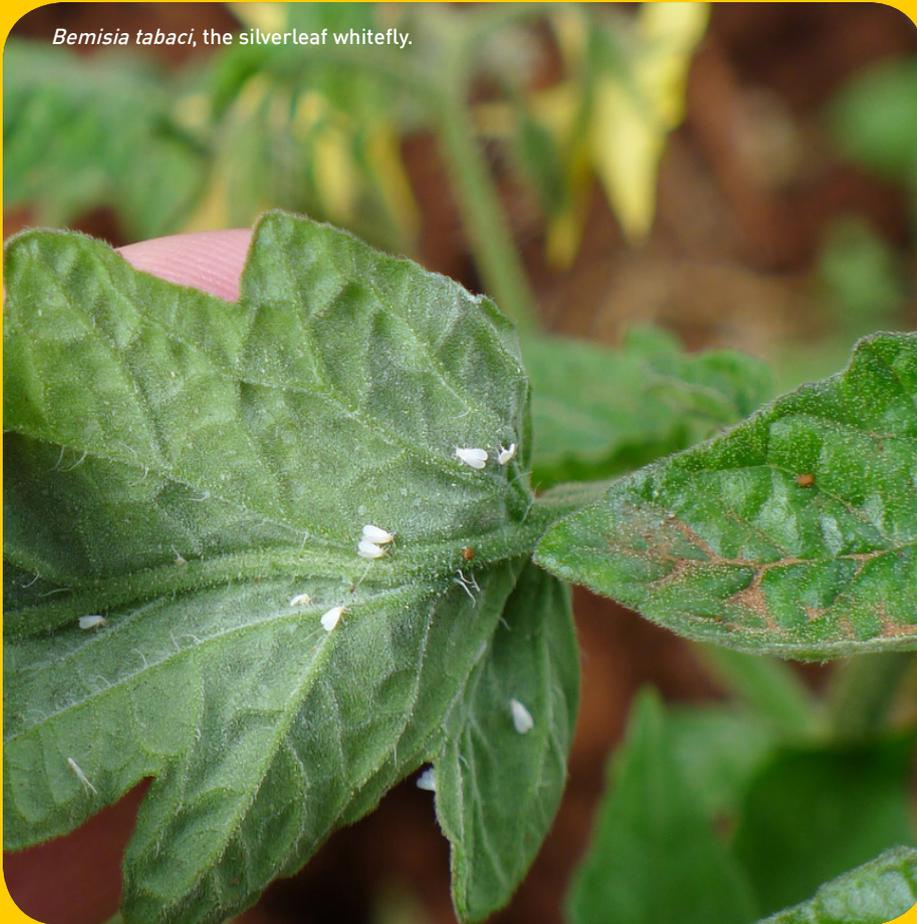


*Bemisia tabaci*, the silverleaf whitefly.



PROJECT LEADER  
A/PROF LAURA BOYKIN

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Main collaborators  
Professor Ian Small  
Peter Beerli

SYSTEM  
MAGNUS

TIME ALLOCATED  
217,832 hours

AREA OF SCIENCE  
PLANT BIOLOGY

APPLICATION USED  
MRBAYES

# SUPERCOMPUTERS AND GLOBAL FOOD SECURITY

## *KNOWING THE ENEMY*

Assistant Professor Laura Boykin of The University of Western Australia's Plant Energy Biology ARC Centre of Excellence is using the Pawsey Supercomputing Centre's resources and expertise to assist farmers in poverty-stricken Eastern Africa by building more accurate identification systems for highly invasive pest species, including *Bemisia tabaci*, the silverleaf whitefly. These systems could potentially bring great benefits to researchers and farmers all over the world, including Australia.

2014



The cassava plant.

# OPTIMAL MCMC STRATEGY FOR BAYESIAN PHYLOGENETIC ANALYSES

A key problem for researchers and farmers is the visual similarity between various species of whiteflies. This makes differentiating between harmless and invasive species almost impossible, as well as hindering management strategies. Different species respond to different strategies, such as pesticides or biological controls.

“It’s a pest which is found all around the world affecting agriculture wherever they go, and the techniques that we’re developing with the East African white flies can be applied with researchers and farmers all around the world,” says A/Prof Boykin.

## THE CHALLENGE

Whiteflies are one of the most pervasive pests on Earth, being found on every continent except Antarctica. While some species of whitefly are harmless native populations, many are highly invasive pests. These invasive species feeds on valuable crops and spread viruses, causing more plants to die.

A/Prof Boykin’s project in particular looks at the silverleaf whitefly, *Bemisia tabaci*. This species is spread throughout the world, including populations in the United States, Australia and Eastern Africa.

## THE SOLUTION

A/Prof Boykin is using phylogenetic techniques to better understand the relationships between white flies around the world. Running a program on ‘Magnus’ using the Markov chain Monte Carlo method, the project is able to genetically distinguish between *Bemisia tabaci* and other harmless species that look identical.

“This project is all about “knowing the enemy”. To a farmer, these species all look the same. This project could help develop diagnostic tests that will tell farmers if they have a harmless species or one they have to get rid of ASAP, which is invaluable,” says A/Prof Boykin.

## OUTCOME

The genetic data sets involved in this project were so large, they would be almost impossible to calculate using a desktop computer. In addition, the sophisticated techniques used in this project are also extremely computationally intensive.

This requires world-class supercomputing power. Using ‘Magnus’ and the Pawsey Supercomputing Centre’s resources and expertise, these calculations can be performed in a practical timeframe. “The Pawsey Supercomputing Centre has really helped,”

says A/Prof Boykin. “The beauty of this particular project is it really is a true engagement. It’s not just me using the resources, I’m interacting with the scientists and staff there as well. It’s made a huge difference in pushing this research forward.”