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Genetic and Molecular Mechanisms and Approaches for Improving Cotton Fiber Quality for Sustainable Agriculture

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ABSTRACT

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Cotton (*Gossypium hirsutum* L.) is an economically important fiber crop whose quality determines textile processing efficiency, yarn performance, fabric durability, and market value. Cotton fiber quality is a complex quantitative characteristic influenced by genetic architecture, molecular regulatory networks, physiological processes, and environmental conditions. This review provides a comprehensive overview of the fundamental properties of cotton fiber, developmental processes, genetic inheritance, and molecular mechanisms underlying fiber quality. Major fiber attributes, including length, strength, uniformity, fineness, and elongation, are examined in relation to fiber initiation, elongation, secondary cell wall formation, and maturation. The genetic architecture of fiber quality is discussed through genetic variability, heritability, quantitative trait loci (QTLs), linkage mapping, genome-wide association studies (GWAS), and genotype-by-environment interactions. Particular attention is given to molecular mechanisms regulating fiber development, including transcription factors, hormonal signaling, carbohydrate metabolism, cellulose biosynthesis, and cell-wall remodeling. Furthermore, advances in cotton genomics, transcriptomics, epigenomics, proteomics, metabolomics, and functional genomics are explored to demonstrate their contributions to candidate-gene identification and functional validation. Emerging breeding technologies, including marker-assisted selection, genomic selection, CRISPR/Cas-mediated genome editing, genetic engineering, and regulatory RNA molecules, offer promising opportunities for improving fiber characteristics. Nevertheless, challenges remain in validating molecular discoveries across diverse genetic backgrounds and environmental conditions, managing genetic diversity, and translating laboratory findings into consistent field performance. Climate change and associated abiotic stresses further emphasize the need to develop cultivars that combine superior fiber quality, high productivity, and environmental resilience. Integrating multi-omics information, high-throughput phenotyping, precision breeding, and multi-environment evaluation could accelerate the development of improved cotton cultivars. Overall, this review highlights the importance of connecting fundamental fiber biology with advanced molecular technologies and conventional breeding to achieve sustainable genetic improvement and maintain cotton quality under changing agricultural conditions. Integrating conventional breeding, molecular markers, genomic selection, and genome editing offers promising opportunities to improve cotton fiber quality sustainably. These approaches can accelerate the development of climate-resilient cultivars with enhanced fiber properties, resource-use efficiency, genetic diversity, and long-term agricultural productivity.

Introduction

Fundamentals of Cotton Fiber Quality and Development

Major Cotton Fiber Quality Traits: Length, Strength, Uniformity, Fineness, and Elongation

Cotton (*Gossypium* spp.) is a globally important natural fiber crop, and its quality directly influences textile processing efficiency, yarn performance, fabric durability, and commercial value. Fiber quality is determined by several interrelated physical properties, including length, strength, uniformity, fineness, and elongation. Fiber length represents the longitudinal dimension of individual fibers and influences yarn-spinning efficiency and the production of fine yarns. Fiber strength measures resistance to tensile failure, whereas length uniformity describes the consistency of fiber lengths within a sample. Higher uniformity generally improves yarn regularity and reduces processing losses. Fiber fineness refers to fiber linear density or mass per unit length and is commonly expressed as micronaire, an indirect measurement influenced by both fineness and maturity. Fiber elongation represents the capacity of a fiber to extend before breaking and contributes to yarn flexibility and resistance to mechanical stress (Bradow & Davidonis, 2000). These traits are genetically controlled quantitative characteristics influenced by multiple genes and environmental conditions. Their relationships are not always straightforward: improving one trait may have limited or unfavorable effects on another, depending on genetic background and growing conditions. Consequently, cotton breeding programs require simultaneous evaluation of multiple fiber-quality parameters rather than selection based on a single characteristic. Understanding the cellular and molecular processes underlying these traits provides a foundation for developing cultivars with improved spinning performance and textile value (Haigler et al., 2012) (Figure 1).

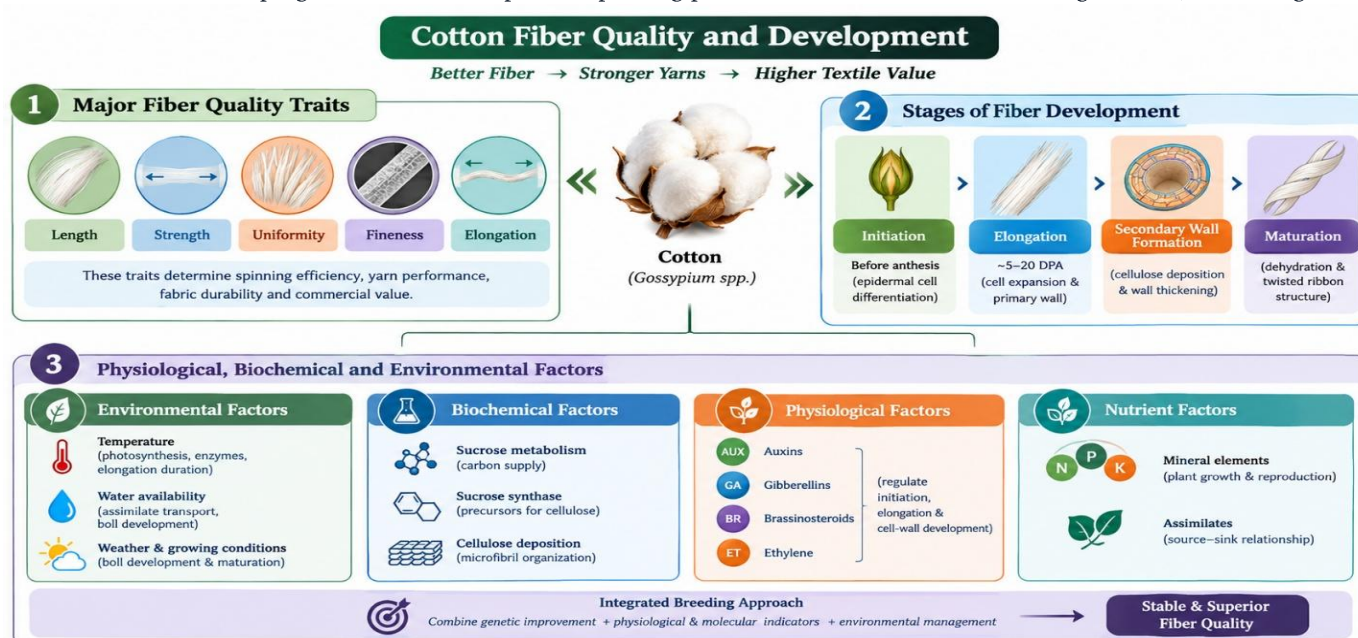


Figure 1: Major cotton fiber quality traits, developmental stages, and physiological, biochemical, and environmental factors influencing fiber quality.

Stages of Cotton Fiber Development: Initiation, Elongation, Secondary Cell Wall Formation, and Maturation

Cotton fibers originate as single-celled trichomes from the epidermal cells of the ovule. Their development is conventionally divided into four overlapping stages: initiation, elongation, secondary cell wall formation, and maturation. Fiber initiation begins shortly before anthesis and involves the differentiation of selected epidermal cells into fiber initials. During elongation, generally occurring most actively during approximately 5–20 days post-anthesis (DPA), rapid cell expansion and primary cell wall synthesis establish the eventual fiber length. This process depends on coordinated cytoskeletal activity, membrane transport, carbohydrate metabolism, and cell-wall loosening (Kim & Triplett, 2001). The transition to secondary cell wall formation involves a shift from longitudinal expansion toward substantial cellulose deposition. During this stage, cellulose synthase complexes produce cellulose microfibrils that accumulate within the cell wall, progressively determining wall thickness and contributing to mature fiber strength. Finally, maturation involves continued wall thickening, dehydration, and the development of the characteristic twisted ribbon-like structure. Although these developmental stages overlap, their timing and intensity strongly influence the final physical properties of the fiber. Genetic differences in developmental duration,

cellulose accumulation, and wall architecture therefore represent important targets for fiber-quality improvement (Haigler et al., 2012; Bai & Scheffler, 2024).

