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Removal of a flower bud for
subsequent hybridization.
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Cotton breeding at CIRAD—from conventional selection to biotechnologies

In addition to conventional breeding methods, cotton breeders have access to new biotechnology tools such as marker-assisted selection and genetic transformation which enable them to create new cotton varieties that are higher yielding and generate a better quality fibre. CIRAD has bred cotton varieties for farmers in developing countries which are adapted to local climatic and cropping conditions, and produce a high technological quality fibre suitable for textile manufacturing.

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Conventional breeding

Varieties bred by CIRAD, alone or in partnership, are cropped yearly on an area of 2.5 million ha (7% of the area under cotton worldwide). They have been obtained by conventional breeding methods (pedigree selection via stabilization of target traits through several selfed generations in the progeny of a cross between two or several varieties). CIRAD is using these standard techniques, in partnerships in Benin, Cameroon, Brazil and Paraguay, with the aim of obtaining varieties that respond to a broad range of specific adaptations.

Participative breeding

CIRAD, with the aim of taking institutional patterns of cotton subsectors into better account, is involved in a "participative breeding" strategy in Benin, with volunteer farmers participating alongside scientists to select strains in populations during the breeding process. Every year these farmers oversee the sowing of new populations. In the field, they choose plants that they consider to be the most interesting from an agricultural standpoint. The breeding process is then focused on technological fibre traits in collaboration with the scientists. New cotton varieties bred in this way will soon be released to farmers.

Genome mapping and marker-assisted selection

DNA molecular markers are used for direct selection of genes in the plant genome. They can accurately identify and pinpoint chromosome regions containing genes underlying agriculturally or technologically interesting traits—these chromosome areas are called quantitative trait loci (QTLs). Breeders strive to accumulate, within the same plant, all QTLs that seem to underlie genes associated with the target trait—this is called marker-assisted selection (MAS). Varieties can thus be screened directly on the basis of the genotype, i.e. from genes contained in the genome, contrary to conventional breeding strategies based on the phenotype (physical manifestation of a trait in a plant induced by the expression of specific genes). Molecular markers are not sensitive to the medium, contrary to phenotypic expression which can be affected by interactions with the environment.

CIRAD's cotton marker-assisted selection programme is currently focused on introgressing a fibre quality QTL from a *Gossypium barbadense* cultivar (cv VH8, which produces a very strong, long thin fibre) into a *Gossypium hirsutum* cultivar (early and high yielding cv Guazuncho 2). QTLs underlying good fibre quality traits were located in around 20 chromosome segments on the cotton genome map. CIRAD breeders hope to enhance the intrinsic fibre quality of *G. hirsutum* through the accumulation of these fibre quality-associated QTLs from *G. barbadense*.

Genetic transformation of cotton

Cotton is one of the first crop plants genetic transformation techniques focused on to obtain commercial varieties. Insect- and herbicide-resistant transgenic varieties are currently grown on 20% of the area under cotton worldwide. They are also being grown to an increasing extent in developing countries. CIRAD considers that it is essential to assess the impact of these varieties in smallholder farming systems in such cotton-producing countries.

Partners

Africa: IRAD, Institut de la recherche agricole pour le développement; SODECOTON, Société de développement du coton, Cameroon • INRAB, Institut national de recherche agronomique, Benin • SODEFITEX, Senegal • University of Pretoria, South Africa

South America: PIEA, Programa de Investigación y Experimentación Algodonera, Paraguay • EMBRAPA, Empresa Brasileira de Pesquisa Agropecuária; COODETEC, Brazil

China: BRI, Biotechnology Research Institute of the Chinese Academy of Agricultural Sciences, CAAS, Beijing

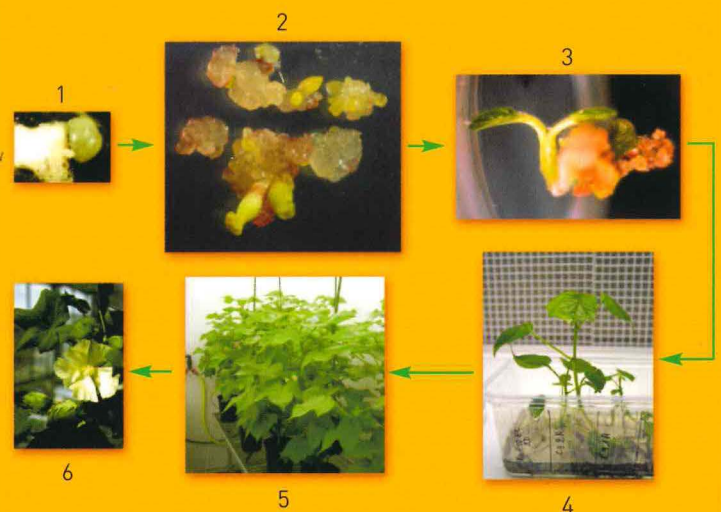
USA: Brookhaven National Laboratory, Upton, New York

Europe: ENSAR, Ecole nationale supérieure agronomique de Rennes; INRA, Laboratoire de biologie cellulaire of the Centre de l'Institut national de la recherche agronomique de Versailles Grignon; Groupe Dagris, France • Faculté des Sciences Agronomiques de Gembloux, Belgium

ICGI, International Cotton Genome Initiative

The genetic transformation process is being developed for cotton at CIRAD—it is an effective tool for unravelling the complexities of the cotton genome. It can, for instance, be used to determine the function of an investigated gene by introducing a construct of two genetic sequences, with one representing a gene and the other promoting the overexpression or extinction of this gene. CIRAD scientists, in collaboration with the Biotechnology Research Institute in Beijing, China, are using this method to study genes involved in cellulose synthesis and cellular elongation, with the aim of generating cotton fibres with novel features, such as crease resistance and dye receptiveness.

OBTAINING TRANSGENIC COTTON PLANTS



1. Callus obtained by propagation of transformed cells • 2. Embryogenic callus bearing somatic embryos • 3. Young plantlet derived from a developing somatic embryo • 4. Plants transformed prior to potting them • 5. Plants transformed in the glasshouse • 6. Fruits (bolls) and flowers of a transgenic plant

For further information

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