

COMMENT

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# Large-scale inversions majorly drive upland cotton population differentiation



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## Abstract

Recently, Li and his team hosted a project on roles of inversion in upland cotton population differentiation. Strikingly, genomic comparison identified, and subsequent RIL population and germplasm panel haplotype analyses confirmed, that large-scale inversions on chromosome At08 are widely distributed and have over time mediated the reduction of meiotic recombination that has ultimately driven genetically isolated haplotypes of *G. hirsutum*. This work is likely to become the new benchmark for cotton functional genomics research, and the scientific insights from the comparative analyses contributed substantially to our basic understanding of how genomic inversions influence meiotic recombination and thus lower genetic diversity in plant populations.

**Keywords:** *Gossypium hirsutum*, Population differentiation, Genome sequencing, TM-1, Zhongmiansuo24

## Main text

Cotton, the most important cash crop for the textile industry, is also an excellent model system for studying polyploidization, cell elongation, and cell wall biosynthesis (Yang et al. 2017; Liu et al. 2018; Hu et al. 2019; Li et al. 2019a; Li et al. 2019b; Zhang et al. 2019). The small structural variations including SNPs (single nucleotide polymorphism) and InDels (insertion-deletion) have been revealed in the cotton genome by different groups (Fang et al., 2017; Wang et al. 2017; Du et al. 2018; Ma et al. 2018), which have accelerated the rate of unraveling the genetic basis for complex agricultural traits. However, the large-scale variations (inversions and translocations) and their genetic effects remain unclear due to the limitation of genome quality and identification of recombination breakpoints. Recently, Li's team from the Institute of Cotton Research, CAAS, successfully identified large-scale inversions on the chromosome At08 in upland cotton, and uncovered their genetic effects on cotton population differentiation (Yang et al. 2019). This work represents new progress and advances our understanding of the mechanism for upland cotton divergence after the completion of the cotton genome and cotton variant genomes (Wang et al.

2012; Li et al. 2014; Li et al. 2015; Du et al. 2018; Ma et al. 2018).

Although multiple cotton genome assemblies are currently available (Paterson et al. 2012; Wang et al. 2012; Li et al. 2014; Li et al. 2015; Zhang et al. 2015; Du et al. 2018; Hu et al. 2019; Wang et al. 2019), the large-scale variations between diverse species and their roles in cotton divergence remain unknown. Comparisons among TM-1, Zhongmiansuo24 (ZM24, an important cultivar released in 1995), and the genomes of the diploid ancestors revealed that the variations between the interspecies are more abundant than those between the intraspecies. It is important that the finding of large-scale inversions on the At08 chromosome of upland cotton deepened our traditional understanding that upland cotton possessed a narrow genetic diversity. They found that the inversions could be used to classify a core collection of upland cotton into two groups, which was consistent with classification by a phylogenetic tree and principal component analysis. Using the artificial population, they found that meiotic recombination was suppressed in the inverted region, which was also validated in the natural cotton population. Further analysis showed that the inversion resulted in a decrease of haplotype and genetic diversity and led to cotton population differentiation. These indicate that there is a need to re-evaluate our understanding about how upland cotton divergence has occurred and how this process has specifically influenced

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extant nucleotide and trait diversity present in upland cotton populations.

Besides, genotype limitation is the most substantial challenge for cotton transformation. Unlike ZM24, TM-1 cannot produce regenerated seedlings through tissue culture to date. The upregulated expression of genes associated with auxin accumulation and transport is beneficial to the cotton transformation efficiency. Unlike auxin, the diminished active GA content in ZM24 calli, rather than as that in difficult to transform TM-1 cultivar, may promote ZM24 to be transformed. These will help guide future studies in improving the efficiency of cotton genetic transformation.

The study also provides a high-quality TM-1 reference genome for upland cotton to date. Meanwhile, a newly published reference genome of ZM24 has been shown to be an effective complement to the TM-1 reference genome. This dataset will benefit the cotton research community and provide better guidance for cotton breeding and functional genomic research.

