Biotech Cotton in China

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Cotton is a China's leading fiber crop and the most important oilseed crop. There are great progresses obtained in cotton biotechnology in China.**1)** Transgenic research. Cotton is the first major crop in which commercialization of biotechnological initiative by the private sector provided various forms of plant protection by use of transgenic technology. So far, many important genes have been transformed into cotton cultivars. These genes included those for insect such as *Bt,GNA,CpTI* etc, herbicide, disease, drought and cold resistance. Among commercial cultivars which have been transformed successfully. Transgenic Bt and/or Bt + CpTI insect-resistant cotton has been popularized in China. In the meantime, studies on genetic mechanism and expression features of time and space on foreign gene in receptor have also been carried out and been reported in detail. **2)** DNA marker screening. Many DNA markers such as RFLP, RAPD, SSR, ISSR, AFLP etc have been used in constructing cotton linkage map, screening molecular markers linked with cotton important agronomic trait genes and studying heterosis mechanism. Many SSR/eSSR markers have been developed. Three genetic maps have been constructed using segregating mapping population such as DH, F_2 and BC_1 etc. Based on this map, DNA markers associated with disease resistance, fertility restorer gene, QTLs for fiber quality, pubescence, lint percent and other yield components have been identified. **3)** Cotton regeneration and transformation. Regeneration of limited cotton genotypes may produces large genetic vulnerability and risk in cotton production. So, research continues to be focused on problems of regeneration and transformation, especially transgenic technology development. Several commercial cultivars have been isolated and are being used in Agrobacterium-mediated transformation, so inserted gene can be used directly. Additionally, genotypic independent pollen tube transformation has been invented and transferred many genes to commercial cotton cultivars in China.

It is estimated that cotton has about 70,000 functional genes. Many studies on these genes have been carried out using DNA markers, maps and gene transfer procedures. However, this is not enough. BAC libraries with 150kb or larger in size have been reconstructed and contigs' identification is being gone by using genetic markers with known chromosome positions .On the other hand, genetic markers and DNA sequences from the physical map which are linked with the important agronomic traits will be used directly for MAS and gene isolation, which show prospective future in cotton genomics.

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