

#### 4. Implementation of a cotton crop module to the TropGENE-DB information system

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The crop information system, TropGENE-DB developed at Cirad for cocoa, sugar cane and banana (Ruiz *et al.*, Nuc Acid Res, 2004, 32: 364-367) has recently been implemented with the marker information and genetic mapping data obtained in our laboratory for cotton. TropGENE-DB is based on the AceDB database management system. The object-oriented system provides usual browsable classes and visualization tools; it also includes a graphical user interface that has been coupled with the Cmap software genetic map viewer (<http://www.gmod.org/cmap/index.shtml>). The data that is now accessible through the internet at <http://tropgenedb.cirad.fr> comprise the primer sequence and loci information derived from the series of 392 in-house cotton microsatellites markers. An always updated version of the interspecific *G. hirsutum* x *G. barbadense* (Guazuncho 2 x VH8) genetic linkage map is also accessible. The nomenclature of markers, loci, and chromosomes / linkage groups, were standardized in order to fit with the most recent international reports on cotton genetic mapping. Data, such as sequence, locus, map data, can be easily submitted for their incorporation in TropGENE-DB using standard Excel submission files. Illustrative of the usefulness of the system, the synteny relationships based on common bridge markers between the 2 densest genetic maps of tetraploid cotton presently publicly available (those of the University of Georgia and of Cirad), can easily be visualized. The future developments of the cotton module of TropGENE-DB include (1) the integration of the phenotypic description and of the microsatellite allelic data of the *Gossypium* collection of Cirad, and (2) the description and localisation of fibre quality QTL data.



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