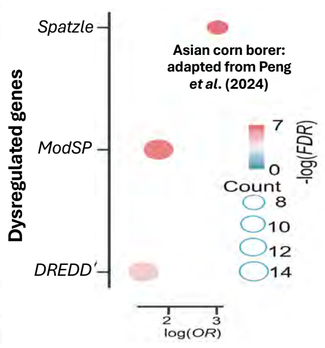
Revista Cultivar

Aim 2: Genomic structural variations in immune-related pathways by constructing a pan-genome

S. frugiperda pangenome: Synteny, genes under selection and enriched pathways and genes



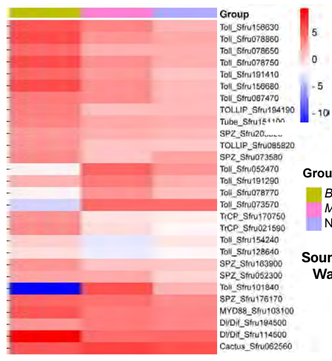


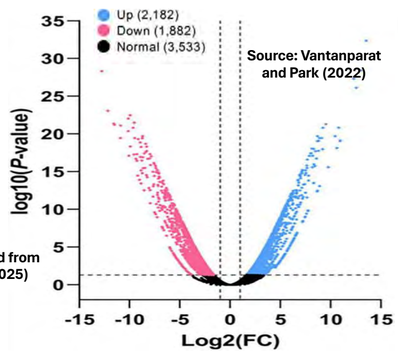


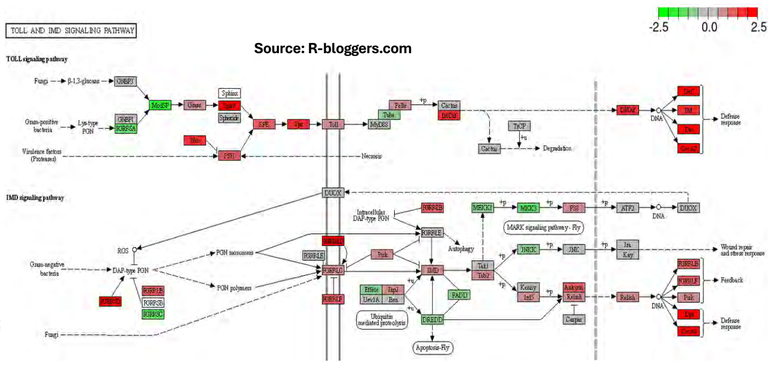
Matt Bertone (2014)

Aim 3: Larval transcriptomic response to biological control agents to identify immunity responses

Differential gene expression and dysregulated metabolic pathways linked to immunity



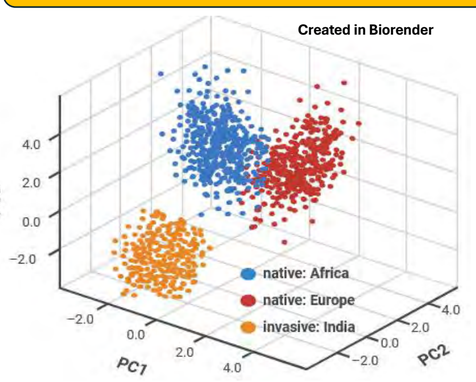


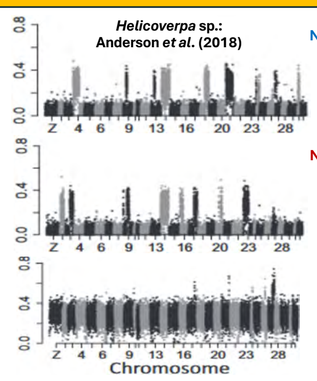


Envirevo Agritech

Aim 4: Egyptian cotton leafworm (*S. littoralis*) population genomics to assess establishment in Australia

Population structure of *Spodoptera littoralis* to address its potential invasion to Australia

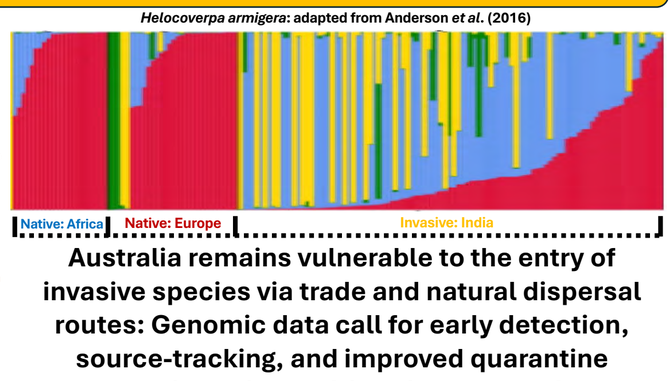




Native: Africa

Native: Europe

Invasive: India



Australia remains vulnerable to the entry of invasive species via trade and natural dispersal routes: Genomic data call for early detection, source-tracking, and improved quarantine strategies using multi-omics approaches

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Petr *et al.* (2023): 10.24072/pcjournal.354
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ARC Training Centre in Plant Biosecurity

Invasive snails as vectors of pathogens and parasites

Bethany Perry[1,2,3] | PhD Candidate | Supervisory Panel: Prof Dianne Gleeson[1,3], Dr Alejandro Trujillo-González[1], Dr Mike Hodda[2], Dr Daniel Huston[2]
[1]University of Canberra, [2]CSIRO, [3]Australian Research Council Training Centre in Plant Biosecurity, Australia

1 Background

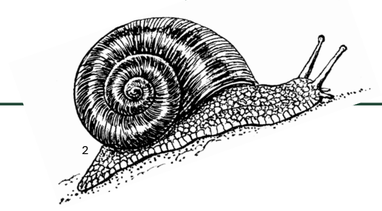
- Invasive snails are able to "hitchhike" across the border by attaching themselves to many objects including **shipping containers**, **tyres**, **machinery**, **vehicles** and **ships**[1].

