

# For the first time, researchers have mapped the complete genome of two closely related megapests

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*Helicoverpa armigera*. Credit: CSIRO

For the first time, researchers from Australia's Commonwealth Scientific and Industrial Research Organisation (CSIRO) have mapped the complete genome of two closely related megapests potentially saving the international agricultural community billions of dollars a year.

Led by CSIRO, in collaboration with a team of renowned experts, the researchers identified more than 17,000 protein coding genes in the genomes of the *Helicoverpa armigera* and *Helicoverpa zea* (commonly known as the Cotton Bollworm and Corn Earworm, respectively).

They also documented how these genetics have changed overtime.

This level of detail makes it easier for scientists to predict both the caterpillars' weak spots, how they will mutate and even breed plants they will not want to eat.

The bollworm and earworm are the world's greatest caterpillar pests of broad-acre crops, causing in excess of US \$5 billion in control costs and damage each year across Asia, Europe, Africa, America and Australia.

The bollworm, which is dominant in Australia, attacks more crops and develops much more resistance to pesticides than its earworm counterpart.

"It is the single most important pest of agriculture in the world, making it humanity's greatest competitor for food and fibre," CSIRO Scientist Dr John Oakeshott said.

"Its genomic arsenal has allowed it to outgun all our known insecticides through the development of resistance, reflecting its name - armigera which means armed and warlike."

In Brazil the bollworm has been spreading rapidly and there have been

cases of it hybridising with the earworm, posing a real threat that the new and improved "superbug" could spread into the United States.

In the mid-90s CSIRO assisted Australian cotton breeders to incorporate Bt insect resistance genes in their varieties to try and tackle the bollworm.

"Bt cotton" plants dispatch an insecticide from a bacteria - *Bacillus thuringiensis* (Bt) - that is toxic to the caterpillar.

In the following 10 years, there was an 80 per cent reduction in the use of chemical pesticides previously required to control bollworms.

However the bollworm soon fought back with a small percentage of them building resistance to BT cotton and scientists introducing further strains of insecticides to manage the problem.

CSIRO Health and Biosecurity Honorary Fellow Dr Karl Gordon said while a combination of BT and some insecticides was working well in Australia, it can be costly and it was important to comprehensive studying the pest themselves to manage the problem world-wide.

"We need the full range of agricultural science," Dr Gordon said.

"Our recent analyses of the complete genome, its adaptations and spread over the years are a huge step forward in combating these megapests."

Identifying pest origins will enable resistance profiling that reflects countries of origin to be included when developing a [resistance](#) management strategy, while identifying incursion pathways will improve biosecurity protocols and risk analysis at biosecurity hotspots including national ports.

As part of the research, CSIRO and the team updated a previously developed potential distribution model to highlight the global invasion threat, with emphasis on the risks to the United States.

The findings further provide the first solid foundation for comparative evolutionary and functional genomic studies on related and other lepidopteran pests, many of considerable impact and scientific interest.

**More information:** S. L. Pearce et al. Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive *Helicoverpa* pest species, *BMC Biology* (2017). DOI: 10.1186/s12915-017-0402-6

Provided by CSIRO

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