

ICGI Functional Genomics Workgroup Co-Chair Candidate

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My research field is molecular biology with a specialization in functional genomics of cotton fiber cell fate determination, epigenetics of the cotton genome, and polyploid cotton genome evolution. My continuous study of cotton fiber fate resulted in the discovery of the critical genes involved in the differentiation of cotton lint and fuzz. The identification of the fuzz determine locus N_1 was narrow down to the *MYBMIXTA-like 3* (*GhMML3*) in upland cotton. We further discovered the natural antisense transcript (NAT) of *GhMML3* is the key component to regulate the fuzz and lint differentiation *via* epigenetic modifications. I also demonstrated microRNAs (miR828 and miR858) can direct their target gene *GhMYB2* in plant trichome differentiation. The cotton fiber fate determination is therefore under the regulation of non-coding RNA genes and epigenetic modifications. My lab continues to investigate the influence of epigenetics on cotton genome evolution. One of my latest finding revealed that the long non-coding RNA (lncRNA) is stimulated by genome shock of hybridization and polyploidization in cotton. These novel lncRNAs can serve as a reservoir of gene neofunctionalization during the evolution of polyploid species. My current research interests are focusing on the functional studies of coding and non-coding genes in cotton abiotic stresses and fiber development. My ongoing research programs are supported by the National Key Research and Development Program, the National Natural Science Foundation of China (NSFC), and 1,000 Talents Plan. To date I have published 23 research papers. These publications have appeared in prestigious journals, including *Genome Biology*, *Nature Communications*, *PNAS*, *Nature Biotechnologies*, *Trends in Plant Science*, and others.