But are these snails travelling alone?

- Many terrestrial snails host **parasites** with **medical**, **veterinary** and **plant health** significance.
- Understanding whether invasive snails **introduce** or **facilitate parasite transmission** is critical for assessing the **full biosecurity risk** posed by these snails.
- **Parasite transmission** by terrestrial snails is poorly understood **in Australia** and is often **overlooked** in an **invasion context**.

2 Overall Aims

1. To evaluate the **role** of terrestrial snails as **vectors** of pathogens and parasites in an invasion context.
2. To assess the overall **biosecurity risk** of terrestrial, invasive snails to Australia from a **human**, **animal** and **plant health** perspective.
3. To determine how **parasite co-invasion** could be **integrated** into future **biosecurity planning** and **frameworks**.



3 Methods

A systematic literature review to identify and assess the parasites being vectored by terrestrial, invasive snails worldwide.

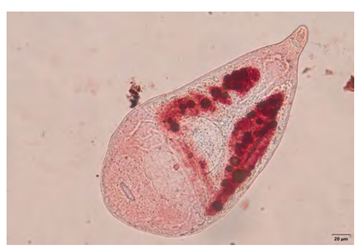
→ **Field sampling across Australia** to investigate the parasite assemblages of terrestrial, invasive snail species.

→ **Evaluation of evidence** to determine if exotic parasite **spillover** is occurring from terrestrial, invasive snails to terrestrial, native snails in Australia.

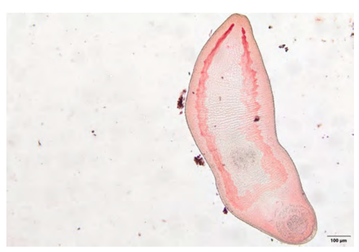
→ **Risk modelling** to assess the variables and risk pathways for parasite co-introduction into Australia through terrestrial, invasive snails.

4 Initial Field Sampling Findings

- **8** different species of terrestrial, invasive snails have been collected from across **Queensland, Western Australia** and **South Australia**.
- **759** specimens were collected and **dissected live**.
- **Nematodes**, **trematodes** and **ciliates** have been found to date.



Trematode **cercariae** found in a terrestrial, invasive snail in Perth, Western Australia.



Trematode **metacercariae** found in a terrestrial, invasive snail in Perth, Western Australia.

Adult nematode found in *Cochlicella acuta* and *Prietocella barbara* snails in South Australia.

Close up of an egg inside an adult nematode found in *Cochlicella acuta* and *Prietocella barbara* snails in South Australia.

Ciliate found in terrestrial, invasive snails across Australia.

5 Project Outcomes

To improve understanding of how invasive snails alter **disease dynamics** and impact **biodiversity**.

To identify **priority risks** for future biosecurity frameworks.

To conduct a **full biosecurity risk assessment** of terrestrial, invasive snails established in Australia.

To provide a **new, exemplar framework** which could be incorporated into Australian biosecurity risk assessments.

To evaluate the main parasites of **medical**, **veterinary** and **agricultural** importance.

To raise awareness of how terrestrial, invasive snails and their parasites **interact** with the environment and native species in Australia.

References:
1. DAFF (Department of Agriculture, Fisheries and Forestry) (2022) *National Hitchhiker (Contaminating) Plant Pest Action Plan 2022-2032*, DAFF, Australian Government, accessed 19 April 2026.
2. Foresman S (2019) *Line art drawing of a snail, Helix sp.* [figure] Wikimedia Commons website, accessed 19th April 2026.

Acknowledgements:
This project is supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027). I would like to acknowledge my supervisory panel from the University of Canberra and CSIRO. I would also like to acknowledge the South Australian Research and Development Institute (SARDI), Dr Storm Martin at Murdoch University and Dr Thomas Cribb and Dr Russell Yong at the Queensland Museum for their help with field sampling and provision of laboratory facilities.

ARC Training Centre in Plant Biosecurity

Absence-Aware GREC for Agriculture

Generalized Referring Expression Comprehension with Controlled Negatives

Xin Zhu[1,2,3], Mohammadreza Haghighat[1,2], Tao Huang[1,2], Mohammad Jahanbakht[1,2,3], Mostafa Rahimi Azghadi[1,2,3,*]

[1] College of Science and Engineering, James Cook University, Townsville, QLD, Australia
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1. What is GREC ?

REC

Query: "car parked beside sidewalk" → **REC Model** →

Output: exactly 1 box. Returns one bounding box (bbox) for the referent assumed to exist.

Generalized REC [2]

Query: "car parked beside sidewalk" → **GREC Model** →

Output: 0, 1, or many boxes. Returns ∅ when nothing matches the text query (phrase).

2. Motivation

The problem: SOTA (State-of-the-Art) GREC rejection (∅) is still weak

- No-target (N-acc) on gRefCOCO [1] measures GREC rejection
- SOTA N-acc sits around **56%-76%** [4, 8] — many absent queries get false bboxes.
- Weak rejection stems from easy training negatives (random, not **close-but-wrong**).

Our goal: A dataset with hard negatives → stronger rejection ability

- 5 controlled negatives per positive
- Train an absence-aware head that **predicts ∅** for null matches.
- Push N-acc higher and apply to agriculture.

