

Review Article

QTL Mapping for Fibre Quality Traits in Cotton: Genetic Architecture, Molecular Markers and Breeding Applications

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Abstract

Cotton (*Gossypium* spp.) is one of the world's most important fibre crops, and fibre quality is a major determinant of its economic value and suitability for textile processing. Important fibre quality characteristics include fibre length, fibre strength, micronaire, fibre elongation, fibre uniformity and fibre maturity. These traits are quantitative in nature and are controlled by multiple genes interacting with environmental factors. Quantitative trait locus (QTL) mapping has therefore become an important approach for dissecting the genetic basis of fibre quality and identifying genomic regions associated with desirable phenotypes. Advances in cotton genome sequencing, molecular marker development and high-density genetic mapping have substantially increased the resolution and reliability of QTL identification. Numerous QTLs have been detected for fibre length, strength, fineness, elongation and uniformity, with several genomic regions repeatedly detected across populations and environments. Recent studies have further combined QTL mapping with genome-wide association studies (GWAS), transcriptomics, meta-analysis and candidate-gene analysis to identify stable loci and genes controlling fibre development. Marker-assisted selection (MAS), genomic selection and genome editing provide opportunities for translating these discoveries into breeding programmes. This review discusses the genetic basis of cotton fibre quality, QTL mapping strategies, important fibre-quality QTLs, molecular markers, QTL $\times$ environment interactions, candidate genes and applications in molecular breeding. Integration of QTL information with high-throughput genomics and precision breeding is expected to accelerate the development of cotton cultivars possessing superior fibre quality together with high yield and environmental adaptability.

Keywords: Cotton, *Gossypium*, fibre quality, QTL mapping, molecular markers, fibre length, fibre strength, micronaire.

1. Introduction

Cotton (*Gossypium* spp.) is a globally important fibre crop whose economic value is strongly associated with the quality and processing performance of its lint. Among cultivated cotton species, upland cotton (*Gossypium hirsutum* L.) is widely grown because of its adaptability and productivity, whereas *G. barbadense* is recognized for superior fibre characteristics, particularly long, strong and fine fibres. Fibre quality is determined by several interrelated characteristics, including fibre length, strength, fineness, elongation and uniformity [1-3]. Fibre length and strength are particularly important for yarn production, while micronaire, which reflects a combination of fibre fineness and maturity, affects processing and dyeing performance. Improving fibre quality through conventional breeding is challenging because these traits are quantitatively inherited and influenced by numerous genes and environmental conditions [4-5]. In addition, favourable fibre characteristics may be genetically associated with undesirable agronomic traits, making simultaneous improvement of yield and quality difficult. Understanding the genomic regions responsible for fibre-quality variation is therefore essential for efficient breeding.

Quantitative trait locus mapping provides a powerful method for identifying chromosome regions associated with quantitative phenotypes. Earlier cotton studies generated numerous QTLs for fibre traits, while advances in molecular markers and genome sequencing have enabled increasingly dense genetic maps and improved QTL resolution [6]. A major review reported more than 1,000 QTLs associated with cotton fibre quality from numerous mapping studies, illustrating the complex genetic architecture of these traits. Recent developments have extended QTL analysis beyond conventional linkage mapping. GWAS can identify marker-trait associations using diverse germplasm, while QTL meta-analysis can integrate results from independent experiments and identify more stable genomic regions. A 2025 meta-analysis integrated 379 original cotton fibre-quality QTLs from 21 mapping studies and identified 74 meta-QTLs distributed across all 26 cotton chromosomes, demonstrating the value of combining independent QTL datasets.