Physiological, Biochemical, and Environmental Factors Influencing Fiber Quality

Cotton fiber quality results from the interaction of genetic potential, physiological processes, biochemical pathways, and environmental conditions during boll development. Temperature is particularly influential because it affects photosynthesis, assimilate partitioning, enzyme activity, and the duration of fiber elongation and secondary cell wall deposition. Excessively high temperatures can disrupt carbohydrate metabolism and shorten developmental periods, potentially reducing fiber length and strength. Similarly, water deficit can restrict photosynthetic activity and assimilate transport to developing bolls, whereas excessive moisture and unfavorable growing conditions may interfere with boll development and fiber maturation. The magnitude and direction of these effects depend on genotype, stress intensity, and developmental timing (Bradow & Davidonis, 2000). Biochemically, sucrose metabolism supplies carbon substrates for cell-wall synthesis, while sucrose synthase contributes to the availability of precursors required for cellulose biosynthesis. Cellulose deposition and microfibril organization are especially important for secondary cell wall development and mature fiber strength. Phytohormones, including auxins, gibberellins, brassinosteroids, and ethylene, regulate different aspects of fiber initiation, elongation, and cell-wall development through interconnected signaling pathways. Their effects depend on concentration, developmental stage, and interactions with other regulatory mechanisms (Haigler et al., 2012; Bai & Scheffler, 2024). Furthermore, nutrient availability, particularly the supply of assimilates and essential mineral elements, influences plant growth and reproductive development. These factors can indirectly affect fiber quality by altering source-sink relationships and the physiological condition of developing bolls. Integrating environmental management with genetic improvement is therefore essential for stabilizing fiber quality across production environments. Breeding strategies should combine direct fiber-quality measurements with physiological and molecular indicators to identify genotypes that maintain desirable fiber characteristics under variable environmental conditions.

Genetic Architecture and Inheritance of Cotton Fiber Quality

Genetic Variability, Heritability, and Quantitative Inheritance of Fiber Quality Traits

Cotton fiber quality is governed by a complex genetic architecture involving multiple genes, allelic variation, and interactions between genetic and environmental factors. Fiber length, strength, uniformity, elongation, and micronaire are generally quantitative traits exhibiting continuous phenotypic variation. Their inheritance reflects the cumulative effects of multiple loci, including genes with relatively large effects and numerous loci contributing smaller effects. Genetic variability within breeding populations provides the essential raw material for improving these characteristics through selection and hybridization (Naoumkina & Kim, 2023). Heritability estimates indicate the proportion of observed phenotypic variation attributable to genetic differences within a particular population and environment. Broad-sense heritability includes additive, dominance, and epistatic genetic variance, whereas narrow-sense heritability considers primarily additive genetic variance. This distinction is important because additive effects are particularly useful for predicting the response to recurrent selection and the transmission of favorable alleles to subsequent generations. A genome-wide association study involving 348 upland cotton accessions evaluated across 10 environments reported broad-sense heritability above 60% for all six investigated fiber-quality traits, demonstrating substantial genetic contributions to phenotypic variation (Wang et al., 2024). Nevertheless, heritability is population- and environment-dependent rather than an immutable property of a trait. Genetic correlations among fiber characteristics also influence selection efficiency. For example, simultaneous improvement of lint yield and fiber quality can be challenging because unfavorable genetic associations may occur in particular breeding populations. Accordingly, breeders should evaluate genetic variance, trait correlations, and selection responses together when designing improvement strategies (figure 2).

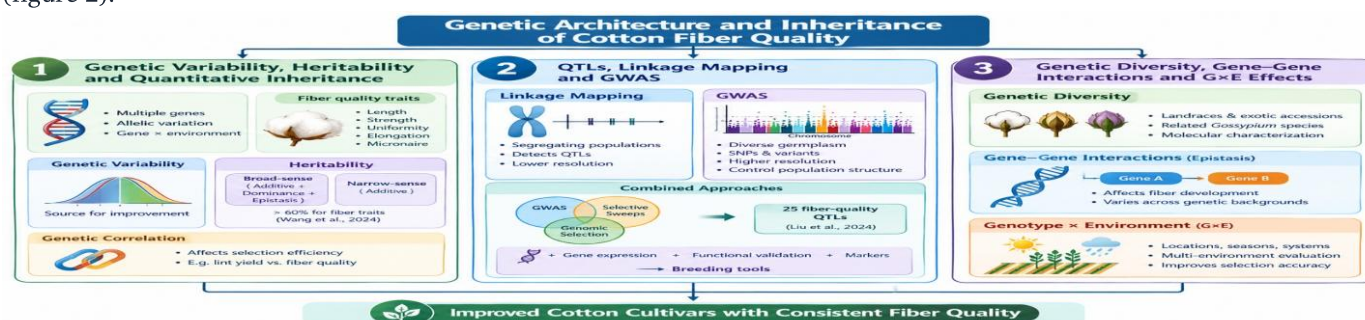


Figure 2: Genetic architecture and inheritance of cotton fiber quality, highlighting genetic variability, heritability, QTL mapping, GWAS, genetic diversity, gene-gene interactions, and genotype-by-environment effects.

Quantitative Trait Loci (QTLs), Linkage Mapping, and Genome-Wide Association Studies (GWAS)

Quantitative trait locus mapping and genome-wide association studies are complementary approaches for identifying genomic regions associated with cotton fiber quality. Traditional linkage mapping uses segregating populations, such as recombinant inbred lines, to identify associations between molecular markers and phenotypic differences inherited from contrasting parents. These studies are useful for detecting QTLs within defined genetic backgrounds, although their resolution depends on population size, recombination frequency, and marker density. GWAS examines genetic associations across diverse germplasm collections using single-nucleotide polymorphisms and other genomic variants. By exploiting historical recombination, this approach can provide finer mapping resolution than conventional linkage analysis, although population structure and relatedness must be controlled to reduce false associations. Yasir et al. (2022) reviewed the application of GWAS in cotton and highlighted its value for identifying loci associated with fiber quality, yield, and other agronomic characteristics. Combining complementary genomic analyses can improve the reliability of candidate-locus discovery. For instance, a study integrating GWAS, genome-wide selective-sweep analysis, and genomic selection identified 25 fiber-quality QTLs in upland cotton breeding lines, including loci that might have been overlooked by GWAS alone (Liu et al., 2024). Integrating mapping results with gene-expression evidence, functional validation, and marker development can facilitate the translation of genomic discoveries into practical breeding tools.

Genetic Diversity, Gene–Gene Interactions, and Genotype-by-Environment Effects

Genetic diversity is fundamental to cotton improvement because it provides alternative alleles for enhancing fiber quality and broadening the adaptive capacity of cultivated varieties. However, repeated use of related elite parents can narrow the genetic base of breeding populations, limiting opportunities for further improvement. Introgression of favorable alleles from landraces, exotic accessions, and related *Gossypium* species can introduce useful variation for fiber length, strength, and other quality attributes. Molecular characterization helps identify genetically distinct parents and favorable haplotypes for crossing and selection (Kushanov et al., 2021). Gene–gene interactions, commonly described as epistasis, occur when the effect of one locus depends on the allelic composition of another locus. Such interactions may influence fiber development through coordinated regulation of cell elongation, cellulose deposition, and associated metabolic pathways. Consequently, the phenotypic contribution of an individual allele may vary across genetic backgrounds, complicating predictions based solely on single-locus effects. Genotype-by-environment (G×E) interactions further influence fiber-quality expression across locations, seasons, and production systems. Gowda et al. (2024) evaluated an upland cotton diversity panel across 10 environments, demonstrating the value of multi-environment assessment for identifying genomic regions associated with fiber-quality traits. Integrating genetic diversity analysis, interaction-aware statistical models, and multi-environment phenotyping can improve selection accuracy and support the development of cotton cultivars with consistently desirable fiber quality.

