

**QTL ANALYSIS OF THE EXPRESSION OF THE LOW-GOSSYPOL SEED AND HIGH
GOSSYPOL PLANT TRAIT IN THE PROGENY OF THE *GOSSYPIUM HIRSUTUM*
X *G. RAIMONDII* X *G. STURTIANUM* TRISPECIFIC HYBRID**

H. Ben Bouza, B. Mbaïkar, J.P. Baudoin, and G. Mergeai

Faculté universitaire des Sciences agronomiques de Gembloux

Gembloux, Belgium

M. Lacape and B. Courtois

CIRAD-CA

Montpellier, France

Abstract

Two hundred and three mapped micro-satellites markers evenly distributed on the 26 chromosomes of *G. hirsutum* L. were used to monitor the introgression of DNA fragments coming from the Australian species *G. sturtianum* Willis in a population of BC₁, BC₂, BC₂S₁, BC₂S₂, BC₂S₃, B₂S₄, BC₂S₅, BC₁/BC₂S₂, S₁/BC₁/BC₂S₂, BC₃, BC₃S₁, BC₃S₂ and BC₃S₃ backcross derivatives obtained from the *G. hirsutum* x *G. raimondii* Ulb. x *G. sturtianum* (HRS) trispecific hybrid. A single marker analysis carried out in this population permitted to associate six *G. sturtianum* microsatellites to putative QTLs controlling the low gossypol-seed and high-gossypol plant trait. These microsatellites are located on chromosomes c02, c13 and c12. They constitute very useful tools to assist the selection of commercial cotton varieties showing a drastic inhibition of the gossypol synthesis in the seed while presenting a normal content of terpenoids in their aerial parts.