

# Chinese scientists crack the genome of diploid cotton

August 28 2012

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The international research team led by Chinese Academy of Agricultural Sciences and BGI have completed the genome sequence and analysis of a diploid cotton— *Gossypium raimondii*. The cotton genome provides an invaluable resource for the study and genetic improvement of cotton quality and output, and sheds new lights on understanding the genetic characteristics and evolutionary mechanism underlying cotton and its close relatives. The study was published online in *Nature Genetics*.

Cotton, also known as "white gold", is an important [cash crop](#) worldwide. Its fiber is one of the oldest fibers under human cultivation, which traces over 7,000 years old recovered from archaeological sites. The [cotton production](#) provides income for approximately 100 million families, and approximately 150 countries are involved in cotton import and export. Additionally, in scientific research, cotton also serves as an excellent model system for studying polyploidization, cell elongation and cell wall biosynthesis.

In this study, researchers sequenced the genome of *G. raimondii* by the next-generation sequencing technology, yielding a draft cotton genome with 103.6-fold genome coverage. Over 73% of the assembled sequences were anchored on 13 *G. raimondii* chromosomes. They identified 2,355 syntenic blocks in the *G. raimondii* genome, and found that approximately 40% of the paralogous genes were present in more than 1 block, which suggests that this cotton genome has undergone substantial chromosome rearrangement during its evolution.

Through comprehensive comparison and analysis, researchers observed that one paleohexaploidization event occurred in the *G. raimondii* genome at approximately 130.8 million years ago, while the event is commonly found in eudicots. They also found the evidence to support a cotton-specific whole-[genome duplication](#) event occurred at approximately 13-20 million years ago.

Cotton is known to produce a unique group of terpenoids such as gossypol. The accumulated gossypol and related sesquiterpenoids produced by cotton in pigment glands can be as a resistance against pathogens and herbivores. The majority of cotton sesquiterpenoids are derived from a common precursor which is synthesized by (+)- $\delta$ -cadinene synthase (CDN) in gossypol biosynthesis. Through the phylogenetic analysis on *G. raimondii* and eight other sequenced plant genomes, they found that the cotton, and probably *Theobroma cacao*, were the only sequenced plant species that possess an authentic CDN1 gene family for gossypol biosynthesis.

Furthermore, the transcriptomic comparison between the fiber-bearing *G. hirsutum* and the non-fibered *G. raimondii* demonstrated that three synthases are important for cotton fiber development, including sucrose synthase (Sus), 3-ketoacyl-CoA synthase (KCS) and 1-aminocyclopropane-1-carboxylic acid oxidase (ACO). Meanwhile, the MYB and bHLH transcription factors preferentially expressed in fiber may be useful to explain the molecular mechanisms that are in charge of governing fiber initiation and early cell growth.

Zhiwen Wang, Project Manager at BGI, said, "The completed *G. raimondii* genome provides a good reference for accelerating the genomic research on tetraploid cotton species such as *G. hirsutum* and *G. barbadense*. It also will lay a solid foundation for researchers to further boost cotton quality and productivity by comprehensively exploring the genetic mechanisms underlying cotton fiber initiation, gossypol

biosynthesis and resistance against pathogens and herbivores."

**More information:**

<http://www.nature.com/ng/journal/vaop/ncurrent/full/ng.2371.html>

Provided by BGI Shenzhen

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