

Biotechnology for Cotton Improvement

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Chapter

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Abstract

Cotton is a natural fiber crop in the world. The ever-increasing demands of the fast-growing population for food, feed, fiber, and fuel, which is estimated to be 11 billion all over the world in 2050, urge to enhance food production 2–3 times. But limitations in conventional breeding program for genetic upgrading are due to limited knowledge about yield and fiber traits. Use of molecular markers and exploitation of DNA polymorphism is one of the noteworthy developments in the field of molecular genetics. Availability of reference genome of *G. raimondii* L., *G. arboreum* L., and next-generation sequencing routed it on fast track for exploring variability among genotypes of cotton. Genomic research could be quantitative trait loci mapping, genome-wide associations, and next-generation sequencing approaches.

Keywords

Marker-assisted selection Quantitative trait locus Deoxyribonucleic acid
Simple sequence repeat

Abbreviations

AFLP

Amplified fragment length polymorphism

CAPS

Cleaved amplified polymorphic sequence

DNA

Deoxyribonucleic acid

EST-SSRs

Expressed sequence tags

GBS

Genotyping by sequencing

GM

Genetically modified

GMO

Genetically modified organisms

GWAS

Genome-wide association

ICAC

International Cotton Advisory Committee

ISAAA

International Service for the Acquisition of Agri-biotech Applications

ISSR

Inter-simple sequence repeat

MAS

Marker-assisted selection

MT

Million metric tons

PCR

Polymerase chain reaction

QTL

Quantitative trait locus

RAPDs

Random amplified polymorphic DNAs

RFLP

Restriction fragment length polymorphism

SCAR

Sequence characterized amplified region

SNP

Single nucleotide polymorphism

SSR

Simple sequence repeat

STS

Sequence-tagged site

USDA

United State Department of Agriculture

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