Molecular Mechanisms Regulating Cotton Fiber Development

Molecular Regulation of Fiber Initiation and Elongation

Cotton fiber development is regulated by coordinated molecular pathways that control the differentiation and expansion of individual ovule epidermal cells. Fiber initiation involves the activation of cell-fate regulators, transcription factors, and genes associated with cellular metabolism. Transcriptome analysis of wild-type cotton and fiberless mutants identified several genes potentially involved in early fiber differentiation, including GhMYB25, homeodomain-related genes, expansins, lipid-transfer proteins, and sucrose synthase (Wu et al., 2006). Functional characterization subsequently demonstrated that GhMYB25-like plays an essential role in fiber initiation, as its silencing substantially disrupts fiber development (Walford et al., 2011). Similarly, Machado et al. (2009) established that GhMYB25 contributes to early fiber and trichome development. Following initiation, fiber elongation depends on cell-wall loosening, cytoskeletal organization, membrane transport, and carbohydrate availability. The homeodomain transcription factor GhHOX3 is an important regulator of elongation because it activates genes associated with cell expansion, including GhRDL1 and GhEXPA1 (Shan et al., 2014). These findings demonstrate that fiber length is determined not only by the initiation of fiber cells but also by the coordinated expression of genes controlling sustained cellular expansion (Figure 3).

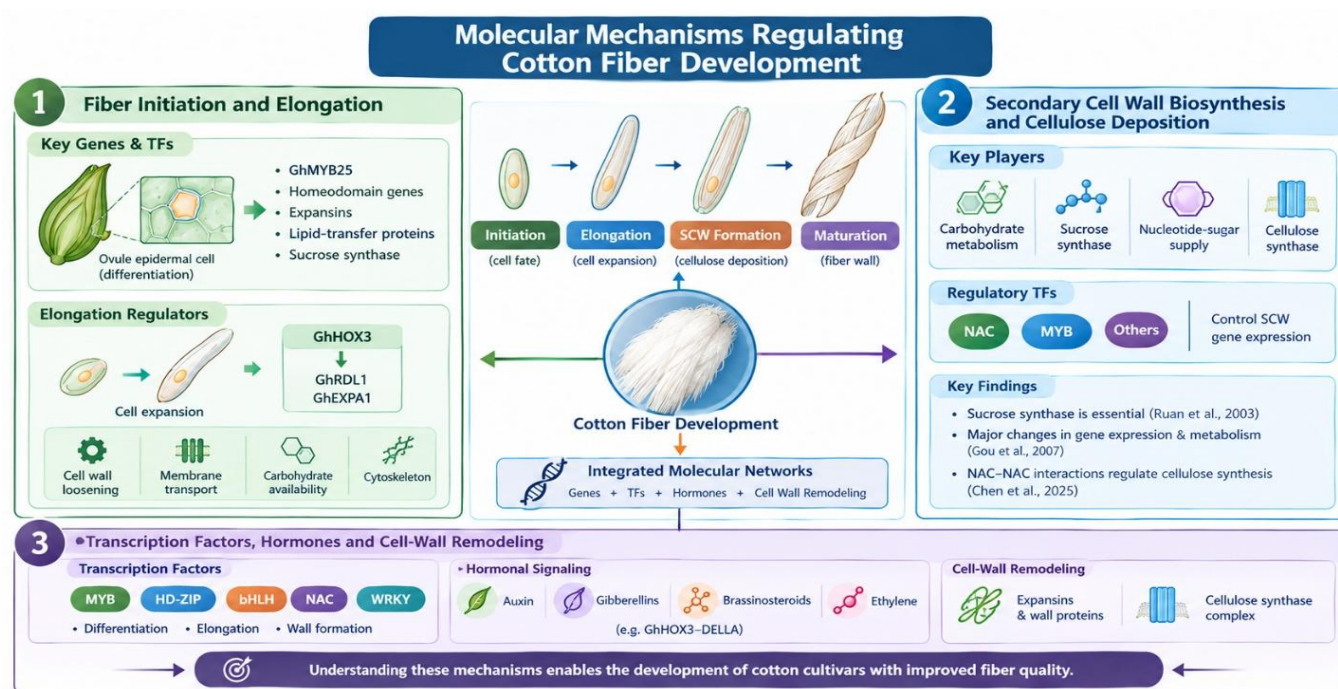


Figure 3: Molecular mechanisms regulating cotton fiber development, including fiber initiation and elongation, secondary cell wall biosynthesis, transcriptional regulation, hormonal signaling, and cell-wall remodeling.

Genes and Regulatory Networks Involved in Secondary Cell Wall Biosynthesis and Cellulose Deposition

Secondary cell wall (SCW) formation is a critical developmental process that determines much of the cellulose content and mechanical properties of mature cotton fibers. During this stage, substantial carbon resources are directed toward cellulose biosynthesis, requiring coordinated regulation of carbohydrate metabolism, nucleotide-sugar availability, and cellulose synthase activity. Sucrose synthase contributes to this process by cleaving sucrose and providing substrates for cellular metabolism and cellulose production. Experimental suppression of sucrose synthase expression has been shown to impair fiber initiation, elongation, and seed development, demonstrating its importance in cotton development (Ruan et al., 2003). Transcriptomic and metabolomic analyses have further revealed substantial changes in gene expression and metabolic activity between fiber elongation and SCW synthesis. Gou et al. (2007) identified extensive developmental differences in genes associated with carbohydrate metabolism, cell-wall formation, and other cellular processes. These findings support the concept that SCW biosynthesis requires a coordinated transition from rapid cell expansion to intensive cellulose deposition. At the regulatory level, transcription factors belonging to NAC, MYB, and related protein families participate in controlling SCW-associated gene expression. Recent molecular research has also demonstrated that interactions among NAC-family transcription factors contribute to the regulation of cellulose biosynthesis in cotton fibers (Chen et al., 2025). Understanding these regulatory networks may enable the identification of genetic targets for improving fiber strength and other quality attributes.

Transcription Factors, Hormonal Signaling, and Cell-Wall Remodeling During Fiber Development

Transcription factors integrate developmental signals to coordinate gene expression throughout cotton fiber development. MYB, homeodomain-leucine zipper (HD-ZIP), basic helix-loop-helix (bHLH), NAC, and WRKY families participate in regulating cellular differentiation, elongation, and wall formation. These regulators frequently operate through interacting transcriptional networks rather than isolated pathways. Wang et al. (2019) reviewed evidence that cotton fiber development involves conserved epidermal differentiation mechanisms alongside regulatory pathways specialized for cotton fibers. Phytohormones further influence these transcriptional networks. Auxin, gibberellins, brassinosteroids, and ethylene participate in different aspects of fiber initiation and elongation, with their effects depending on developmental stage and interactions with other signaling components. GhHOX3, for example, interacts with a DELLA protein associated with gibberellin signaling, linking hormonal regulation to the activation of cell-expansion genes (Shan et al., 2014). Cell-wall remodeling is equally important because developing fibers must maintain sufficient wall flexibility for expansion before establishing the cellulose-rich secondary wall. Expansins and other wall-modifying proteins facilitate cellular extension, whereas cellulose synthases contribute to subsequent wall deposition. Recent evidence that multiple NAC proteins interact to regulate cellulose synthase genes highlights the complexity of this process (Chen et al., 2025). Collectively, these mechanisms provide potential molecular targets for improving cotton fiber properties through precision breeding and functional genomics.

Advanced Genomics, Transcriptomics, and Functional Genomics

Cotton Genome Organization, Polyploidy, and Homoeologous Gene Regulation

The development of advanced genomic resources has substantially improved understanding of the genetic mechanisms underlying cotton fiber quality. Upland cotton (*Gossypium hirsutum* L.) is an allotetraploid species containing A- and D-subgenomes, designated At and Dt, which originated through hybridization between ancestral diploid species followed by chromosome doubling. Its complex genome provides duplicated genes that may retain overlapping functions, acquire specialized roles, or undergo regulatory divergence. The reference genome of the TM-1 cultivar established an essential foundation for investigating genome organization, gene evolution, and fiber-associated loci (Zhang et al., 2015). Comparative genome analysis subsequently revealed extensive structural variation and evolutionary differences between the two subgenomes (Li et al., 2015). Homoeologous genes inherited from the ancestral genomes may exhibit biased expression, developmental specialization, or partial functional redundancy. Such differences can influence fiber initiation, elongation, and cellulose accumulation. Bao et al. (2019) demonstrated that cis- and trans-regulatory changes contributed to gene-expression evolution during cotton domestication. Understanding homoeolog-specific expression is therefore important for identifying favorable alleles and designing breeding strategies that exploit both subgenomes (Figure 4).