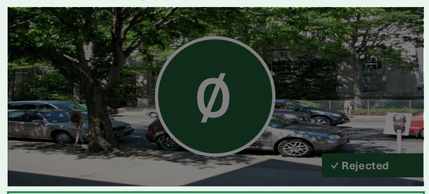
GREC: False bbox

"sidewalk parked beside car"
(no relation in image)

✗ predicts false boxes

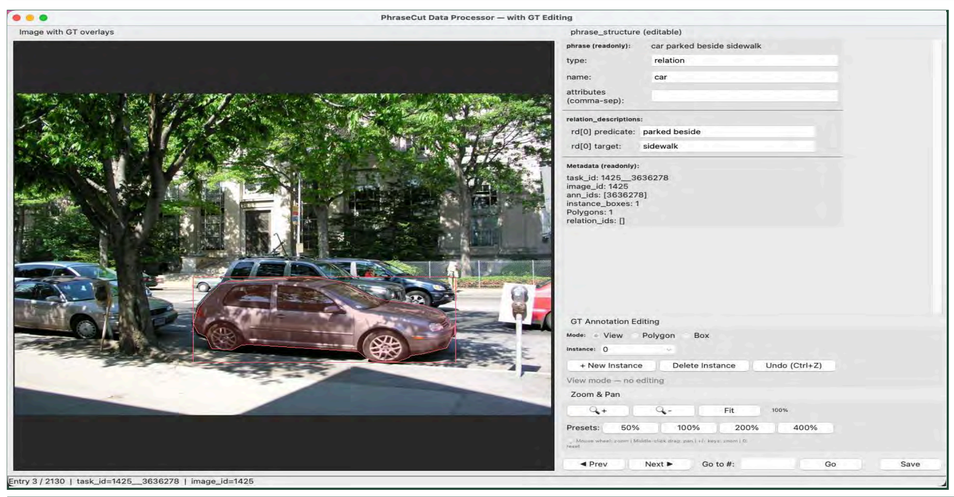
Ours: Success rejection

"sidewalk parked beside car"
(no relation in image)



✓ rejects — no target (∅)

3. Our Developed Annotator & Novel gPhraseCut Dataset based on PhraseCut [5]



Phrase template

<att> <cat> <rel> <rel_object>

Example — 1 positive + 5 controlled negatives

POS	"silver car parked beside sidewalk"	
NEG	"red car parked beside sidewalk"	(attribute replacement)
NEG	"silver building parked beside sidewalk"	(category replacement)
NEG	"silver car apart from sidewalk"	(relation replacement)
NEG	”sidewalk parked beside car"	(subject object swap)
NEG	"silver wood paved with helmet"	(random replacement)

Dataset statistics

Split	#Images	#Phrases	Pos : Neg
Train	~47,000	~282,000	1 : 5
Val	~3,000	~18,000	1 : 5
Test	~2,000	~12,000	1 : 5
Total	**~52,000**	**~312,000**	**1 : 5**

4. Method — Absence-Aware GREC Pipeline

1. Input

Query
"car parked beside sidewalk"
(may or may not be present)

2. Grounded matching with absence head

Visual encoder image → regions
Text encoder phrase → tokens
→ **Region scorer** matches each region to the text tokens
→ **Presence gate** decides: box or ∅

The presence gate makes the model say "rejection" (∅) instead of forcing a wrong box — the key to absence-aware grounding.

3. Output

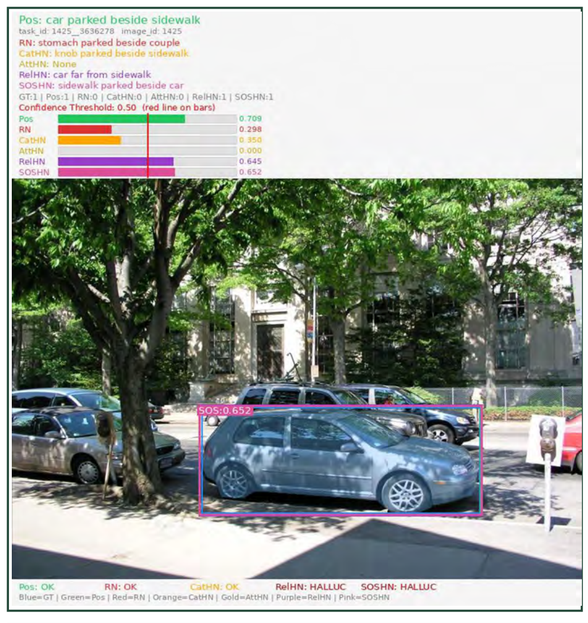
If present
☐ bounding box on the real target

If absent
∅ refuse directly (no false detection)

