Hewlett Packard Enterprise

AMAZING IMPACT

Dr. Laura Boykin of the University of Western Australia and Dr. Titus Alicai of Uganda's NaCRRI are fighting famine in East Africa.

In 2012, computational biologist Laura Boykin visited a smallholder farm in Kenya as part of a Bill and Melinda Gates Foundation-hosted workshop. What she saw there changed her.

"I saw the devastation caused by whiteflies and viruses," Dr. Boykin says. "The situation was unacceptable, and my skills could be applied to the problem. I was also blown away by the amazing scientists in East Africa battling on the front lines of this devastation. At that moment, I decided the best use of my time on Earth was to make a difference by partnering with the team on the ground."

The silverleaf whitefly, or bemisia tabaci, attacks the cassava plant, a crucial food source for the East African region and transmits two devastating viruses, cassava mosaic disease and cassava brown streak disease. Farmers rely on cassava to bridge the gap between growing seasons after other crops such as beans and sweet potatoes have been consumed.

But when the virus-carrying whitefly descends, it can completely wipe out a year's product. For a family, an infestation suddenly means no food. For the region, it can mean widespread economic hardship and famine. And on a global level, the whitefly costs global agriculture billions of dollars a year.

Case study
Pawsey Supercomputing Centre

Industry
Academic

"I saw the devastation caused by whiteflies and viruses. The situation was unacceptable, and my skills could be applied to the problem."

– Laura Boykin, computational biologist

Pawsey Supercomputing Centre
The Pawsey Supercomputing Centre supports researchers with supercomputing, data, and visualization services across a range of scientific fields. Their supercomputer, Magnus, is a petascale Cray XC system and one of the most powerful systems in the southern hemisphere.

System details

- Cray XC series supercomputer
- Cray Sonexion storage system
- 1+ PF peak performance
- 93 TB memory
- 1,488 compute nodes
- 35,712 cores
- 3 PB Sonexion capacity

Cray was acquired by Hewlett Packard Enterprise in 2019, and this case study was originally published in 2019. Browse hpe.com/info/hpc for our latest supercomputing technologies and solutions.

Coming face to face with the devastation, Boykin, a senior research fellow at the University of Western Australia, dedicated herself to fighting the famine-causing insect.

She's joined in the effort by an international team of like-minded researchers—Dr. Titus Alicai of Uganda's NaCRRI, Drs. Joseph Ndunguru, Peter Sseruwagi, and Fred Tairo from Mikocheni Agricultural Research Institute (Tanzania), Dr. Laura Kubatko from Ohio State University, Dr. Monica Kehoe from the Department of Agriculture and Food, Western Australia, and Dr. Elijah Ateka from Jomo Kenyatta University of Agriculture and Technology (Kenya).

Their goal? To give farmers a whitefly- and virus-resistant cassava plant and equip African scientists with the knowledge to tackle future insect and virus outbreaks.

Step one lies in understanding the enemy. To expose the whitefly's vulnerabilities, the team is using genomics and supercomputing.

Awarded time on the Pawsey Supercomputing Centre's Cray XC supercomputer Magnus, Boykin and team have already overturned one long-held assumption. Scientists had thought they were battling a single silverleaf whitefly species. Turns out it's a species complex of at least 34. Additionally, they're battling more species of cassava-destroying viruses, too.

Understanding the species' genetic differences will help scientists and farmers distinguish between harmless and invasive whiteflies, develop defense strategies, and breed whitefly- and virus-resistant strains of cassava.

Computationally speaking, the challenge is vast. "We have the task of trying to make sense out of billions of base pairs—billions of As, Ts, Gs, and Cs at a time," says Boykin.

But with the petascale power of Magnus, the team is making significant progress. They've been able to generate phylogenetic trees of whitefly species from around the world. Phylogenetic trees represent evolutionary relationships, or genealogy, among species. Even with only 500 whiteflies in a data set the possible relationships between them run into the octillions (a 1 followed by 27 zeros)—a calculation impossible without a supercomputer.

Boykin and the team are making meaningful progress toward distinguishing damaging whiteflies and viruses from others and arming scientists with the information they need to develop management strategies. As proof, a disease-resistant cassava plant is already on trial in Tanzania.

"Magnus is changing the world in agricultural development," Boykin says.

LEARN MORE AT
hpe.com/info/hpc

Hewlett Packard Enterprise

a50002422ENW, August 2020