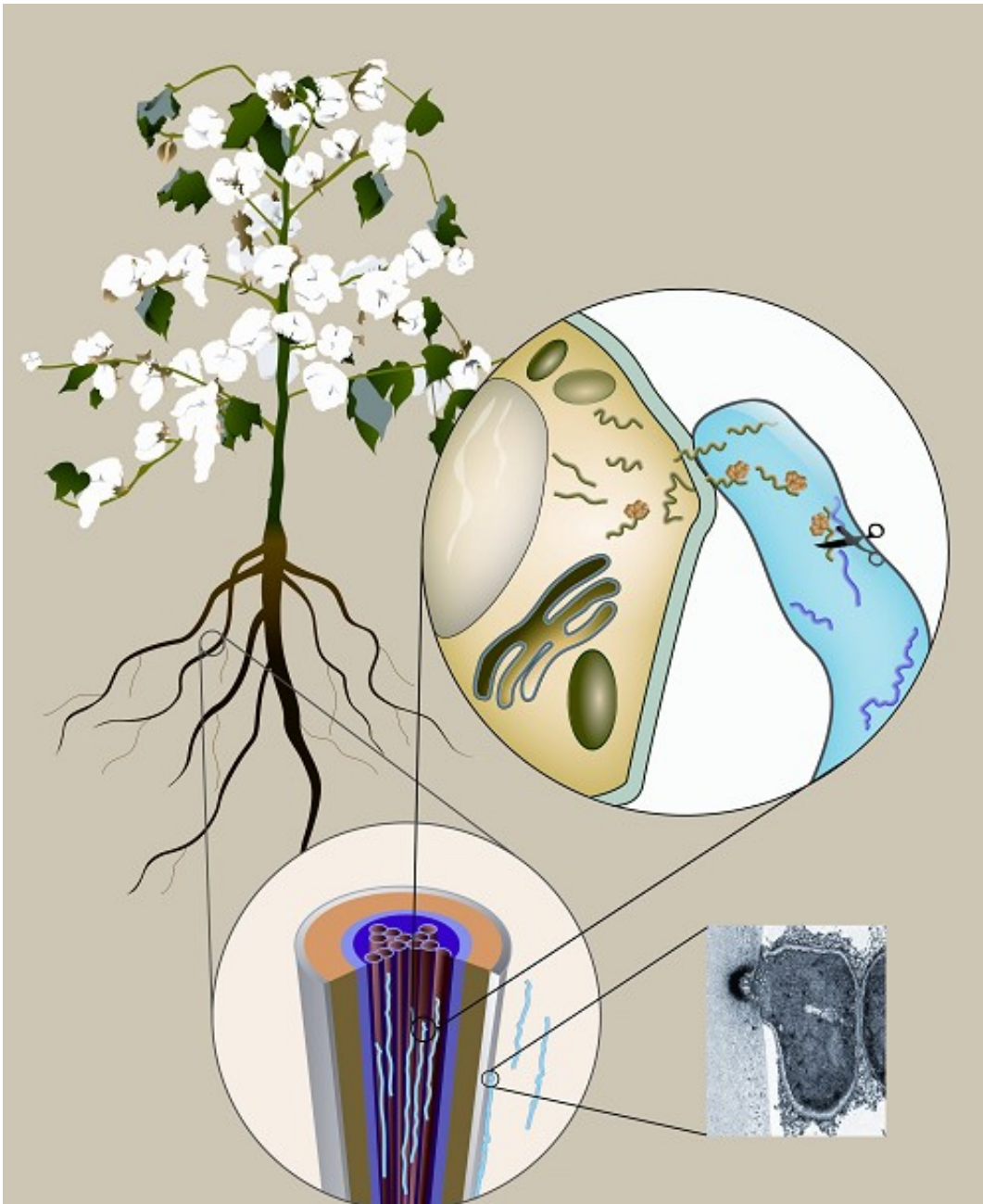


Scientists unravel weapons of defense against 'cotton cancer'