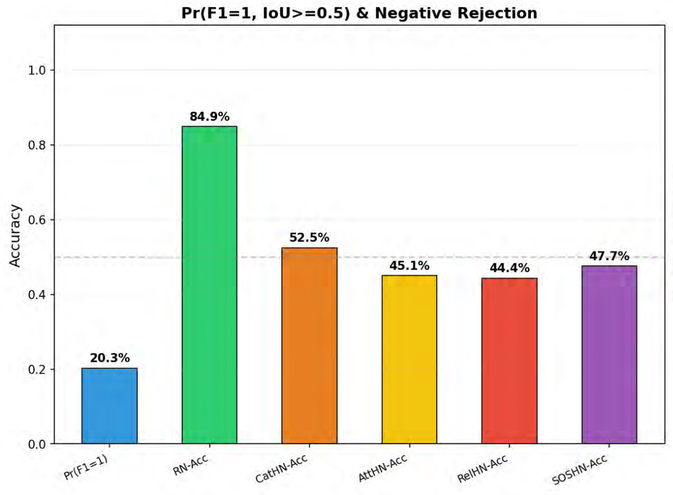
Train once, transfer to many

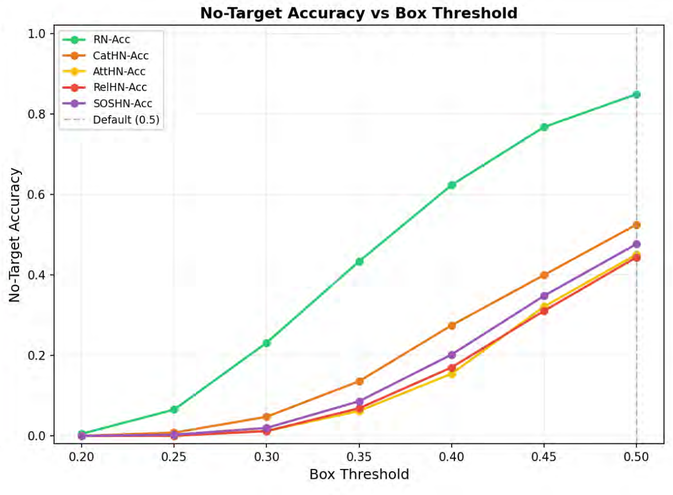
- **Pre-train on gPhraseCut:** yields a generalised, absence-aware GREC model.
- **Adapt to each domain:** light fine-tuning on a small domain-specific dataset.
- **Why generalised > specialised:** one model covers many tasks, fewer labels per task, inherits absence-aware refusal.
- **Examples:** fruit counting, weed mapping, plant disease prevention.

5. Experiments & Results (gPhraseCut)

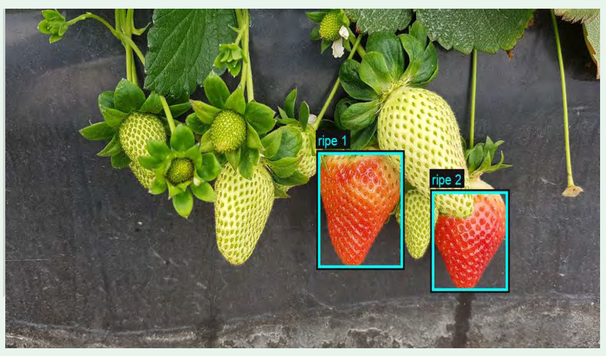


Benchmark results (Precision@(F1=1, IoU>=0.5), N-acc) on gPhraseCut test set





6. Application — Multi-label Visual Grounding in Agriculture



Fruit counting [7]

Success query: "how many ripe strawberries?"

Counts ripe fruit, ignores unripe — drives yield estimation & harvest scheduling.

Weed mapping [3]

Failure query: "any weeds near the crop seedling"

Locates weeds and ignores crop seedlings — enables spot-spraying and increases crop yields.

Plant disease prevention [6]

Success query: "any leaves of cauliflower with brown spots?"

Spots early infections, says ∅ on healthy plants — targeted spraying, less chemical use.

Conclusion: gPhraseCut + absence-aware GREC model delivers reliable grounding and transfers to agricultural multi-label grounding.

References: [1] GRES (CVPR'23) [2] GREC (arXiv'23) [3] Multi-label Instance-level Generalised VG in Agriculture [4] GREx (IJCV'26) [5] PhraseCut (CVPR'20) [6] Benchmarking In-the-Wild Multimodal Plant Disease Recognition and A Versatile Baseline [7] The Strawberry Digital Images Data Set [8] Improving Generalized Visual Grounding With Instance-Aware Joint Learning (TPAMI'26)

Acknowledgement: This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

ARC Training Centre in Plant Biosecurity

Sampling Irrigation Water to Detect Vegetable Plant Pathogens

Presented by: Addam Corallo[1,2]
Supervised by: Dianne Gleeson [1], Brendan C Rodoni [2], Fiona E Constable [2]

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[2] Agriculture Victoria, 5 Ring road Bundoora, Victoria, Australia

Australian Horticulture is under persistent threat of **exotic and endemic pathogens**

Monitoring and Surveillance tools are essential for management strategies to improve outcomes

Irrigation networks are major pathways for pathogen movement into and out of production sites (1).

Sampling this irrigation substrate for pathogens could offer an **efficient** means to **monitor these sites at scale**

Project goals

START

1. Risk mapping and pathways

Understanding the flow and expected volume of plant pathogens in irrigation networks will **inform project potential** and **sampling / handling methodology.** Characterising irrigation infrastructure and pathogen interplay can inform **risk**.

2. Optimising sampling

Ideal sampling methods can **maximise sensitivity** while **reducing costs**, improving outcomes and management strategies.

Case Study

Cucumber green mottle mosaic virus (CGMMV)
Highly transmissible and stable in water. Can use irrigation networks as a pathway to spread through facilities, to other plants or natural reservoirs (2).

GOAL

3. Surveillance Pipeline

Ability to enter a production site, map the system and efficiently monitor and triangulate pathogen presence using irrigation water.

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

References:
1. Lamichhane JR, Bartoli C. Plant pathogenic bacteria in open irrigation systems: what risk for crop health? Plant Pathology. 2015;64(4):757-66.
2. Li J-X, Liu S-S, Gu Q-S. Transmission Efficiency of Cucumber green mottle mosaic virus via Seeds, Soil, Pruning and Irrigation Water. Journal of Phytopathology. 2016;164(5):300-9.

Accelerating post-entry quarantine for tissue culture plants

Stephanie Morgan[1,2], Dr Matt Barrett[1], Prof Lori Lach[1], Dr Adrian Dinsdale[2], Dr Shamila Abeynayake[2]

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The Problem: Plant virus diagnostics are too slow and inefficient to meet current biosecurity needs

- Viruses cause 40% of agricultural crop losses annually, equating to $30 billion [1, 2].
- Increased global trade is putting biosecurity systems under increasing pressure [3].
- Tissue culture imported through Australia's post-entry quarantine is a lengthy process.
- Virus diagnostics are challenging – latencies, uneven distribution, low titre, absence of universal barcode [4, 5].

