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**Personal statement:**

Allotetraploid cotton is a model crop for polyploid research. My research field focus on the evolution and domestication of cotton genome, the mining of elite genes for important traits, and their application in cotton breeding. To date, I have published more than 20 research papers, published in Nature Biotechnology, Nature Genetics, Genome Biology and others. 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. 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 from tree cotton to American upland cotton. By comparing the genetic diversity among wild *G. hirsutum* cultivars and races, we identified 109 domestication-related selective sweeps, closely related to fiber and seed domestication.

(3) Genetic basis of cotton variety improvement in China. 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. We also identified elite alleles with multiple-effect on distinct traits which contain significant utilization value in breeding.

(4) Divergent improvement of two cultivated allotetraploid cotton species. Most associated loci or functional haplotypes for agronomic traits were highly divergent. We addressed the direct biological impact of interspecific haplotypes on variation in growth and agronomic traits. Actually, it is very difficult to simultaneously improve yield and fiber qualities by incorporating a single common haplotype or natural hybridization.

My aim is to improve cotton fiber yield and quality by combing their elite alleles identified from comparative genomic program. I will combine my professional expertise with more teams to carry out cooperative research and further promote the development of cotton genomics.