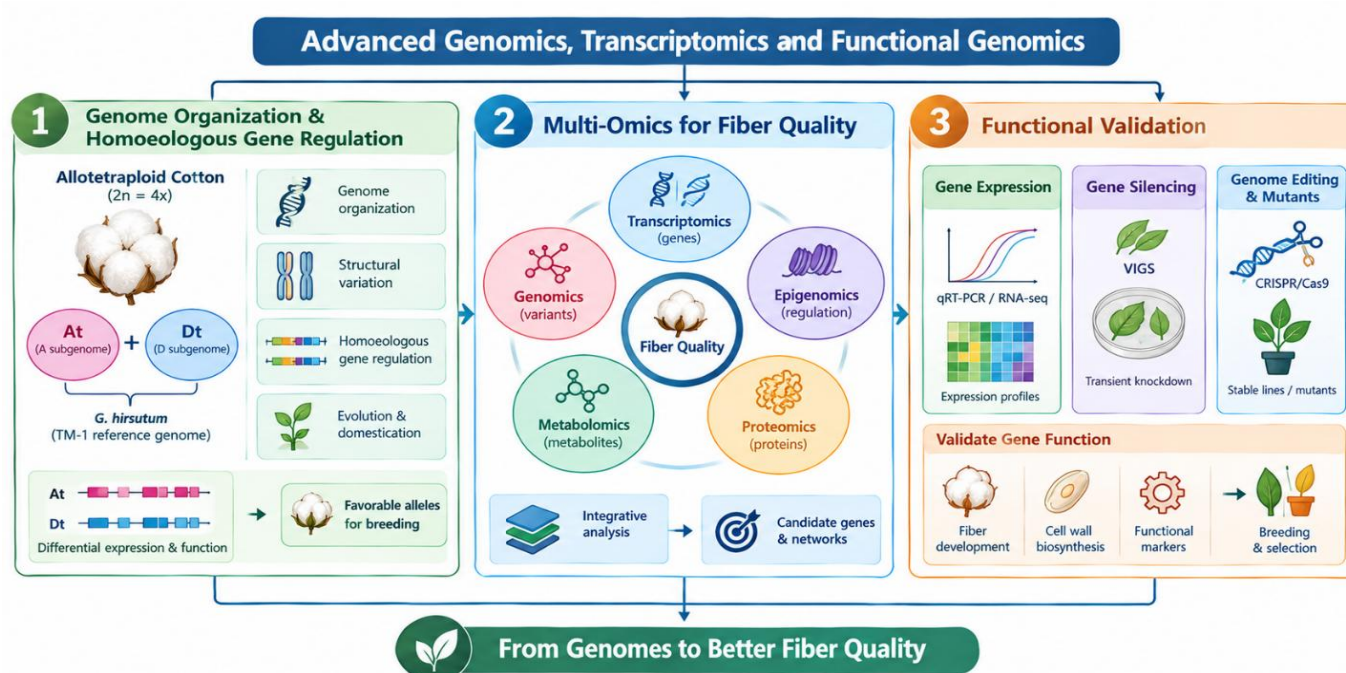


Figure 4: Applications of advanced genomics, multi-omics approaches, and functional genomics in elucidating the molecular basis of cotton fiber quality and accelerating precision breeding.

Transcriptomics, Epigenomics, Proteomics, and Metabolomics in Fiber Quality Research

Multi-omics approaches provide complementary information about the molecular processes governing cotton fiber development. Transcriptomics identifies genes expressed at different developmental stages, enabling researchers to distinguish molecular signatures associated with fiber initiation, elongation, and secondary cell wall formation. Large-scale genome and transcriptome analyses of diverse upland cotton accessions have revealed developmental expression patterns, expression quantitative trait loci, and regulatory networks associated with fiber characteristics (You et al., 2023). Epigenomics investigates DNA methylation, histone modifications, chromatin accessibility, and three-dimensional genome organization, which influence when and where genes are expressed. Huang et al. (2024) integrated epigenomic, transcriptomic, and chromatin-conformation datasets across cotton tissues and developmental stages, revealing dynamic regulatory organization and differences between the At and Dt subgenomes. These findings demonstrate that fiber quality depends not only on DNA sequence variation but also on the regulatory environment surrounding genes. Proteomics identifies proteins and their abundance, providing evidence about whether transcriptional changes are reflected in functional cellular machinery. Metabolomics complements these analyses by examining changes in sugars, organic acids, amino acids, and other metabolites associated with cellular growth and wall biosynthesis. Integrating these datasets can connect genetic variation with molecular activity and fiber phenotypes, improving candidate-gene prioritization and mechanistic interpretation (Wu et al., 2017).

Functional Validation of Candidate Genes Through Gene Expression Analysis, Mutant Studies, and Gene-Silencing Approaches

Functional genomics establishes causal relationships between candidate genes and fiber-quality traits. Differential gene-expression analysis using quantitative reverse-transcription PCR (qRT-PCR) and RNA sequencing helps identify genes whose expression correlates with specific developmental stages or fiber characteristics. However, expression correlations alone cannot establish gene function; experimental validation is required to determine whether a candidate gene directly contributes to a particular phenotype. Virus-induced gene silencing (VIGS) provides a relatively rapid approach for transiently suppressing gene expression and examining associated developmental changes. Its applications in cotton include investigating gene functions, defense responses, and physiological processes (Tian et al., 2024). Stable transformation, mutant analysis, and CRISPR/Cas-mediated genome editing offer complementary strategies for testing gene function through targeted disruption or modification. These methods can reveal whether candidate genes influence fiber initiation, elongation, cellulose deposition, or mature fiber properties. Combining functional experiments with transcriptomic and genomic information strengthens candidate-gene validation. For example, You et al. (2023) integrated population genomics and developmental transcriptomics to identify favorable alleles and regulatory relationships associated with cotton fiber development. Ultimately, validated genes and functional markers can support marker-assisted selection, genomic selection, and precision breeding for improved fiber quality.

5. Emerging Molecular Technologies for Cotton Fiber Quality Improvement

Marker-Assisted Selection, Genomic Selection, and Integration of Multi-Omics Data

Molecular breeding technologies provide opportunities to accelerate genetic improvement of cotton fiber quality by combining genomic information with conventional phenotypic selection. Marker-assisted selection (MAS) uses DNA markers linked to favorable quantitative trait loci (QTLs) to identify desirable plants during early generations. Its effectiveness depends on marker-trait association strength, linkage stability, and validation across breeding populations. Genomic selection (GS), in contrast, estimates the breeding values of individuals using genome-wide markers and is particularly suitable for complex traits controlled by numerous loci. Li et al. (2022) evaluated 1,385 cotton breeding lines and demonstrated that integrating genomic and pedigree information improved prediction accuracy for fiber length, strength, and lint yield. Similarly, Gapare et al. (2018) showed that historical multi-environment datasets can support genomic prediction of cotton fiber-quality traits. Integrating genomic selection with transcriptomic, metabolomic, and other omics datasets may further improve the identification of favorable alleles and biological pathways. However, the practical value of these approaches depends on reliable phenotyping, representative training populations, and validation across environments. Genomic prediction models must also account for population structure, relatedness, and genotype-by-environment interactions to maintain selection accuracy (Yang et al., 2023) (figure 5).