My project will develop a single diagnostic assay using high-throughput sequencing (HTS)

1. Compare plant tissue culture sampling times and tissue types.
2. Compare HTS methods (RNA-Seq, sRNA-Seq and dsRNA-Seq) and platforms (Illumina and Oxford Nanopore).
3. Compare HTS viral diagnostics on tissue culture plants to mature glasshouse-grown plants.

HTS virus screening directly on tissue culture plants

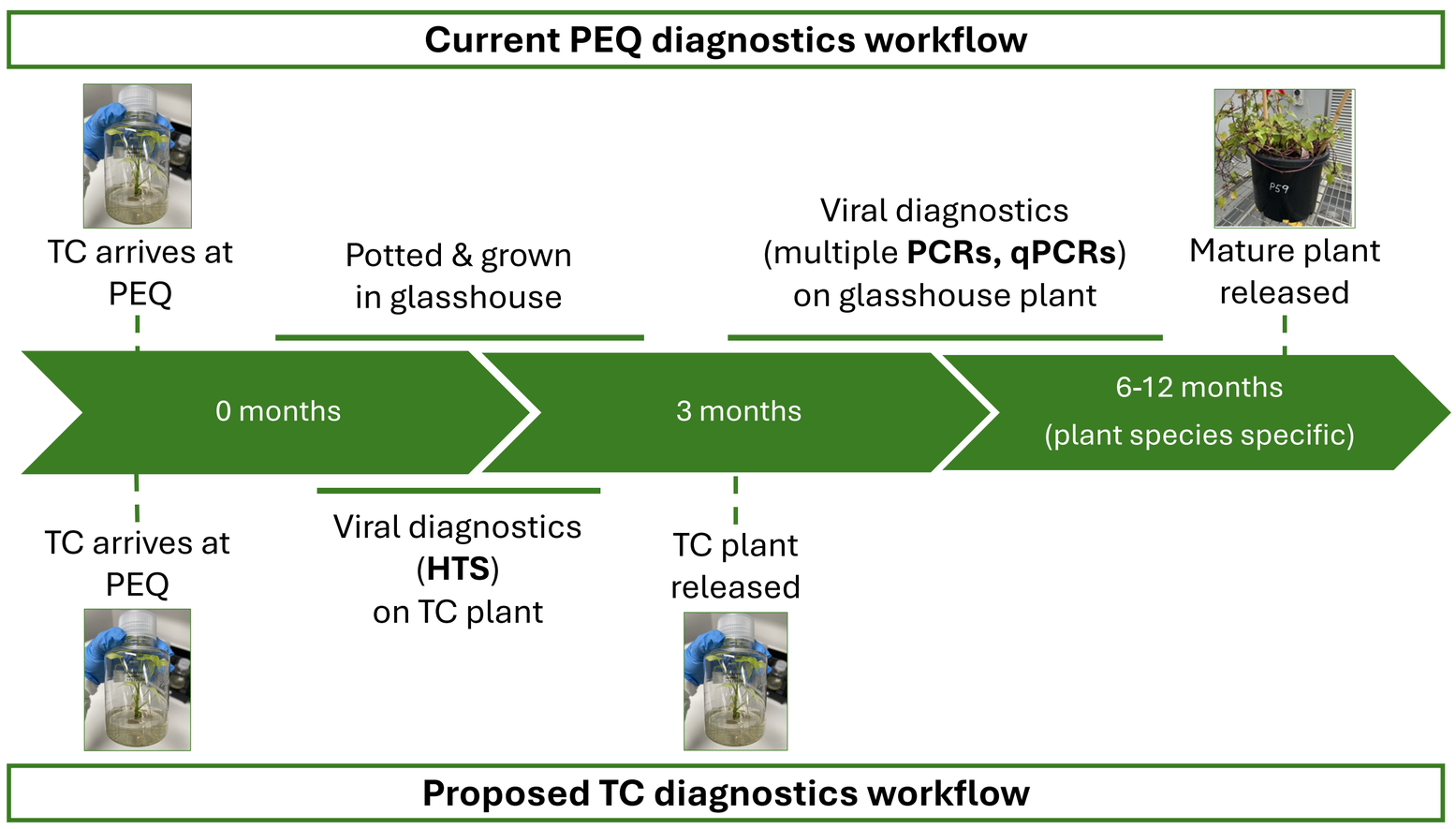

Figure 1. PEQ workflows demonstrating the current PEQ virus diagnostic workflow to the proposed tissue culture (TC) workflow that could offer accelerated virus diagnostics in PEQ.

Expected Outcomes

- ✓ Rapid and reliable diagnostic assay for tissue culture plants.
- ✓ Accelerate post-entry quarantine process (Figure 1).
- ✓ Faster access to new germplasm for Australian farmers.
- ✓ Reduced PEQ cost.
- ✓ Improved biosecurity outcomes.

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- [3] Rodoni, B. (2009). The role of plant biosecurity in preventing and controlling emerging plant virus disease epidemics. Virus research, 141(2), 150-157. https://doi.org/10.1016/j.virusres.2008.11.019
- [4] Valenzuela, S. L., Norambuena, T., Morgante, V., García, F., Jiménez, J. C., Núñez, C., Fuentes, I., & Pollak, B. (2022). Viroscope: plant viral diagnosis from NGS data using biologically-informed genome assembly coverage. bioRxiv. https://doi.org/10.1101/2022.09.14.507814
- [5] Maina, S., Donovan, N. J., Plett, K., Bogema, D., & Rodoni, B. C. (2024). High-throughput sequencing for plant virology diagnostics and its potential in plant health certification. Frontiers in Horticulture, 3. https://doi.org/10.3389/fhort.2024.1388028

