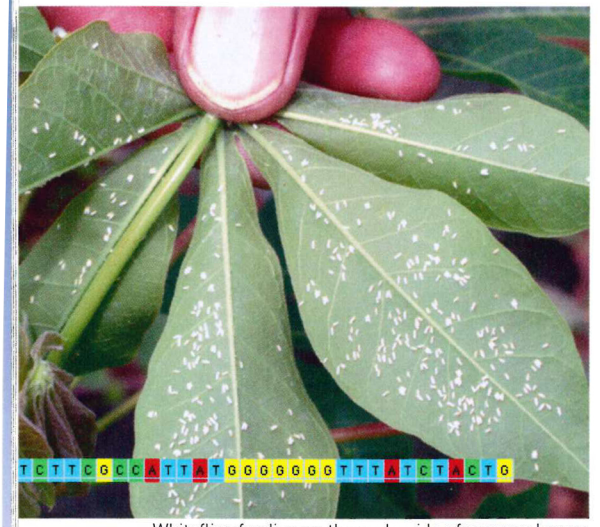
KNOWING THE ENEMY



Whiteflies feeding on the underside of cassava leaves

A/Prof 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 in Australia.

The Problem

Species of whitefly 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, leaving many smallholder farmers without enough food to feed their families.

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

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 of whiteflies respond differently to varying 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 whiteflies can be applied with researchers and farmers all around the world," says A/Prof Boykin.

The Solution

A/Prof Boykin is using phylogenetic techniques to better understand the relationships between whiteflies 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.

How the Pawsey Supercomputing Centre Helped

The genetic data sets involved in this project involved upwards of thousands of base pairs. Even with only 500 whiteflies in a dataset, the possible relationships between these flies would be an almost impossible calculation using a desktop computer.

"There's not enough computing power to do it using normal methods," says A/Prof Boykin.

As well as the size of the data sets, the sophisticated techniques used in this project are also extremely computationally intensive, necessitating 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."


Bemisia tabaci

Image courtesy A/Prof Laura Boykin