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Genetic  
resources  
*Genomics*  
Plant  
biotechnology



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## Quality of cotton fibre

Cotton fibre is the natural fibre most used by the textile industry. It has a unicellular structure which develops from epidermal cells of the seed integument. We currently have few molecular data that would enable a correlation to be made between gene expression and the technological quality of the fibres (length, strength, resistance to stretching ...). It is now possible to identify which genes account for the different qualities of fibres in diverse mutants, varieties and species of cotton plant. For this, patterns of expression of cDNA (complementary DNA) and of Expressed Sequence Tags (ESTs) during cotton fibre development are investigated. This indicates which genes are involved in this agronomic trait and, in each case, identifies the favourable alleles. It will thus be possible to locate important genes whose expression determines in fine intrinsic fibre quality, and possibly to assign a biological function to these genes. The candidate genes thus identified are of agronomic interest and can be genetically tested in the analysis of Quantitative Trait Loci involved in the fibre technological quality.

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What genes are controlling technological quality in cotton (fibre length, strength, resistance...)?



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All this presupposes access to genetic resources, land for field trials, laboratory facilities, and a capacity to raise offspring in confinement.

- **Structural genomics** reveals the physical organization of the genome in the form of chromosomes bearing various types of sequences which contain genes of interest.

- **physical mapping of the genome** constructs a replica of a whole genome in the form of large DNA fragments that are cloned (inside bacteria in the case of Bacterial Artificial Chromosome clones) and ordered with respect to one other. This mapping translates a genetic map – which locates the genomic regions implicated in the expression of particular traits – into DNA fragments that contain the genes governing these traits. It is

typically applied to positional cloning (see page 11 "*Syteny and parallel chromosome walking in the Poaceae*") of genes of agronomic interest. It also serves to recover the complete version of genes detected by means of their transcribed sequences, or Expressed Sequence Tags (ESTs);

- **systematic sequencing of the genome** gives access to all the genes of a plant, i.e. between 20,000 and 50,000. Large industrial groups and laboratory networks generate this type of information using model plants like *Arabidopsis* and rice. The Languedoc-Roussillon laboratories have participated in the setting up of such an initiative in France for the chromosome 12 of rice (see page 16 "*The Montpellier and Languedoc-Roussillon Génopole*")....