ARC Training Centre in Plant Biosecurity

Resolving the taxonomy of the *Zeugodacus tau* (pumpkin fruit fly) species complex

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Background

Tephritidae: **500** genera, **5000** spp.
Dacini: >**900** spp., ~**10%** pests of crops

- Market access
- Trade regulations
- Quarantine
- Crop yield

→ **Food stability** (especially developing countries)

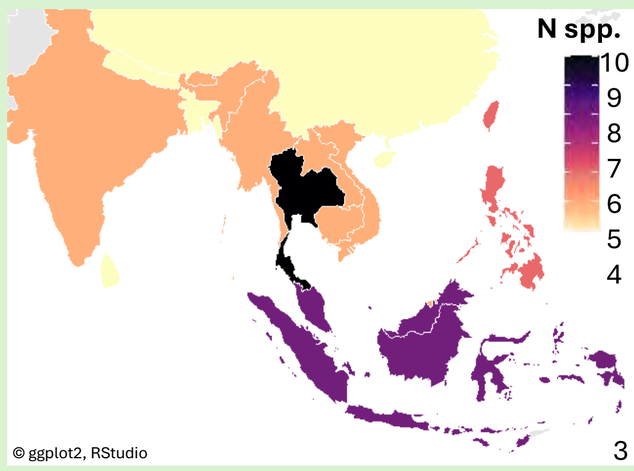
- High intraspecific variability [Fig.1]
- Low interspecific variability

***Zeugodacus tau* complex** [Fig.2]

→ Many **cryptic** species complexes (e.g. *Bactrocera dorsalis* — 88 spp.) → **Ambiguous taxonomy**

SE Asia [Fig.3] — hotspot of differentiation in **Thailand**
62 plant species across **25** families (mainly Cucurbitaceae [Fig.4])

- 21 species (Drew & Romig, 2013)
- 7 'forms' (Zaelor & Kitthawee, 2018)



Objective

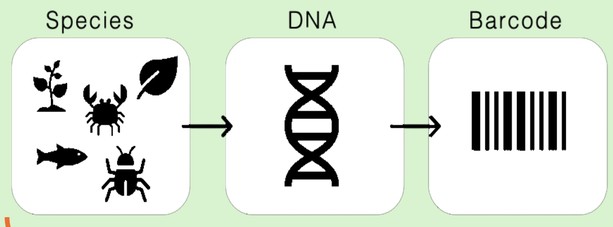
Resolve the *Zeugodacus tau* species complex with an **integrative taxonomic** approach, to underpin stable and accurate taxonomy for **effective Plant Biosecurity** (e.g. rapid pre- and post-border diagnosis)

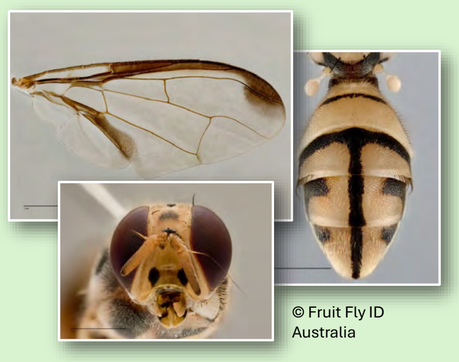
Methods

a) Genome-wide population sequencing and phylogenetic tree reconstruction (both **museum** and **field** specimens)

Qld Dept. of Primary Industries collection

Thailand cultivated fields & orchards



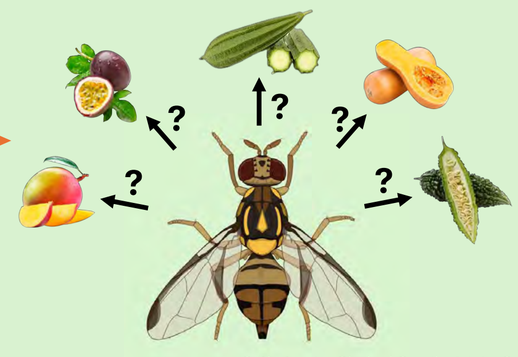


b) Morphology:

- Reliability of current characters
- Evaluation of new characters

c) Ecology and behavior:

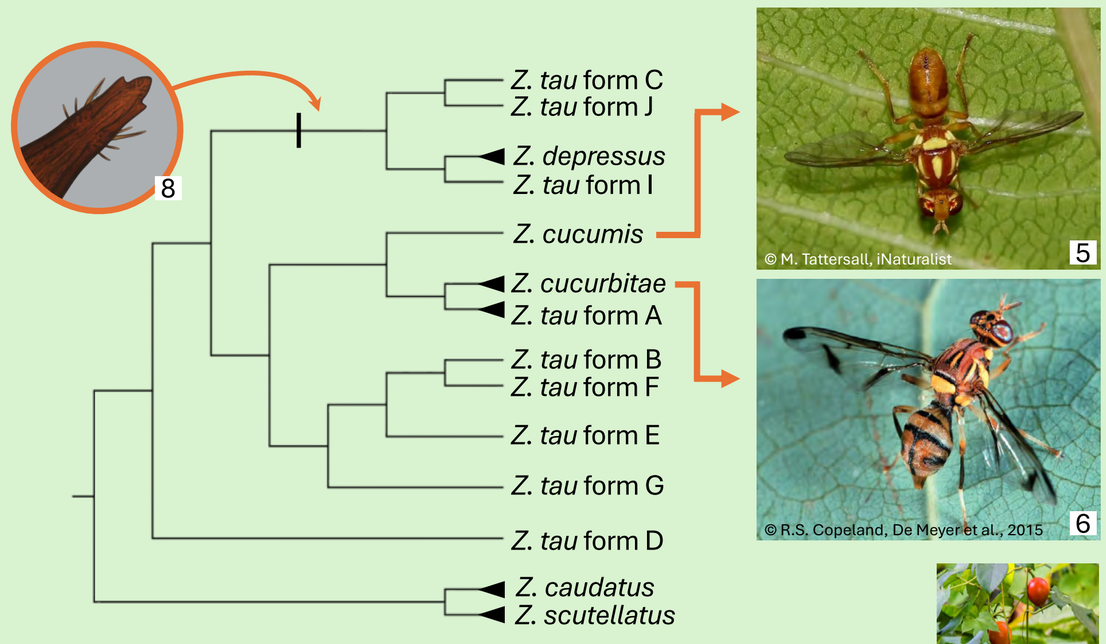
- Host breadth and preferences
- Response to male lures
- Other reproductive barriers