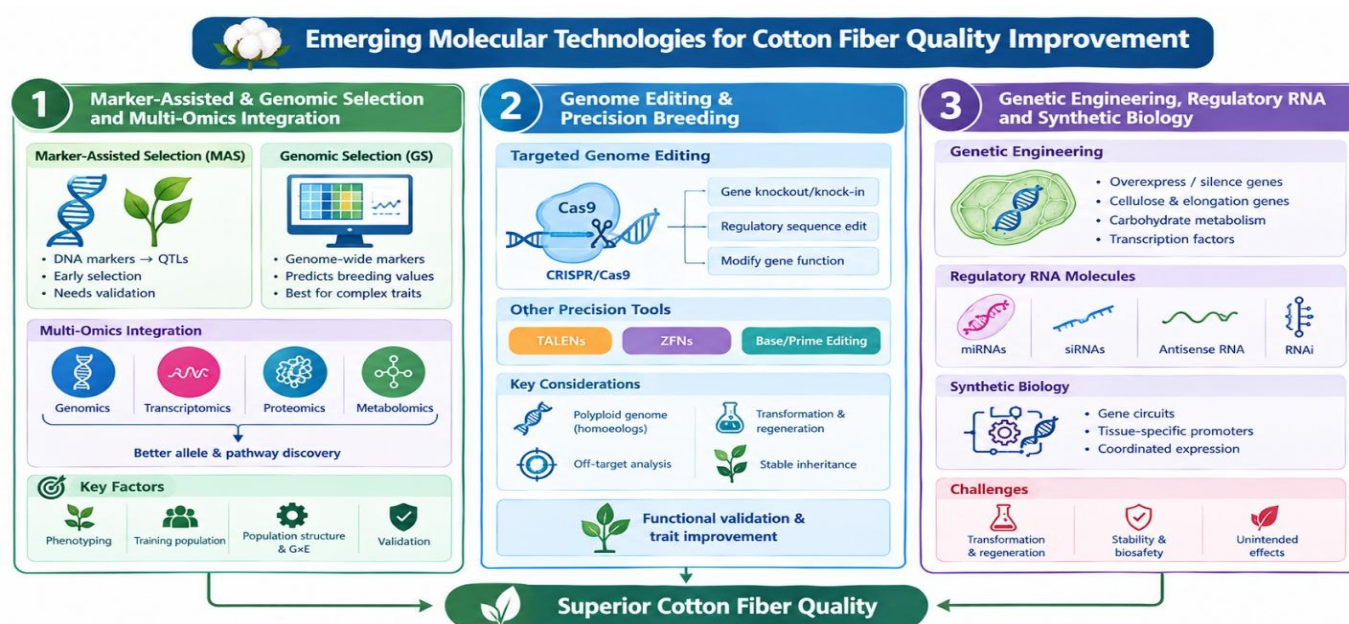


Figure 5: Emerging molecular technologies for cotton fiber quality improvement, highlighting marker-assisted and genomic selection, multi-omics integration, genome editing, genetic engineering, regulatory RNA, and synthetic biology.

Genome Editing Using CRISPR/Cas Systems and Other Precision Breeding Approaches

CRISPR/Cas genome editing enables targeted modifications in genes regulating fiber initiation, elongation, and secondary cell wall development. Unlike conventional breeding, which recombines existing alleles, genome editing can introduce specific mutations into candidate genes, modify regulatory sequences, or alter gene function directly. Other precision tools, including transcription activator-like effector nucleases (TALENs) and zinc-finger nucleases (ZFNs), also enable targeted genome modification, although their design and implementation can be more technically demanding. In cotton, CRISPR/Cas9 has been used to modify fiber-associated genes, including GhMYB25, demonstrating its potential for functional validation and trait improvement (Saleem et al., 2024). Newer approaches, including base editing, prime editing, and multiplex editing, may enable more precise nucleotide changes and simultaneous modification of multiple targets. Nevertheless, cotton's polyploid genome presents challenges because homoeologous gene copies may require coordinated editing. Efficient transformation, regeneration, off-target assessment, and stable inheritance remain essential considerations for practical applications (Khan et al., 2023; Vijay et al., 2025).

Genetic Engineering, Regulatory RNA Molecules, and Synthetic Biology for Fiber Quality Enhancement

Genetic engineering offers an alternative strategy for improving cotton fiber properties by introducing, suppressing, or modifying genes involved in fiber development. Transgenic approaches can manipulate genes associated with cellulose biosynthesis, cell elongation, carbohydrate metabolism, and transcriptional regulation. Regulatory RNA molecules, particularly microRNAs (miRNAs), small interfering RNAs (siRNAs), and natural antisense transcripts, provide additional mechanisms for controlling gene expression. Wan et al. (2016) demonstrated that siRNAs generated from bidirectional transcripts of GhMML3_A12 participate in cotton fuzz fiber development, illustrating the importance of RNA-mediated regulation in fiber differentiation. RNA interference (RNAi) can reduce the expression of undesirable genes, whereas targeted genetic engineering can enhance the activity of beneficial pathways. Synthetic biology extends these approaches through the design of regulatory circuits, tissue-specific promoters, and coordinated gene-expression systems. Such strategies could enable developmental-stage-specific manipulation of fiber elongation and cellulose deposition while minimizing unintended effects on other plant tissues. Nevertheless, genetic engineering requires careful evaluation of transformation efficiency, transgene stability, unintended phenotypic effects, and biosafety considerations. The development of efficient transformation and regeneration systems remains an important technical challenge in cotton improvement (Aluko et al., 2025). Integrating transgenic approaches, regulatory RNA technologies, genome editing, and conventional breeding could provide complementary routes for developing cotton cultivars with superior fiber quality and stable agronomic performance.

Future Perspectives and Sustainable Improvement of Cotton Fiber Quality

Integrating Genetic, Molecular, and Phenotypic Information for Precision Cotton Breeding

Future cotton improvement will increasingly depend on integrating conventional breeding with genomic selection, molecular markers, high-throughput phenotyping, and multi-omics technologies. Fiber length, strength, uniformity, and micronaire are complex traits influenced by numerous genetic loci and environmental conditions. Consequently, combining genome-wide marker data with accurate phenotypic measurements can improve breeding-value prediction and accelerate the identification of superior parental lines. Genomic prediction models can also incorporate pedigree information, gene-expression profiles, and environmental variables to improve selection decisions across breeding populations (Yang et al., 2023). High-throughput phenotyping technologies, including imaging, spectroscopy, and automated plant measurements, can facilitate the rapid evaluation of large cotton populations. When integrated with genomic and environmental datasets, these technologies may help identify genotypes that combine desirable fiber properties with high yield and stress tolerance. However, effective implementation requires standardized fiber-quality measurements, representative training populations, and validation across multiple locations and seasons. Integrative genomics and precision breeding therefore offer a pathway toward more efficient and environmentally responsive cotton improvement (Zhang et al., 2019) (Figure 6).

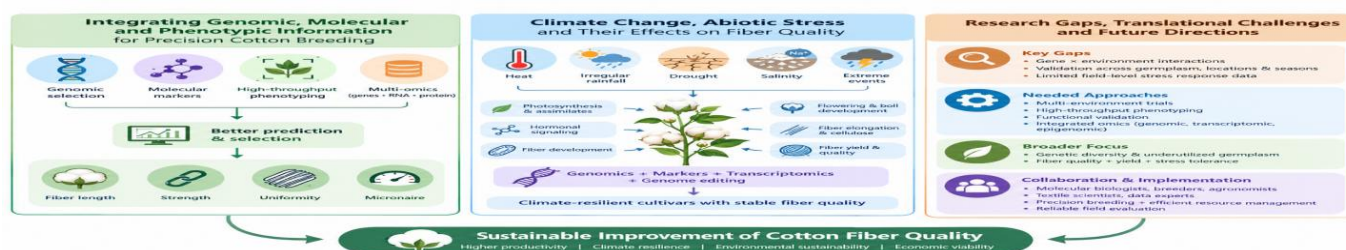


Figure 6: Integrating Precision Breeding, Climate Resilience, and Sustainable Strategies for Cotton Fiber Quality Improvement.

Climate Change, Abiotic Stress, and Their Effects on the Genetic Regulation of Fiber Quality

Climate change presents an increasing challenge to sustainable cotton production through elevated temperatures, irregular rainfall, drought, salinity, and extreme weather events. These stresses can disrupt photosynthesis, carbohydrate allocation, hormonal signaling, and the developmental processes responsible for fiber elongation and cellulose deposition. High day and night temperatures may also affect flowering, boll development, and assimilate availability, ultimately reducing fiber yield and quality (Saini et al., 2023). Drought further restricts the transport of photosynthetic assimilates toward developing reproductive tissues, potentially impairing fiber development and mature fiber properties (Ul-Allah et al., 2021). Importantly, combined stresses may produce responses that differ from those observed under individual stress conditions. Liu et al. (2025) reported increasing exposure of global cotton-growing regions to compound drought and heat events, with significant associations between these events and cotton yield failures. Future breeding programs should therefore investigate the genetic regulation of fiber quality under realistic combinations of environmental stresses rather than relying exclusively on controlled single-stress experiments. Genomic selection, molecular markers, transcriptomics, and genome editing offer opportunities to identify and utilize favorable alleles associated with stress resilience and fiber-quality stability. Integrating these approaches with field-based phenotyping may accelerate the development of climate-resilient cotton cultivars while maintaining desirable textile properties (Luqman et al., 2025; Khan et al., 2025).

