

Why the whitefly is such a formidable threat to food security

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Adult whiteflies on a watermelon leaf. Credit: CSIRO

Researchers have sequenced the genome of the whitefly (*Bemisia tabaci*), an invasive insect responsible for spreading plant viruses worldwide, causing billions of dollars in crop losses each year.

The genome study, led by Associate Professor Zhangjun Fei of the

Boyce Thompson Institute (BTI), offers many clues to the insect's remarkable ability to resist pesticides, transmit more than 300 plant viruses, and to feed on at least 1,000 different plant species. Published today in the journal *BMC Biology*, the study will serve as a foundation for future work to combat this global pest.

"Whitefly is an economically important pest for agriculture crops. It causes direct damage and also is a major vector for viruses, like Tomato yellow leaf curl virus, Cassava mosaic virus and Cassava brown streak virus, so it creates huge [crop losses](#) and poses serious threats to food security, especially in Africa and other parts of the developing world," said Fei.

In collaboration with a group of international colleagues, BTI researchers created a high-quality draft [genome sequence](#) of the whitefly and identified [genes](#) that code for proteins. The genome sequence can be accessed at the [whitefly genome database](#) developed by the Fei lab.

An analysis showed that, compared to related species, the whitefly has expanded families of detoxification genes. It also has extra genes that code for proteins related to virus acquisition and transmission, as well as insecticide resistance.

In an impressive example of horizontal gene transfer, the whitefly has acquired 142 genes from bacteria or fungi, including some coding for enzymes that break down foreign chemicals. These genes likely allow the whitefly to feed on diverse types of plants and to rapidly evolve resistance to insecticides.

Because pesticides are ineffective at keeping whitefly populations in check, collaborators at USDA plan to use the genome sequence to develop a control strategy using RNA interference (RNAi). Once scientists pinpoint the genes necessary for virus transmission and

survival in the whitefly genome, they can develop new varieties of crops that will produce RNA molecules that block the expression of those necessary genes, killing the whitefly or preventing it from spreading the virus .

The genome will also be vital for mapping out genetic diversity in whitefly populations around the world. Whiteflies represent a group that is likely composed of a collection of species and subspecies, which may have implications for whitefly control. For example, the "superabundant" whitefly populations that are decimating cassava harvests in parts of Africa are a different variant from the insect sequenced in the current study, but sequence information generated here is aiding in the development of strategies for control of African whiteflies as well.

"The whitefly is among the top 100 invasive species in the world," said Fei. "It's everywhere."

More information: Wenbo Chen et al, The draft genome of whitefly *Bemisia tabaci* MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance, *BMC Biology* (2016). [DOI: 10.1186/s12915-016-0321-y](https://doi.org/10.1186/s12915-016-0321-y)

Provided by Boyce Thompson Institute

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