Species delimitation will integrate a robust foundation of **molecular** evidence with **morphological** characteristics and **ecological** traits. The objective is to apply the biological species concept as rigorously as possible, as non-integrative evidence is often insufficient for reliable species delimitation (Schlick-Steiner et al. 2010).

Where are we now (8 months in PhD candidature)

- *Z. tau* complex probably **not monophyletic**; clade of polyphagous species and successful pests — *Z. cucumis* [Fig.5] + *Z. cucurbitae* [Fig.6] + *Z. tau* sensu strictu ("form A")
- Baseline of hosts: Cucurbitaceae (e.g. *Momordica cochinchinensis* [Fig.7])
- Evolution of trilobed aculeus [Fig.8] in clade that kept ancestral hosts (Cucurbitaceae) vs. needle-shaped aculeus in clades with larger host breadth
- **Evolutionary trend to generalism?**



Cryptic species in the southern region of Thailand occurring on *Trichosanthes and Gymnopetalum* lesser crops [Fig.9]

◄ *T. scabra*

▲ *T. kirilowii*

▲ *T. tricuspidata*

© Wikipedia
9

References: Drew & Romig (2013) CABI England 644pp. ; Zaelor & Kitthawee (2018) Zoological Systematics 43: 27–36; Schlick-Steiner et al. (2010) Annual Review of Entomology 55: 421–438.

JAMES COOK UNIVERSITY AUSTRALIA

Queensland Government

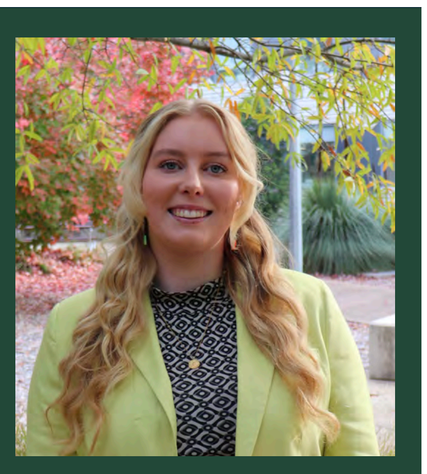
ARC Training Centre in Plant Biosecurity

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027).

Improved sugarcane biosecurity preparedness with the genetic characterisation of the fungal orange rust pathogen (*Puccinia kuehnii*) of sugarcane in Australia

Samantha Whitling[123], Lavi Singh[123], John Rathjen[1], Celeste Linde[1], Seona Casonato[3], Benjamin Schwessinger[1]

1 - Australian National University, 2 - ARC Training Centre in Plant Biosecurity, 3 - Sugar Research Australia



Sugarcane orange rust epidemics cause crop and financial loss

- 2025 Australian sugarcane industry contributes AUD $2.5 billion to the Australian economy
- Orange rust (*Puccinia kuehnii*) is a fungal foliar pathogen of sugarcane
- In epidemic conditions *P. kuehnii* lead to 40% crop loss
- *Puccinia kuehnii* has been present in Australia since late 1800s, however little is known about the genomics or population diversity of *P. kuehnii*

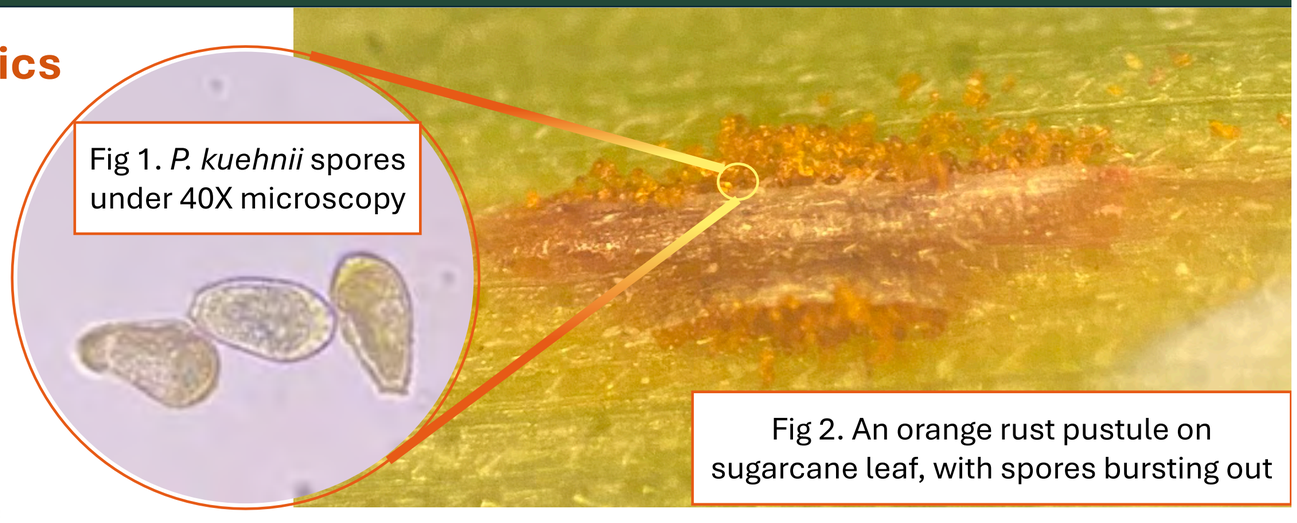


Fig 1. *P. kuehnii* spores under 40X microscopy

Fig 2. An orange rust pustule on sugarcane leaf, with spores bursting out

My PhD research aims to understand the infection biology and genetics of *P. kuehnii* to inform disease management