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#### Authors' contributions

Tian SL wrote the manuscript, Ma ZY revised the manuscript. All authors read and approved the final manuscript.

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Not applicable.

#### Consent for publication

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#### Competing interests

The authors declare that they have no competing interests.

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#### References

Du X, Huang G, He S, et al. Resequencing of 243 diploid cotton accessions based on an updated a genome identifies the genetic basis of key agronomic traits. *Nat Genet.* 2018;50:796–802. <https://doi.org/10.1038/s41588-018-0116-x>.  
Hu Y, Chen J, Fang L, et al. *Gossypium barbadense* and *Gossypium hirsutum* genomes provide insights into the origin and evolution of allotetraploid cotton. *Nat Genet.* 2019;51:739–48. <https://doi.org/10.1038/s41588-019-0371-5>.

Li FG, Fan GY, Lu CR, et al. Genome sequence of cultivated upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nat Biotechnol.* 2015;33:524–30. <https://doi.org/10.1038/nbt.3208>.  
Li FG, Fan GY, Wang KB, et al. Genome sequence of the cultivated cotton *Gossypium arboreum*. *Nat Genet.* 2014;46:567–72. <https://doi.org/10.1038/ng.2987>.  
Li Z, Li L, Zhou K, et al. *GhWRKY6* acts as a negative regulator in both transgenic Arabidopsis and cotton during drought and salt stress. *Front Genet.* 2019a; 10:392. <https://doi.org/10.3389/fgene.2019.00392>.  
Li ZK, Chen B, Li XX, et al. A newly identified cluster of glutathione S-transferase genes provides Verticillium wilt resistance in cotton. *Plant J.* 2019b;98:213–27. <https://doi.org/10.1111/tpj.14206>.  
Liu Z, Qanmber G, Lu L, et al. Genome-wide analysis of *BES1* genes in *Gossypium* revealed their evolutionary conserved roles in brassinosteroid signaling. *Sci China Life Sci.* 2018;61:1566–82. <https://doi.org/10.1007/s11427-018-9412-x>.  
Ma ZY, He SP, Wang XF, et al. Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield. *Nat Genet.* 2018;50:803–13. <https://doi.org/10.1038/s41588-018-0119-7>.  
Paterson AH, Wendel JF, Gundlach H, et al. Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres. *Nature.* 2012;492:423–7. <https://doi.org/10.1038/nature11798>.  
Wang KB, Wang Z, Li FG, et al. The draft genome of a diploid cotton *Gossypium raimondii*. *Nat Genet.* 2012;44:1098–103. <https://doi.org/10.1038/ng.2371>.  
Wang M, Tu L, Lin M, et al. Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. *Nat Genet.* 2017;49:579–87. <https://doi.org/10.1038/ng.3807>.  
Wang M, Tu L, Yuan D, et al. Reference genome sequences of two cultivated allotetraploid cottons, *Gossypium hirsutum* and *Gossypium barbadense*. *Nat Genet.* 2019;51:224–9. <https://doi.org/10.1038/s41588-018-0282-x>.  
Yang ZE, Ge XY, Yang ZR, et al. Extensive intraspecific gene order and gene structural variations in upland cotton cultivars. *Nat Commun.* 2019;10:2989. <https://doi.org/10.1038/s41467-019-10820-x>.  
Yang ZE, Gong Q, Qin WQ, et al. Genome-wide analysis of *WOX* genes in upland cotton and their expression pattern under different stresses. *BMC Plant Biol.* 2017;17:113. <https://doi.org/10.1186/s12870-017-1065-8>.  
Zhang T, Hu Y, Jiang W, et al. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. *Nat Biotechnol.* 2015;33:531–7. <https://doi.org/10.1038/nbt.3207>.  
Zhang Y, Jin Y, Gong Q, et al. Mechanism analysis of resistance to *Verticillium dahliae* in upland cotton conferred by overexpression of *RPL18A-6* (*Ribosomal Protein L18A-6*). *Ind Crop Prod.* 2019;141:111742. <https://doi.org/10.1016/j.indcrop.2019.111742>.

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