

ICGI Comparative Genomics & Bioinformatics Workgroup Co-Chair Candidate

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In order to improve the yield and quality traits of cotton, my research field focus on the evolution and domestication of crop genome, the mining of elite genes related to important traits, and their application in cotton breeding. My main findings are summarized as follows: (1) Asymmetric evolution and domestication in allotetraploid cotton. More structural rearrangements, transposable elements, lost and disrupted genes have been characterized in the A subgenome than in the D subgenome. Correspondingly, faster evolution has been identified in the A subgenome. Interestingly, more positively selected genes for fiber yield and quality in the A subgenome and more for stress tolerance in the D subgenome. (2) Domestication and improvement of cotton: from tree cotton to American upland cotton and to the world's largest fiber crop. By comparing the genetic diversity among wild *G. hirsutum* cultivars and races, we identified 109 domestication-related selective sweeps. To further unveil the improvement history, we reported 119 GWAS loci in modern improved upland cotton and found 54.8% of the elite GWAS alleles were transferred from three founder landraces. (3) Discovery of elite alleles with multiple-effect on distinct traits which contain significant utilization value in breeding. My current research interests are focusing on comparative genomics study on genetic improvement of two tetraploid cultivated cottons, *G. hirsutum* and *G. barbadense*. The goal is to improve cotton fiber yield and quality by combing their elite alleles. My research programs are supported by the National Key Research and Development Program, the National Natural Science Foundation of China (NSFC). To date, I have published 19 research papers, which have appeared in Nature Biotechnology, Nature Genetics, Genome Biology and others.