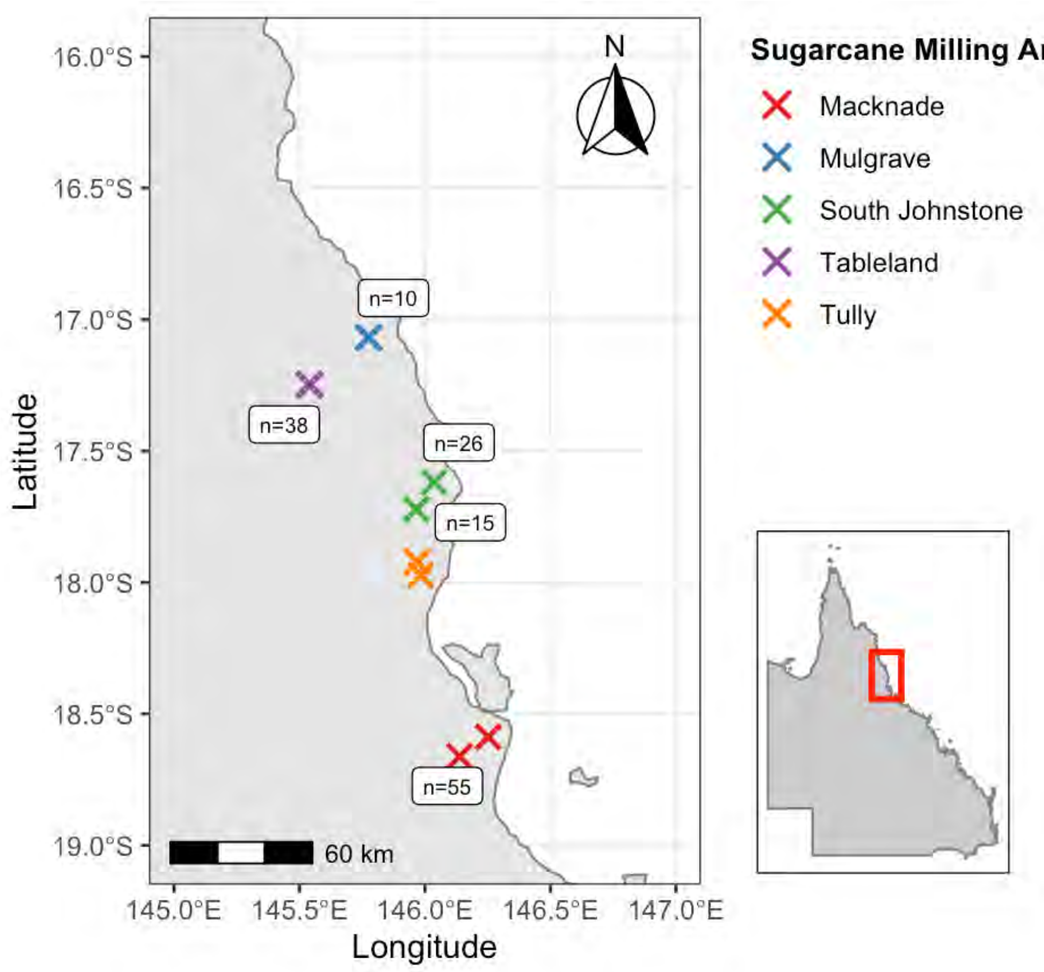
I have optimised controlled *P. kuehnii* infections to obtain sufficient spore stocks for DNA extraction, genome assembly, transcriptomic studies, and confocal microscopy.

Are there different strains of *P. kuehnii* present in Australia?

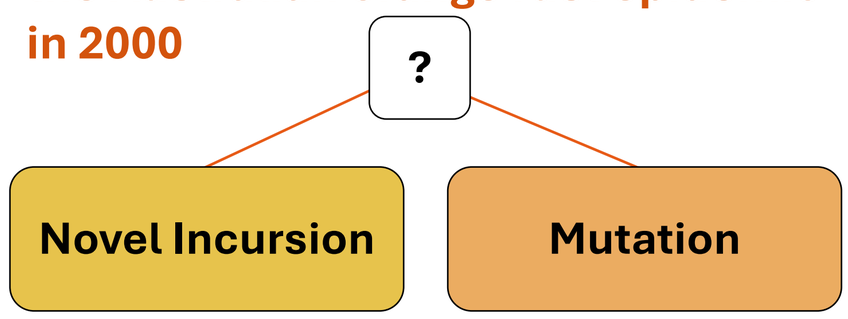
Understanding *P. kuehnii* genetics, infection biology and population structure will increase preparedness for orange rust epidemics.

A high-quality genomic resource will contribute to future surveillance and diagnostics.

Fig 3. *P. kuehnii* isolates collected per sugarcane milling area in Far North Queensland 2026



Comparing current *P. kuehnii* populations to historical samples could tell us what caused the breakdown of resistance that led to the Australian orange rust epidemic in 2000



To date, I have :

- collected isolates from various sugarcane growing regions (Figure 3) to compare the potential genetic diversity of *P. kuehnii* in Australia.
- received historical herbarium samples from NSW DPIRD for comparison with present isolates.

This project was supported by the Australian Government through the Australian Research Council Training Centre in Plant Biosecurity (IC230100027)