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Trans-kingdom small RNAs target *Verticillium dahliae* genes during plant-microbe interaction. The soil-borne fungal pathogen *V. dahliae* (blue in the lower figure) develops infectious structure "hyphopodium" (Transmission electron microscopy image in the lower figure on the right) to penetrate and infects cotton roots and colonizes plant vascular tissues (red tubes in the lower figure). Small RNAs (green lines in the figure on the right) transmit from the plant cell to the colonized hyphae (blue in the figure on the right), targeting and "cutting" fungal gene transcripts (purple lines in the figure on the right). Credit: Prof. GUO's group

As world's largest cotton producer, China yields six to eight million tons cotton (30% of total world production) every year. However, high quality cotton cultivars are vulnerable to *Verticillium* wilt disease. Due to their long-term survival and vascular colonization of pathogen, the disease cannot be controlled by fungicides. How *V. dahliae* infects cotton was largely unknown and very limited resistance genes can be used for cotton breeding.

A group of Chinese scientists led by Prof. GUO Huishan from Institute of Microbiology of Chinese Academy of Sciences discovered that trans-kingdom small RNAs (sRNAs) can be used to protect crops from infection of fungal pathogens. This RNAi-based mechanism has been successfully manipulated to protect [cotton](#) from infection of a soil-borne fungal pathogen *Verticillium dahlia* (*V. dahliae*), the causal agent of vascular wilt disease so-called "Cotton Cancer" in China. This study has been published online in *Nature Plants*.

GUO's focus on the research of cotton-*V. dahliae*'s infection process can be traced back to her visit in 2008 to Xinjiang in Northwest China, where she was astonished by the scene of huge area of infected cottons and desperate farmers. She began to try to search for a novel strategy to

target *V. dahliae*.

Eight years of laboratory experiment and field research have brought GUO's team consecutive achievements in understanding *Verticillium* wilt disease.

The team finds that trans-kingdom sRNAs exist during cotton-*V. dahliae* interactions, and some target virulence genes of pathogens. A novel penetration structure "hyphopodium" helps *V. dahliae* to "break" plant cell, which determines successful fungal infection (<http://dx.doi.org/10.1371/journal.ppat.1005793>). Most importantly, cotton cultivars expressing specific sRNAs are resistant to *Verticillium* wilt disease (<http://dx.doi.org/10.1016/j.molp.2016.02.008>).

Taking advantage of RNA and genome sequencing, the team found that cotton sRNAs exist in *V. dahliae* hyphae retrieved from infected cotton, which means sRNAs naturally transmit from host to pathogens during cotton-*V. dahliae* interaction.

They also demonstrated that some transmitted sRNAs target fungal genes were involved in pathogenicity and efficiently degraded gene transcripts. This phenomenon gave confidence to GUO that cotton would gain disease resistance by stably expressing sRNAs that target *V. dahliae* virulence genes.

"It was really time-consuming to generate the cottons stably expressing specific sRNAs, but we obtained them finally," said GUO. Their research proved to be successful both in the lab and in the field. sRNA expressing cottons showed 22.25% more disease resistance compared to the other cotton cultivars in the same cotton production base. The new generated cottons show resistance to wilt disease, especially in the field where the fungal populations are diverse.

More efficient fungal targets need to be found based on the established systems, which can also be guidelines for other un-controlled crop diseases in the future.

More information: Yun-Long Zhao et al, Hyphopodium-Specific VdNoxB/VdPls1-Dependent ROS-Ca²⁺ Signaling Is Required for Plant Infection by *Verticillium dahliae*, *PLOS Pathogens* (2016). [DOI: 10.1371/journal.ppat.1005793](https://doi.org/10.1371/journal.ppat.1005793)

Tao Zhang et al. Host-Induced Gene Silencing of the Target Gene in Fungal Cells Confers Effective Resistance to the Cotton Wilt Disease Pathogen *Verticillium dahliae*, *Molecular Plant* (2016). [DOI: 10.1016/j.molp.2016.02.008](https://doi.org/10.1016/j.molp.2016.02.008)

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