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Abstract

Fiber from cotton (*Gossypium hirsutum* and *G. barbadense*) is a major product in the world economy. It is a botanically unique plant as it is a perennial allotetraploid derived from diploid *Gossypium* species, one of which does not produce lint, which is grown as an annual row crop. Cotton is an especially appropriate system for research into the molecular basis of plant response to water deficit and salinity, as it originates from wild perennial plants adapted to semi-arid, sub-tropical environments which experienced periodic drought and temperature extremes that are associated with soils with high salt content. The current primary molecular breeding approaches include transgenic modification and quantitative trait mapping with marker-assisted selection. The preliminary work in QTL mapping for drought response and the relationships of the QTLs with the drought-associated measurements is developing a foundation for understanding and using the molecular basis of drought tolerance. QTL mapping for salt tolerance is not moving apace. Using and/or regulating transgene effects on the plant responses to drought and salinity has shown success and will continue to increase our understanding of the complexity of plant's physiological pathways. Improvements in all areas of molecular breeding are almost certain, but the most effective improvements will come from exploiting our improved understanding of the genetic architecture

Keywords QTL - MAS - abiotic stress - water-use efficiency - stable carbon isotope ratio/discrimination