Research Gaps, Translational Challenges, and Future Directions for Developing Superior Cotton Cultivars

Despite substantial advances in cotton genomics, several challenges remain in translating molecular discoveries into commercially valuable cultivars. One major limitation is the incomplete understanding of how fiber-quality genes interact with environmental conditions and genetic backgrounds. Many candidate genes and molecular markers have been identified, but their effectiveness requires validation across diverse germplasm, locations, and seasons. Furthermore, experiments conducted under controlled conditions may not fully represent field-level responses to fluctuating temperatures, water availability, and combined stresses (Dabbert & Gore, 2014). Future research should prioritize multi-environment trials, high-throughput phenotyping, functional validation of candidate genes, and integration of genomic, transcriptomic, and epigenomic datasets. Greater attention is also needed to genetic diversity, underutilized *Gossypium* germplasm, and the simultaneous improvement of fiber quality, yield, and stress tolerance. Recent experimental evidence confirms that cotton cultivars differ substantially in their responses to reproductive-stage heat stress, highlighting opportunities for identifying and transferring favorable physiological and genetic characteristics into elite backgrounds (Bista et al., 2025). Sustainable improvement will require collaboration among molecular biologists, plant breeders, agronomists, textile scientists, and computational researchers. Combining precision breeding with efficient resource management and reliable field evaluation can help develop cotton cultivars that maintain superior fiber properties under changing climatic conditions. Ultimately, the objective should be to achieve durable genetic improvement without compromising productivity, environmental sustainability, or economic viability.

7. Genetic and Molecular Approaches to Improving Cotton Fiber Quality for Sustainable Agriculture

Integrating Conventional Breeding, Molecular Markers, and Genomic Selection for Sustainable Cotton Improvement

Sustainable cotton improvement requires integrating conventional breeding with molecular markers, genomic selection, and high-throughput phenotyping. Conventional hybridization remains essential for combining desirable fiber characteristics, yield potential, and stress tolerance, whereas molecular markers facilitate the identification and transfer of favorable alleles. Genomic selection estimates breeding values using genome-wide marker information, enabling earlier selection of superior genotypes for complex quantitative traits. Billings et al. (2022) demonstrated the potential of genomic prediction for fiber-quality improvement in public cotton breeding programs. More recently, Abdurakhmonov (2026) highlighted how advanced mapping approaches, including graph-based pan-genomes, can improve gene discovery and sustainable cotton breeding. Integrating these methods with multi-environment trials can accelerate genetic gain while maintaining fiber quality and agronomic performance (figure 7).

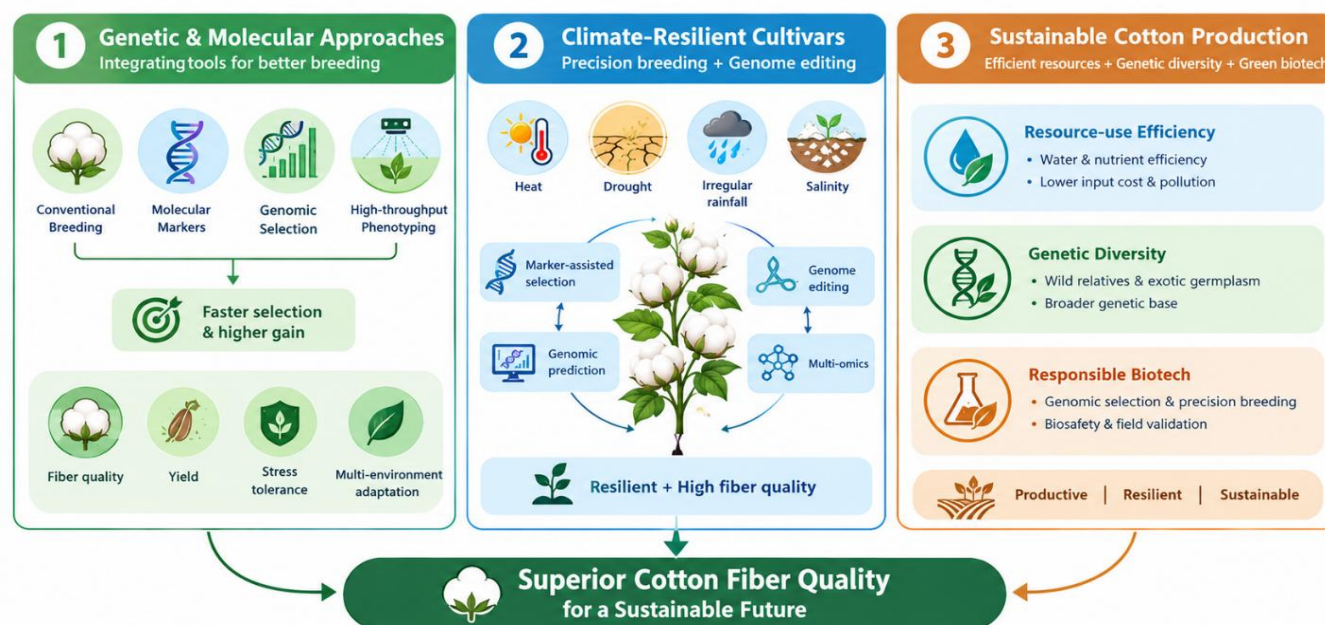


Figure 7: Integrating Genetic and Molecular Breeding, Climate Resilience, and Sustainable Resource Management for Cotton Fiber Quality Improvement.

Developing Climate-Resilient Cotton Cultivars with Superior Fiber Quality Through Precision Breeding and Genome Editing

Climate change, particularly drought and heat stress, threatens cotton productivity and fiber quality by disrupting photosynthesis, carbohydrate metabolism, reproductive development, and fiber elongation. Developing resilient cultivars therefore requires combining stress-tolerance traits with desirable textile characteristics. Zafar et al. (2023) reviewed physiological and molecular mechanisms associated with cotton drought tolerance, emphasizing the importance of integrating genetic improvement with appropriate crop-management strategies. Genome editing, marker-assisted selection, and genomic prediction offer complementary approaches for identifying and modifying favorable alleles. Luqman et al. (2025) further highlighted the potential of multi-omics and molecular breeding to improve cotton heat tolerance. However, candidate genes and edited lines must be evaluated under field conditions to establish their effectiveness across genetic backgrounds and environments.

Sustainable Cotton Production Through Resource-Use Efficiency, Genetic Diversity, and Environmentally Responsible Biotechnological Innovations

Sustainable cotton production requires genetic improvement alongside efficient management of water, nutrients, and biological resources. Developing cultivars with improved water-use and nitrogen-use efficiency can reduce production costs and environmental pollution while maintaining yield and fiber quality. A meta-analysis of 61 studies across nine countries identified substantial opportunities to optimize irrigation and nitrogen inputs in cotton production (Wang et al., 2024). At the molecular level, nitrogen transporters, transcription factors, and microRNAs represent potential targets for improving nutrient acquisition and utilization (Ninkuu et al., 2023). Genetic diversity is equally important for long-term sustainability. Wild cotton relatives and exotic germplasm contain useful alleles that may improve fiber quality and expand the narrow genetic base of cultivated cotton. Sakthipriya et al. (2025) emphasized the potential of wild relatives as sources of favorable fiber-quality genes. Integrating these resources with genomic selection and precision breeding can support the development of cultivars combining superior fiber properties, stress tolerance, and efficient resource utilization. Environmentally responsible biotechnology should complement conventional breeding, with careful evaluation of genetic stability, biosafety, and field performance.

Conclusion

Cotton fiber quality is a complex quantitative trait governed by genetic architecture, molecular regulatory networks, physiological processes, and environmental interactions. Advances in genomics, transcriptomics, epigenomics, and functional genomics have enhanced understanding of fiber initiation, elongation, cellulose biosynthesis, and secondary cell wall formation.

Integrating molecular markers, genomic selection, genome editing, and multi-omics approaches offers promising opportunities to accelerate genetic improvement. However, challenges associated with genotype-by-environment interactions, genetic diversity, and translating laboratory discoveries into field performance remain. Future research should prioritize precision breeding, climate resilience, and sustainable management to develop high-yielding cotton cultivars with superior fiber quality and stable performance. Integrating conventional breeding, molecular technologies, and sustainable resource management can accelerate cotton fiber quality improvement while enhancing climate resilience, productivity, and long-term agricultural sustainability.

