ICGI Germplasm & Genetic Stocks Workgroup Co-Chair Candidate

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Research interests: Cotton germplasm evaluation and development
Recent researches 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. Thirty-eight associated regions had pleiotropic effects controlling more than one trait (Plant Biotechnol J, 2017, 15, 1374-1386).

(2) The genetic basis of brown fibre cotton: we dissected Lc_1 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*. Haploid analysis showed that most tetraploid modern brown cotton accessions exhibit the introgression signature of *G. barbadense*. We identified 10 QTL for fibre yield and 19 QTL for fibre quality through a GWAS and found that *qBF-A07-2* negatively affects fibre yield and quality through an epistatic interaction with *qBF-A07-1* (Plant Biotechnol J, 2018, 16, 1654-1666).

(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, 125: 1263-1274; Int J Mol Sci, 2008, 19, 243; Nat Genet, 2019, 51, 224-229).