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Molecular Breeding of Cotton

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Abstract

Molecular characterization provides comprehensive information about the extent of genetic diversity, it assists for the development of an effective, highly accurate, and rapid marker-assisted cotton breeding program. Due to one of the world's leading fiber crops, molecular studies of cotton are being explored widely by cotton researchers. Cotton provides raw material to the textile industry among other products. Limitations in conventional breeding program for genetic improvement are due to the complexity and limited knowledge on economically important traits. The use of molecular markers for the detection and exploitation of DNA polymorphism is one of the most significant developments in molecular genetics. In the present scenerio, cotton molecular breeding has become a reliable source through the study and exploitation of its genetic diversity and due to better understanding of the cotton genomes using the next-generation sequencing technologies. Cotton breeders should utilize genomics in breeding programs for effective selection of best parents for agronomic and fiber-related traits, as well as for the development of resistance against biotic and abiotic stresses. The genomic research work could be based upon genotyping using DNA markers, quantitative trait loci mapping, genome-wide associations, and next-generation sequencing. The objective of this chapter is to describe evolution as well as utilization of various molecular markers and review the contribution of marker-assisted selection (MAS) in cotton breeding.

Keywords: cotton, DNA markers, genotyping by sequencing (GBS), genome-wide association studies (GWAS), marker-assisted selection (MAS)