References

- Abdurakhmonov, I. Y. (2026). Cotton genetic mapping for plant biotechnology: From markers to graph pan-genomes and sustainable breeding. *Frontiers in Plant Science*, 17, Article 1825852. <https://doi.org/10.3389/fpls.2026.1825852>
- Aluko, O. O., Ninkuu, V., & Liu, Z. (2025). Recent advances in cotton transformation and genome editing techniques: The prospects and challenges. *Modern Agriculture*, 3(1), Article e70014. <https://doi.org/10.1002/moda.70014>
- Bai, F., & Scheffler, J. (2024). Genetic and molecular regulation of cotton fiber initiation and elongation. *Agronomy*, 14(6), Article 1208. <https://doi.org/10.3390/agronomy14061208>
- Bao, Y., Hu, G., Grover, C. E., Conover, J., Yuan, D., & Wendel, J. F. (2019). Unraveling cis and trans regulatory evolution during cotton domestication. *Nature Communications*, 10, Article 5399. <https://doi.org/10.1038/s41467-019-13386-w>
- Billings, G. T., Jones, M. A., Rustgi, S., Bridges, W. C., Jr., Holland, J. B., Hulse-Kemp, A. M., & Campbell, B. T. (2022). Outlook for implementation of genomics-based selection in public cotton breeding programs. *Plants*, 11(11), Article 1446. <https://doi.org/10.3390/plants1111446>
- Bista, M. K., Kodadinne Narayana, N., Chakravaram, A., Pieralisi, B., Dhillon, J., Reddy, K. R., & Bheemanahalli, R. (2025). Intensifying heat stress impacts cotton flowering and boll development efficiency. *BMC Plant Biology*, 25, Article 984. <https://doi.org/10.1186/s12870-025-06934-8>
- Bradow, J. M., & Davidonis, G. H. (2000). Quantitation of fiber quality and the cotton production-processing interface: A physiologist's perspective. *Journal of Cotton Science*, 4(1), 34-64.
- Chen, F., Qiao, M., Chen, L., Liu, M., Luo, J., Gao, Y., Li, M., Cai, J., Persson, S., Huang, G., & Xu, W. (2025). Dimerization among multiple NAC proteins mediates secondary cell wall cellulose biosynthesis in cotton fibers. *The Plant Journal*, 121(2), Article e17223. <https://doi.org/10.1111/tpj.17223>
- Dabbert, T. A., & Gore, M. A. (2014). Challenges and perspectives on improving heat and drought stress resilience in cotton. *Journal of Cotton Science*, 18(3), 393-409. <https://doi.org/10.56454/IOSW7990>
- Gapare, W., Liu, S., Conaty, W., Zhu, Q.-H., Gillespie, V., Llewellyn, D., Stiller, W., & Wilson, I. (2018). Historical datasets support genomic selection models for the prediction of cotton fiber quality phenotypes across multiple environments. *G3: Genes, Genomes, Genetics*, 8(5), 1721-1732. <https://doi.org/10.1534/g3.118.200140>
- Gou, J.-Y., Wang, L.-J., Chen, S.-P., Hu, W.-L., & Chen, X.-Y. (2007). Gene expression and metabolite profiles of cotton fiber during cell elongation and secondary cell wall synthesis. *Cell Research*, 17, 422-434. <https://doi.org/10.1038/cr.2007.39>
- Gowda, S. A., Fang, H., Tyagi, P., Bourland, F., Dever, J., Campbell, B. T., Zhang, J., Abdelraheem, A., Sood, S., Jones, D. C., & Kuruparth, V. (2024). Genome-wide association study of fiber quality traits in US upland cotton (*Gossypium hirsutum* L.). *Theoretical and Applied Genetics*, 137, Article 214. <https://doi.org/10.1007/s00122-024-04717-7>
- Haigler, C. H., Betancur, L., Stiff, M. R., & Tuttle, J. R. (2012). Cotton fiber: A powerful single-cell model for cell wall and cellulose research. *Frontiers in Plant Science*, 3, Article 104. <https://doi.org/10.3389/fpls.2012.00104>
- Huang, X., Wang, Y., Zhang, S., Pei, L., You, J., Long, Y., Li, J., Zhang, X., Zhu, L., & Wang, M. (2024). Epigenomic and 3D genomic mapping reveals developmental dynamics and subgenomic asymmetry of transcriptional regulatory architecture in allotetraploid cotton. *Nature Communications*, 15, Article 10721. <https://doi.org/10.1038/s41467-024-55309-4>

- Khan, M. A., Anwar, S., Abbas, M., Aneeq, M., de Jong, F., Ayaz, M., Wei, Y., et al. (2025). Impacts of climate change on cotton production and advancements in genomic approaches for stress resilience enhancement. *Journal of Cotton Research*, 8, Article 17. <https://doi.org/10.1186/s42397-025-00223-3>
- Khan, Z., Khan, S. H., Ahmed, A., Iqbal, M. U., Mubarik, M. S., Ghouri, M. Z., Ahmad, F., Yaseen, S., Ali, Z., Khan, A. A., et al. (2023). Genome editing in cotton: Challenges and opportunities. *Journal of Cotton Research*, 6, Article 3. <https://doi.org/10.1186/s42397-023-00140-3>
- Kim, H. J., & Triplett, B. A. (2001). Cotton fiber growth in planta and in vitro: Models for plant cell elongation and cell wall biogenesis. *Plant Physiology*, 127(4), 1361–1366. <https://doi.org/10.1104/pp.010724>
- Kushanov, F. N., Turaev, O. S., Ernazarova, D. K., Gapparov, M. M., Oripova, B. B., Kudratova, M. K., Rafieva, F. M., Khalikov, K. K., Erjigitov, D. S., Khidirov, M. T., Kholova, M. S., Khusenov, N. N., Amanboyeva, S. U., Saha, S., Yu, J. Z., & Abdurakhmonov, I. Y. (2021). Genetic diversity, QTL mapping, and marker-assisted selection technology in cotton (*Gossypium* spp.). *Plants*, 10(12), Article 2642. <https://doi.org/10.3390/plants10122642>
- Li, F., Fan, G., Lu, C., Xiao, G., Zou, C., Kohel, R. J., Ma, Z., Shang, H., Ma, X., Wu, J., Liang, X., Huang, G., Percy, R. G., Liu, K., Yang, W., Chen, W., Du, X., Shi, C., Yuan, Y., ... Yu, S. (2015). Genome sequence of cultivated upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature Biotechnology*, 33(5), 524–530. <https://doi.org/10.1038/nbt.3208>
- Li, Z., Liu, S., Conaty, W., Zhu, Q.-H., Moncuquet, P., Stiller, W., & Wilson, I. (2022). Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. *Heredity*, 129, 103–112. <https://doi.org/10.1038/s41437-022-00537-x>
- Liu, S., Zhang, W., Shi, T., Li, T., Li, H., Zhou, G., Wang, Z., & Ma, X. (2025). Increasing exposure of cotton growing areas to compound drought and heat events in a warming climate. *Agricultural Water Management*, 308, Article 109307. <https://doi.org/10.1016/j.agwat.2025.109307>
- Luqman, T., Hussain, M., Ahmed, S. R., Ijaz, I., Maryum, Z., Nadeem, S., Khan, Z., Khan, S. M. U. D., Aslam, M., Liu, Y., et al. (2025). Cotton under heat stress: A comprehensive review of molecular breeding, genomics, and multi-omics strategies. *Frontiers in Genetics*, 16, Article 1553406. <https://doi.org/10.3389/fgene.2025.1553406>
- Machado, A., Wu, Y., Yang, Y., Llewellyn, D. J., & Dennis, E. S. (2009). The MYB transcription factor GhMYB25 regulates early fibre and trichome development. *The Plant Journal*, 59(1), 52–62. <https://doi.org/10.1111/j.1365-313X.2009.03847.x>
- Manivannan, A., & Cheeran, A. T. (2023). Deciphering the complex cotton genome for improving fiber traits and abiotic stress resilience in sustainable agriculture. *Molecular Biology Reports*, 50(8). <https://doi.org/10.1007/s11033-023-08565-4>
- Naoumkina, M., & Kim, H. J. (2023). Bridging molecular genetics and genomics for cotton fiber quality improvement. *Crop Science*, 63(4), 1794–1815. <https://doi.org/10.1002/csc2.20987>
- Ninkuu, V., Liu, Z., & Sun, X. (2023). Genetic regulation of nitrogen use efficiency in *Gossypium* spp. *Plant, Cell & Environment*, 46(6), 1749–1773. <https://doi.org/10.1111/pce.14586>
- Ruan, Y.-L., Llewellyn, D. J., & Furbank, R. T. (2003). Suppression of sucrose synthase gene expression represses cotton fiber cell initiation, elongation, and seed development. *The Plant Cell*, 15(4), 952–964. <https://doi.org/10.1105/tpc.010108>
- Saini, D. K., Impa, S. M., McCallister, D., Patil, G. B., Abidi, N., Ritchie, G., Jaconis, S. Y., & Jagadish, K. S. V. (2023). High day and night temperatures impact on cotton yield and quality—Current status and future research direction. *Journal of Cotton Research*, 6, Article 16. <https://doi.org/10.1186/s42397-023-00154-x>
- Sakthipriya, M., Subramanian, A., Premalatha, N., Marimuthu, S., & Chitra, N. (2025). Weaving the wild: Harnessing the potential of cotton relatives for superior fibre quality. *Genetic Resources and Crop Evolution*, 72, 9147–9164. <https://doi.org/10.1007/s10722-025-02533-6>
- Shan, C.-M., Shangguan, X.-X., Zhao, B., Zhang, X.-F., Chao, L.-M., Yang, C.-Q., Wang, L.-J., Zhu, H.-Y., Zeng, Y.-D., Zhou, C.-F., Zhang, M.-Q., & Chen, X.-Y. (2014). Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. *Nature Communications*, 5, Article 5519. <https://doi.org/10.1038/ncomms6519>

