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Research progress in the population differentiation and geographical adaptation of cotton

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Abstract

Recently, Du and his team revealed the genomic basis of population differentiation and geographical distribution of Chinese cultivated *G. hirsutum* (upland cotton). Our previous study showed that the large-scale inversions on chromosome A08 are widely distributed in a core collection of upland cotton and have driven population differentiation in *G. hirsutum*. With 3248 tetraploid cotton germplasms, He et al. identified new inversions on chromosome A06, and found these inversions together with those in chromosome A08 caused subpopulation differentiation Chinese cultivars that were highly consistent with their corresponding geographical distributions. This work provides new perspectives to further understand environmental adaptation of Chinese upland cotton germplasms.

Keywords: *Gossypium hirsutum*, Inversion, Introgression, Germplasm

In nature, species have evolved into a variety of ecotypes to adapt to different environments. The genetic basis of environmental adaptation is a major concern for all evolutionary biologists, including those who study crop plants. *Gossypium hirsutum*, a cultivated tetraploid cotton grown worldwide with good adaptability, accounts for more than 95 % of the natural cotton fiber production (Niles and Feaster 1984; Wendel et al. 2010). Although, cotton breeders and researchers focus on fiber yield and fiber quality for decades, the genetic basis of cotton adaptability is still unknown.

In animals, large-scale structural variations are often accompanied by changes in complex traits, such as mimicry in butterflies (Jay et al. 2021; VanKuren et al. 2019; Zhang et al. 2017), social habits in ants (Avril et al. 2019; Pracana et al. 2017), and alternative mating behavior in ruffs (Küpper et al. 2016; Lamichhaney et al. 2016). In plants, adaptability-related haplotypes have been identified in sunflower, located in genomic regions with high degrees of differentiation and accompanied by large-scale structural variation (Todesco et al. 2020). In crops, genetic differentiation always coexists with geographical distribution in both foxtail millet (Jia et al. 2013) and soybean (Zhou et al. 2015). These results implied that the genomic differentiation driven by structural variation functions might be related to environmental adaptation (Hoffmann and Rieseberg 2008; Wellenreuther and Bernatchez 2018).

In cotton, Du et al. (2018) found that Asian cotton (*G. arboreum*) was possibly domesticated in southern China, then gradually adapted to local environments as it moved northward, eventually categorized into three subpopulations. Genomic divergence was widely existed between *G. hirsutum* landraces and *G. hirsutum* cultivars populations (Nazir et al. 2021). Differentiation of upland cotton core collection had an obvious geographical distribution and phenotypic characteristics (Ma et al. 2018; Dai et al. 2020), which might be driven by three large-scale inversions on chromosome A08 and A06 by

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directly comparing genome assembles and using population genetics approaches (Yang et al. 2019; Dai et al. 2020). This phenomenon was also found in other Upland cotton populations (He et al. 2019, 2020).

He et al. (2021) published a study in *Nature Genetics* that provided insights into the genomic basis of population differentiation and geographical distribution in cultivated *G. hirsutum*. Based on an analysis of genomic variation in 3 248 tetraploid cotton germplasms, he and colleagues, mainly from the Institute of Cotton Research, Chinese Academy of Agricultural Sciences (ICR, CAAS), clearly illuminated large-scale inversions on chromosomes A06 and A08. Accessions differentiated by these inversions were highly consistent with their corresponding geographical distributions, which might determine the formation of different ecotypes in cultivated *G. hirsutum*. To confirm the origin of these chromosomal inversions, four major haplotypes were identified on chromosomes A06 and A08. Almost all Chinese registered cultivars carrying two A06-haplotypes and one A08-haplotype were geographically distributed in the highest- and lowest-latitude regions, respectively, exhibiting a regular distribution pattern. They found that the landraces carried these three haplotypes (A06–A08 haplotype) consistent with both chromosomes. This study therefore demonstrated that chromosomal inversions of A06 and A08 originated from a landrace and were related to geographic differentiation of cultivated *G. hirsutum*. They also comprehensively analyzed registered cultivars ($n = 851$) by integrating their A06–A08 haplotype combination and clearly described the genomic landscape of chromosomes A06 and A08 for cotton germplasm introduction, breeding preferences, and regional relocation in China.

This study revealed the genetic basis of population differentiation in Chinese upland cotton cultivars, and laid an important theoretical foundation for further understanding the adaptive evolution of *G. hirsutum*. This study could also guide new cultivars development to rapidly adapt Chinese Northwestern regions where has been the most important cotton cultivation region in recent years.

Additionally, this study comprehensively identified and evaluated the origin and effect of all favorable alleles related to fiber quality of *G. hirsutum*. Two new and favorable allelic variations were identified from introgression of the diploid species *G. arboreum* and *G. thurberi*, demonstrating that introgression of exogenous fragments and recombination of elite loci have great potential for enhancing fiber quality. Further identification causal genes of these new loci could accelerate to develop super fiber-quality cultivars in future.

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