

## Major Results and Research Challenges in Cotton Molecular Genetics at CIRAD (France)

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CIRAD (Montpellier, France) develops research activities centered on tropical and sub-tropical agricultural systems. Among others crops, cotton is the focus of a series of research programs in different disciplines from economics to breeding. Major areas in genetics and breeding relate to (1) genetic diversity, (2) cultivar development through classical and molecular breeding, and (3) applied genomics. An important but under-exploited reservoir of genetic diversity exists within the genus *Gossypium*. With over 3000 accessions CIRAD has one of the few important gene banks worldwide. It includes cultivars, landraces, and wild *Gossypium* species. DNA molecular markers have shown their usefulness and validity for fingerprinting plant resources and for structuring diversity of large collections. In our case, after a preliminary step centered on the screening of microsatellite markers over a limited set of accessions of the gene bank (a genotyping kit has been proposed), our future plans include the use of high-throughput methods of genotyping (a DArT platform will soon be available in our unit). Opportunities for exploiting this large diversity relate to the development core-collections and of genetic association studies for a given set of traits (fiber quality, stress response). After a past and fruitful period of collaboration in different tropical countries (varieties co-obtained by CIRAD are cultivated on over 2.5 million hectares worldwide), CIRAD has more recently engaged research programs in molecular genetics. Focus has initially been on fiber quality as a target trait and on marker-assisted interspecific breeding for introgressing fiber quality traits from *G. barbadense* into *G. hirsutum*. Achievements in this area (genetic maps, fiber quality QTLs) have been published and are posted on the web. The database of CIRAD, TropGene DB (available at <http://tropgenedb.cirad.fr/>) is regularly updated and presently displays various genetic maps as well as QTL data. Based upon QTL detected in the BC1 and BC2 (backcross to the Gh parent) generations, marker-assisted selection in further generations (BC3 to BC6) was conducted and advanced lines introgressed with 3~5 QTLs were tested under tropical conditions. Using the same material, libraries of segmental introgression lines are being created for a few specific target chromosomes. More recently, through collaboration with Embrapa (Brazil), CIRAD has initiated research on disease and nematode resistances in order to clarify the genetic basis of resistance; prepare segregating populations, and develop marker-assisted selection programs. A new collaborative project coordinated by CIRAD on the genetics and genomics of cotton fiber quality has been launched in 2007. CIRAD and its partners, Bayer CS and CSIRO, are engaged in ambitious research aimed at elucidating the genetic basis of fiber quality. The project is centered on an interspecific RIL population (a cross between 2 well studied parents, Guazuncho 2 (*G. hirsutum*) and VH8 (*G. barbadense*)). It is innovative by the approach combining (1) phenotypic assessment of fiber quality from field and greenhouse experiments on four continents, and (2) transcriptome profiling using complementary platforms, hybridization-based (microarrays) and PCR-based (cDNA-AFLP). Comparison of QTL and eQTL results is expected to help in identifying candidate genes important in fiber quality.