- Tan, H., Tang, B., Sun, M., Yin, Q., Ma, Y., Li, J., Wang, P., Li, Z., Zhao, G., Wang, M., Zhang, X., You, C., & Tu, L. (2024). Identification of new cotton fiber-quality QTL by multiple genomic analyses and development of markers for genomic breeding. *The Crop Journal*, 12(3), 866–879. <https://doi.org/10.1016/j.cj.2024.03.014>
- Thangaraj, A., Kaul, R., Sharda, S., & Kaul, T. (2025). Revolutionizing cotton cultivation: A comprehensive review of genome editing technologies and their impact on breeding and production. *Biochemical and Biophysical Research Communications*, 742, Article 151084. <https://doi.org/10.1016/j.bbrc.2024.151084>
- Tian, Y., Fang, Y., Zhang, K., Zhai, Z., Yang, Y., He, M., & Cao, X. (2024). Applications of virus-induced gene silencing in cotton. *Plants*, 13(2), Article 272. <https://doi.org/10.3390/plants13020272>
- Ul-Allah, S., Rehman, A., Hussain, M., & Farooq, M. (2021). Fiber yield and quality in cotton under drought: Effects and management. *Agricultural Water Management*, 255, Article 106994. <https://doi.org/10.1016/j.agwat.2021.106994>
- Ul-Allah, S., Sugumar, T., Ahmed, J. S., Bhandari, B., et al. (2026). Genetic and biotechnological innovations for drought and heat resilient cotton production: A review. *Journal of Cotton Research*, 9, Article 21. <https://doi.org/10.1186/s42397-026-00266-0>
- Vijay, S., Harikrishnan, M., Phanikanth, J., Anshu, A., Khan, R. G., et al. (2025). CRISPR/Cas genome editing for cotton precision breeding: Mechanisms, advances, and prospects. *Journal of Cotton Research*, 8, Article 4. <https://doi.org/10.1186/s42397-024-00206-w>
- Walford, S.-A., Wu, Y., Llewellyn, D. J., & Dennis, E. S. (2011). GhMYB25-like: A key factor in early cotton fibre development. *The Plant Journal*, 65(3), 359–372. <https://doi.org/10.1111/j.1365-313X.2010.04464.x>
- Wan, Q., Zhang, H., Ye, W., Wu, H., Zhang, T., & Wang, X. (2016). Small interfering RNAs from bidirectional transcripts of GhMML3_A12 regulate cotton fiber development. *New Phytologist*, 210(4), 1298–1311. <https://doi.org/10.1111/nph.13860>
- Wang, Z., Yang, Z., & Li, F. (2019). Updates on molecular mechanisms in the development of branched trichome in Arabidopsis and nonbranched in cotton. *Plant Biotechnology Journal*, 17(9), 1706–1722. <https://doi.org/10.1111/pbi.13167>
- Wang, Z., Zhang, K., Shao, G., Lu, J., Gao, Y., & Song, E. (2024). Water and nitrogen use efficiencies in cotton production: A meta-analysis. *Field Crops Research*, 309, Article 109322. <https://doi.org/10.1016/j.fcr.2024.109322>
- Wu, Y., Machado, A. C., White, R. G., Llewellyn, D. J., & Dennis, E. S. (2006). Expression profiling identifies genes expressed early during lint fibre initiation in cotton. *Plant and Cell Physiology*, 47(1), 107–127. <https://doi.org/10.1093/pcp/pci228>
- Wu, Z., Yang, Y., Huang, G., Lin, J., Xia, Y., & Zhu, Y. (2017). Cotton functional genomics reveals global insight into genome evolution and fiber development. *Journal of Genetics and Genomics*, 44(11), 511–518. <https://doi.org/10.1016/j.jgg.2017.09.009>
- Yang, Z., Ge, X., Yang, Z., Qin, W., Sun, G., Wang, Z., Li, Z., Liu, J., Wu, J., Wang, Y., & Li, F. (2023). Recent progression and future perspectives in cotton genomic breeding. *Journal of Integrative Plant Biology*, 65(2), 548–569. <https://doi.org/10.1111/jipb.13388>
- Yasir, M., Kanwal, H. H., Hussain, Q., Riaz, M. W., Sajjad, M., Rong, J., & Jiang, Y. (2022). Status and prospects of genome-wide association studies in cotton. *Frontiers in Plant Science*, 13, Article 1019347. <https://doi.org/10.3389/fpls.2022.1019347>
- You, J., Liu, Z., Qi, Z., Ma, Y., Sun, M., Su, L., Niu, H., Peng, Y., Luo, X., Zhu, M., Huang, Y., Chang, X., Hu, X., Zhang, Y., Pi, R., Liu, Y., Meng, Q., Li, J., Zhang, Q., ... Wang, M. (2023). Regulatory controls of duplicated gene expression during fiber development in allotetraploid cotton. *Nature Genetics*, 55(11), 1987–1997. <https://doi.org/10.1038/s41588-023-01530-8>
- Zafar, S., Afzal, H., Ijaz, A., Mahmood, A., Ayub, A., Nayab, A., Hussain, S., Ul-Hussan, M., Sabir, M. A., Zulfikar, U., Zulfikar, F., & Moosa, A. (2023). Cotton and drought stress: An updated overview for improving stress tolerance. *South African Journal of Botany*, 161, 258–268. <https://doi.org/10.1016/j.sajb.2023.08.029>
- Zhang, T., Hu, Y., Jiang, W., Fang, L., Guan, X., Chen, J., Zhang, J., Saski, C. A., Scheffler, B. E., Stelly, D. M., Hulse-Kemp, A. M., Wan, Q., Liu, B., Liu, C., Wang, S., Pan, M., Wang, Y., Wang, D., Ye, W., ... Yu, J. Z. (2015). Sequencing of allotetraploid

cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. *Nature Biotechnology*, 33(5), 531–537. <https://doi.org/10.1038/nbt.3207>

Zhang, X., Wang, J., & Fu, J. (2025). Improving cotton yield and fiber quality based on QTL mapping and genomic selection. *Cotton Genomics and Genetics*, 16(3), 117–125. <https://doi.org/10.5376/cgg.2025.16.0012>

Zhu, Y., Li, F., & colleagues. (2018). Recent insights into cotton functional genomics: Progress and future perspectives. *Plant Biotechnology Journal*.



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