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Chinese scientists sequence cotton genome

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Chinese scientists sequence genome of diploid cotton

Singapore: An international research team, led by the Chinese Academy of Agricultural Sciences and BGI, completed the genome sequence and analysis of a diploid cotton, *Gossypium raimondii*. The cotton genome provides an invaluable resource for the study and provides oppurtunity for genetic improvement of cotton quality and output.

It also 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*.

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 percent 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 percent of the paralogous genes were present in more than one block, which suggests that this cotton genome has undergone substantial chromosomal 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. They also found evidence to infer that a cotton-specific whole-genome duplication event occurred between 13-to-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 act as resistance against pathogens and herbivores. The majority of cotton sesquiterpenoids are derived from a common precursor which is synthesized by (+)- Î´ -cadinene synthase (CDN) in gossypol biosynthesis. Through the phylogenetic analysis on *G. raimondii* and eight other sequenced plant genomes, they found that cotton and probably *Theobroma cacao*, were the only sequenced plant species that possesed 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.

Mr Zhiwen Wang, project manager, BGI, said that, "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."

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