

Genetic road map may bring about better cotton crops

April 20 2015



Upland allotetraploid cotton (right) comes from two extant diploid species, closely related to today's *G. raimondii* (left) and *G. arboreum* (middle) or *G. herbaceum*. The interactions between the genes of these two ancestral species

are what give modern-day cotton its best qualities. Somehow, these two different lineages come together to create something greater than the sum of its parts. Credit: Laboratory of Z. Jeffrey Chen.

A University of Texas at Austin scientist, working with an international research team, has developed the most precise sequence map yet of U.S. cotton and will soon create an even more detailed map for navigating the complex cotton genome. The finding may help lead to an inexpensive version of American cotton that rivals the quality of luxurious Egyptian cotton and helps develop crops that use less water and fewer pesticides for a cotton that is easier on the skin and easier on the land.

Z. Jeffrey Chen and his collaborators, Tianzhen Zhang and Wangzhen Guo at Nanjing Agricultural University (NAU) in China, describe the new draft genomic sequence in a paper published today in *Nature Biotechnology*. Chen and another group of scientists also learned earlier this month that they will receive \$2.3 million in funding from the National Science Foundation to take the draft road map to completion.

Having a detailed genetic road map of an American crop that has recently fallen on tough times could prove critical to the industry. Cotton is known as the most important renewable fiber crop, and its seeds and oils are used in food for humans and livestock, as well as in fertilizer.

The species of [cotton](#) Chen's team is sequencing is Upland (or American) cotton (*Gossypium hirsutum*), which makes up 95 percent of all cotton grown. A well-defined map of the Upland cotton's [genome](#) would allow researchers and growers to better understand the interactions between genes that determine the species' ability to produce better fibers and oils in seeds.

"Only about 20-30 percent of the cells on the cotton seed surface actually produce fibers, and no one knows why," said Chen, the D.J. Sibley Centennial Professor in Plant Molecular Genetics. "Knowing more about the sequence map could allow for more and better cotton to be produced on every seed or plant."

The U.S. is a leading exporter of cotton, and Texas grows more cotton than any state, producing nearly 30 percent of the nation's supply. The crop generates an estimated \$2 billion per year for the state's economy, but droughts and other weather-related changes since 2010 have led to steep losses for Texas cotton farmers, with yields down in some areas by as much as 50 percent.

Within this context, scientists have made several efforts to sequence the cotton genomes. The task is complicated for Upland cotton, a plant formed by two ancestral species 1.5 million years ago and that carries twice as many copies of genes as the presumed parent plants. Sequencing parent species, as previous researchers have done, is relatively easier but offers only a rough approximation of American cotton, much the way that using a map from the 1800s would provide incomplete information for someone trying to navigate a modern city.

"This sequence will accelerate genetic and breeding improvement of cotton production," said Zhang, director of the Cotton Research Institute at NAU.

David Stelly of Texas A&M, a collaborator with Chen on both the paper and the new grant, noted that the draft cotton genome sequence will be a "game-changer," launching a new era in cotton research, education and breeding.

Although the new map is accurate, with the new grant, Chen and researchers from Texas A&M University, Clemson University, Alcorn

State University and HudsonAlpha Institute for Biotechnology will create a higher resolution or "gold standard" map of the Upland cotton genome. Their novel sequencing method will be able to account for changes that occurred in Upland cotton over more than a million years and could also be applied to other important crops.

"Most crop species are also polyploid," said Chen, referring to plants whose DNA contains more than two of each chromosome. "Wheat, oats, canola, coffee, bananas, strawberries, sugarcane and basically everything that we eat, that we drink, and that we live on is polyploid."

More information: Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement, *Nature Biotechnology*, [DOI: 10.1038/nbt.3207](https://doi.org/10.1038/nbt.3207)

Provided by University of Texas at Austin

Citation: Genetic road map may bring about better cotton crops (2015, April 20) retrieved 17 April 2024 from <https://phys.org/news/2015-04-genetic-road-cotton-crops.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--