

ICGI Structural Genomics Workgroup Co-Chair Candidate



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Since 1990 joining the Institute of Cotton Research, Chinese Academy of Agricultural Sciences, Youlu Yuan has been involved with studies related to genome sequencing, genetic mapping, QTL identification, and molecular marker assisted selection about fiber quality, focus on cotton variety molecular design, especially on excellent fiber quality variety development. Since 2013 worked as a Director of Biotechnology Research Department and PI of cotton variety molecular design unit. Until to now, Published 142 papers with 32 SCI papers for first or Corresponding author, and developed the cotton varieties: CCRI60, CCRI70, CCRI78, CCRI96, CCRI101, and CCRI112. Recent publications include:

1.Genome sequence of the cultivated cotton *Gossypium arboreum*. Nature Genetics. 2014,46 (6),567—572, Co-first author

2.Transcriptomic and biochemical analysis of upland cotton (*Gossypium hirsutum*) and a chromosome segment substitution line from *G. hirsutum* × *G. barbadense* in response to *Verticillium dahliae* infection, BMC Plant Biology, (2019) 19:19, Corresponding author

3.GWAS analysis and QTL identification of fiber quality traits and yield components in upland cotton using enriched high-density SNP markers, Frontiers in Plant Science. 2018, 9:9:1067, Corresponding author

4.Quantitative trait locus mapping for *Verticillium* wilt resistance in an Upland cotton recombinant inbred line using SNP-based high-density genetic map. Frontiers in Plant Science. 2017, 8:382, Corresponding author

5.Construction of a high-density genetic map and its application to QTL identification for fiber strength in upland cotton. Crop Science 2017, 57:774-788, Corresponding author

6.Identification of stable quantitative trait loci (QTLs) for fiber quality traits across multiple environments in *Gossypium hirsutum* recombinant inbred line population. BMC Genomics, 2016, 17:197, Corresponding author

7.Construction of a high-density genetic map by specific locus amplified fragment sequencing (SLAF-seq) and its application to quantitative trait loci (QTL) analysis for boll weight in upland cotton (*Gossypium hirsutum*). BMC Plant Biology, 2016, 16:79, Corresponding author