

GERMPLASM ENGINEERING IN COTTON

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Abstract

DNA markers have been applied sparingly in cotton improvement. Their use is limited to areas of proprietary protection, transgene conversion and tagging simple qualitative traits. This is due, in part, to the paucity of intra-specific polymorphism for most available DNA markers. An immediate and appropriate use of DNA marker technology is introgressive breeding or germplasm engineering. This involves molecular characterization of the genetic diversity of cotton germplasm resources. Careful discovery of novel quantitative trait loci (QTL) alleles are undertaken at the same time they are being introgressed into an elite genetic background. This can be used to exploit the secondary *Gossypium* gene pools, such as the *G. hirsutum* primitive race stocks. Microsatellite or simple sequence repeats (SSR) markers are very suitable for introgressive breeding. They can be modified to high-throughput systems essential to efficiency of germplasm engineering. Advanced Backcross QTL strategies, such as those successfully applied in rice and tomato, should be appropriate to germplasm engineering in cotton. The strategic use of DNA markers can “mine” the novel QTL alleles from exotic germplasm for genetic enhancement of the elite primary gene pool. This is a more appropriate use of DNA markers in cotton than trying to use marker-assisted selection within intra-specific elite populations for QTLs.