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**Research interests:** Theoretical and Applied Genetics of Cotton Germplasm



**Recent research on cotton germplasm:**

**(1) Population structure and genetic basis of the agronomic traits of Upland cottons in China:** a diverse and nation-wide population containing 503 *G. hirsutum* accessions was collected for a GWAS on 16 agronomic traits. These accessions were divided into 3 subpopulations based on 11,975 SNPs, but geographic distribution and breeding period were not the determinants of genetic structure. A total of 324 SNPs and 160 candidate QTL regions were identified as significantly associated with 16 agronomic traits (Plant Biotechnol J, 2017). Based on re-sequencing data, the recombination maps of core upland cotton was constructed and found that there were more QTLs overlapping with recombination regions in upland cotton, revealing that genetic improvement of upland cotton cultivars in China was realized by high frequency genetic recombination from a few germplasm in a short time (Plant J, 2019). A study in *G. hirsutum* and 70 *G. barbadense* cultivars of Xinjiang revealed that asymmetric introgression contributed to the improvement of the two species (Plant J, 2020).

**(2) The genetic basis of brown fibre cotton:** we dissected *Lc1* into two loci, *qBF-A07-1* and *qBF-A07-2*. The *qBF-A07-1* locus mediates the initiation of brown fibre production, whereas the shade of the brown fibre is affected by the interaction between *qBF-A07-1* and *qBF-A07-2*. We found that *qBF-A07-2* negatively affects fibre yield and quality through an epistatic interaction with *qBF-A07-1* (Plant Biotechnol J, 2018; The Crop J, 2020).

**(3) Germplasm development by interspecific hybridization:** in order to broaden the narrow genetic basis of upland cotton, nearly 2000 introgression lines were developed by crossing upland cotton with *G. barbadense*, *G. darwinii*, *G. tomentosum* and *G. mustelinum*. These introgression lines were phenotyped and genotyped to discover new variations, QTL mapping was conducted to reveal favorite alleles (Theor Appl Genet, 2012; Int J Mol Sci, 2008; Nat Genet, 2019; BMC Genomics, 2020, Plant Biotechnol J, 2021).

I am passionate in cotton research and it will be my great pleasure and honor to co-chair the Breeding and Applied Genomics workgroup. I would like to avail myself of this opportunity to serve ICGI and strengthen ties with other ICGI members. Any opportunities for me to help ICGI grow in the future would be cherished and highly appreciated.