



Genetically cryptic but behaviourally distinct: the sympatric pest *Bactrocera tryoni* and sibling *B. neohumeralis* species of fruit fly (Diptera: Tephritidae).

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Better Border Biosecurity (B3)
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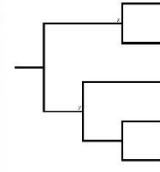


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Collaborators: Sally Cowan, AQIS QLD
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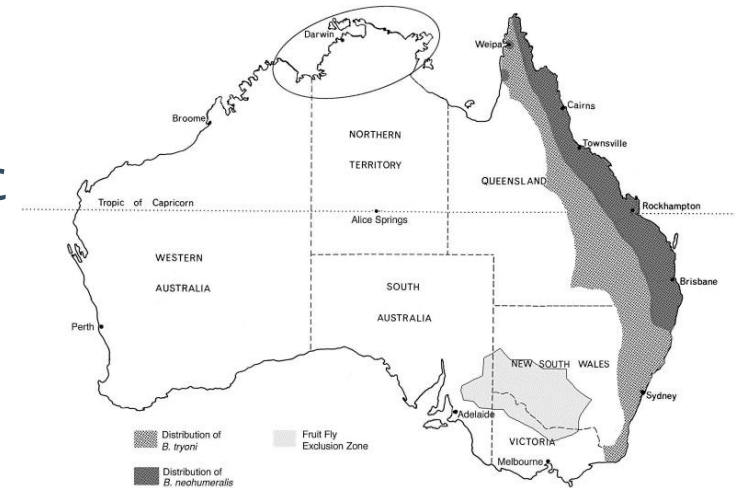
My background

- Interested in insects since a young age
- Bachelor of Science majoring in Bio-Protection & Biosecurity and Ecology & Conservation:
East Timor Fruit fly genetics
Tussock butterfly taxonomy & phylogenetics
- 1st Class Honours majoring in Entomology:
Black mountain ringlet butterfly taxonomy & phylogenetics
Arctesthes moth taxonomy and phylogenetics
New Zealand native fruit fly taxonomy and phylogenetics
- Coauthor of 'Butterflies of the South Pacific'



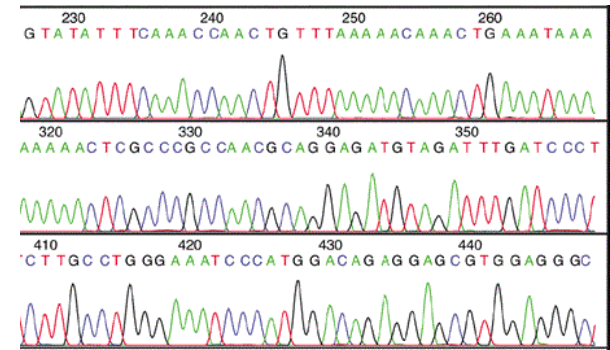
The *Bactrocera tryoni* species complex

- 4 named species
- *B. tryoni* & *B. neohumeralis* are sympatric
- *B. tryoni* is a serious pest
- Recorded from 117 hosts
- Occasionally intercepted in NZ
- Differ in two characteristics
- Species status of other two unknown



What do we know about their DNA?

- Several genetic regions sequenced
- No fixed differences found
- *B. tryoni* genome recently sequenced



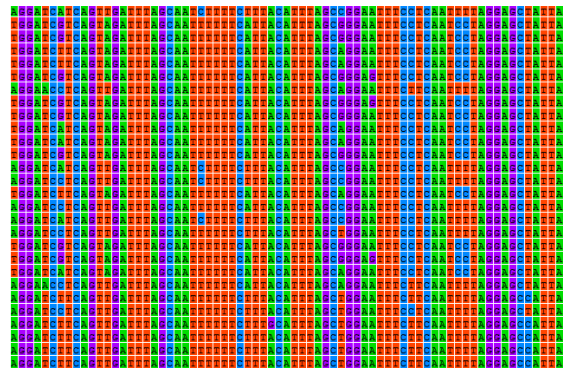
This is a problem

- Genetic methods often used to ID and discover source
- Can't differentiate between members of the complex

Project Aims

To use modern Next Generation Sequencing methods to:

- Find genetic differences useful for identification
- Learn more about evolutionary history
- Evaluate the species status of the complex members



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Methods: Collecting & DNA extraction

- Collect flies throughout the native range
- Bring back to NZ for identification and DNA extraction



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Methods: DNA sequencing & analysis

- Sequencing using Genome By Sequencing (GBS)
- Align to reference genome of *B. tryoni*
- Use a variety of programs to analyse sequence data



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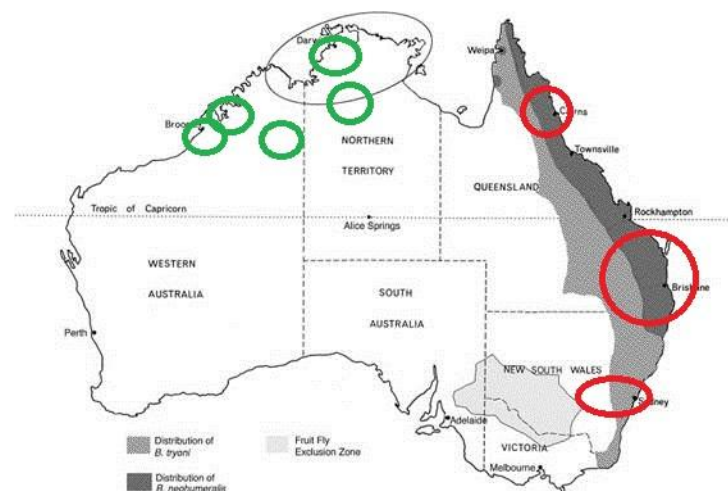
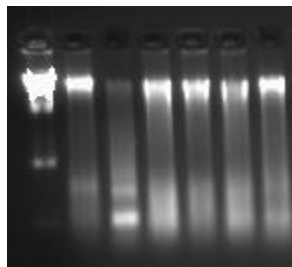


The logo for Stacks, featuring a stylized 'S' icon composed of horizontal lines above the word 'Stacks' in a large, bold, black, sans-serif font.



Results so far

- 1000+ specimens collected from a total of three expeditions
- 190 samples sent for sequencing
- Have learnt how to ID these species
- Transportation method developed for bringing specimens back to NZ without degrading DNA
- Sequence data due in June



Potential outcomes

- The development of a novel genetic marker for identifying members of the complex when they come into NZ
- Updated and accurate taxonomy
- A fuller understanding of the role genetics play in the development of pest status and the speciation of this complex



My future intentions

Continue working to resolve difficult taxonomic groups utilising the modern genetic tools learnt from this PhD



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Questions

