

Dr. Xianlong Zhang is a full professor of Huazhong Agricultural University, China. He got his Ph.D. in 1990 from HZAU and then he became a faculty member of HZAU. Dr. Zhang worked in cotton science for thirty years, his research involves in cotton fiber development, cotton tissue culture and cell biology, interaction between cotton and *Verticillium* wilt disease, high temperature stress, abiotic stress tolerance, and molecular breeding. He is leading a research group consisting of 9 members, and the cotton group is one of the groups in National Key Laboratory of Crop Genetic Improvement. In cotton fiber development, Dr. Zhang constructed a normalized cDNA library at the early time, and then sequenced more than ten thousand clones with which he and his students identified the potential candidate genes possibly confers fiber development. In the recent 10 years, they analysed the functions of genes, such as GbPDF1, GbF3H, GhCaM7, GbTCP, GbEXPATR, and GbPSK, by genetic transformation. Recently, Dr. Zhang and his students analysed the involvement of miRNA and LincRNA, and identified some key miRNAs and LincRNAs which may regulate fiber development. These results contribute a lot to understanding cotton fiber development.

#### **Books:**

- Plant Biotechnology, edited by Xianlong Zhang, 2004 (1<sup>st</sup> edition) , 2012 (2<sup>nd</sup> edition), Chinese Science Press, Beijing.
- Cotton Biotechnology: Challenge the Future for Cotton Improvement, In: Biotechnology in Crop Improvement, GP Rao (ed.), 2008, Studium Press, LLC, Houston, Texas, USA. Pp. 251-311
- Developmental and molecular aspects of somatic embryogenesis (nonzygotic embryogenesis), In: Plant Tissue Culture, Development, and Biotechnology, Robert N. Trigiano and Dennis J. Gray Eds., CRC Press, 2011, p. 307-325
- Genome sequencing, In: Cotton, 2<sup>nd</sup> edition, edited by David Fang and Richard G. Percy, published by American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America, 2015, p. 289-302

#### **Representative papers:**

##### **(1) Fiber development**

- GbEXPATR, a species-specific expansin, enhances cotton fibre elongation through cell wall restructuring. **Plant Biotechnol J**, 2015 doi: 10.1111/pbi.12450
- Long noncoding RNAs and their proposed functions in fibre development of cotton (*Gossypium* spp.), **New Phytologist**, 2015, 207: 1181–1197
- Small RNA and degradome profiling reveals a role for miRNAs and their targets in the developing fibers of *Gossypium barbadense*, **Plant Journal**, 2014, 80: 331–344
- The calcium sensor GhCaM7 promotes cotton fiber elongation by modulating ROS production, **New Phytologist**, 2014, 202: 509-520
- A peptide hormone gene, GhPSK promotes fiber elongation and

contributes to longer and finer cotton fiber, **Plant Biotechnol J**, 2014, 12: 861-871

- A Genetic and Metabolic Analysis Revealed that Cotton Fiber Cell Development Was Retarded by Flavonoid Naringenin, **Plant Physiology**, 2013, 162: 86-95
- GbTCP, a cotton TCP transcription factor, confers fibre elongation and root hair development by a complex regulating system, **J Exp Bot**. 2012, 63: 6267-6281
- GbPDF1 (PROTODERMAL FACTOR 1) is involved in cotton fiber initiation *via* the core *cis*-element HDZIP2ATATHB2, **Plant Physiology**, 2012, 158: 890-904

## (2) Others

- Defective pollen wall contributes to male sterility in the male sterile line 1355A of cotton, **Scientific Reports**, 5, 9608; DOI:10.1038/srep09608 (2015)
- Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway, **Nature Communications**, 2014, 5:5372 doi: 10.1038/ncomms6372
- Sugar and auxin signaling pathways respond to high temperature stress during anther development as revealed by transcript profiling analysis in cotton, **Plant Physiology**, 2014, 164: 1293-1308
- Cotton WRKY1 Mediates the Plant Defense-to-Development Transition during Infection of Cotton by *Verticillium dahliae* by Activating JASMONATE ZIM-DOMAIN1 Expression. **Plant Physiology**, 2014, 166(4): 2179-2194
- Proteomic and virusinduced gene silencing (VIGS) analyses reveal that Gossypol, Brassinosteroids and Jasmonic acid contribute to the resistance of cotton to *Verticillium dahlia*, **Molecular & Cellular Proteomics**, 2013, 12: 3690-3703
- Cotton *GhCKI* disrupts normal male reproduction by delaying tapetum programmed cell death via inactivating starch synthase, **Plant Journal**, 2013, 75: 823-835
- Small RNA and degradome sequencing reveal complex miRNA regulation during cotton somatic embryogenesis, **J of Exp Bot**, 2013, 64(6): 1521-1536
- Regulation of Somatic Embryogenesis in Higher Plants, **Critical Review in Plant Science**, 2010, 29: 36-57