2. Fibre Quality Traits in Cotton

Cotton fibre quality is a multidimensional characteristic comprising several physical and technological properties. Fibre length is generally expressed through measurements such as upper-half mean length and is associated with spinning performance and yarn

strength. Longer fibres can generally produce finer and stronger yarns when other characteristics are favourable [7]. Fibre strength represents the force required to break a fibre bundle and is an important determinant of yarn durability. Strong fibres are particularly desirable for modern high-speed spinning technologies. Fibre elongation describes the ability of fibres to extend before breaking and contributes to processing behaviour. Micronaire is an indirect measure associated with fibre fineness and maturity [8]. Extremely low or high micronaire values can negatively affect processing efficiency and textile quality. Fibre uniformity reflects the consistency of fibre length within a sample, while the short fibre index represents the proportion of relatively short fibres. Together, these traits determine the suitability of cotton for ginning, spinning, weaving and dyeing.

3. Genetic Basis of Cotton Fibre Quality

Cotton fibre quality traits exhibit complex inheritance because they are controlled by multiple loci with different effects. Some loci contribute relatively large effects, whereas numerous minor-effect loci collectively influence phenotypic variation. Consequently, fibre-quality traits generally exhibit continuous variation rather than discrete phenotypic classes. The allotetraploid genome of cultivated cotton further complicates genetic analysis. Upland cotton contains A and D subgenomes, and interactions between homoeologous loci can influence fibre development. Comparative analyses indicate that QTLs for fibre traits are distributed across both subgenomes, although some chromosomes contain relatively greater concentrations of particular trait-associated loci. For example, studies of tetraploid cotton have reported substantial concentrations of fibre-quality QTLs on several A and D subgenome chromosomes [9]. Fibre development itself occurs through distinct developmental stages involving initiation, elongation, secondary cell-wall synthesis and maturation. Different genes and regulatory pathways become active during these stages. Hormonal signalling, transcription factors, cell-wall biosynthesis, carbohydrate metabolism and cytoskeletal processes all contribute to fibre development. This developmental complexity explains why different QTLs may control fibre characteristics at different stages.

4. QTL Mapping Approaches in Cotton

QTL mapping identifies genomic regions statistically associated with phenotypic variation within a segregating population. In cotton, commonly used mapping populations include F populations, recombinant

inbred lines, backcross populations, chromosome substitution lines, introgression lines and other advanced populations. These populations are genotyped with molecular markers and phenotyped for fibre-quality characteristics. Linkage maps are constructed by determining the order and genetic distances between molecular markers. Statistical analysis is then used to identify genomic intervals associated with variation in fibre traits [10]. Depending on the mapping population and experimental design, interval mapping, composite interval mapping and inclusive composite interval mapping can be used. The accuracy of QTL identification depends on population size, marker density, phenotyping accuracy and environmental replication. QTLs detected repeatedly across generations, locations and years are particularly valuable because their stability increases the likelihood of successful application in breeding. Recent studies have demonstrated that stable QTLs can be identified through multi-environment evaluation and subsequent validation.

5. Major QTLs Associated with Fibre Quality Traits

Numerous QTLs have been identified for fibre length, strength, micronaire, elongation and uniformity. Fibre length is particularly well studied, and QTLs have been identified across many cotton chromosomes. A recent overview reported that approximately 1,850 QTLs have been mapped for fibre length, fibre strength and fineness over the past two decades, although only a subset have been sufficiently validated for direct breeding or gene-editing applications. Fibre strength QTLs have also been detected across the cotton genome. For example, high-resolution mapping on chromosome 25 identified a stable fibre-strength QTL, qFS-chr25-4, that was detected across seven environments and explained approximately 6.53–11.83% of phenotypic variation. Such stable loci are especially valuable for marker-assisted breeding [11]. Micronaire is influenced by numerous genomic regions and is often associated with fibre maturity and fineness. Because micronaire can show complex relationships with other fibre traits, breeding strategies must carefully evaluate correlated responses when selecting favourable alleles.

6. Molecular Markers for QTL Detection

Molecular markers are fundamental tools for constructing genetic maps and detecting QTLs. Earlier cotton mapping studies extensively used restriction fragment length polymorphisms, amplified fragment length polymorphisms and simple sequence repeats. SSR markers were particularly useful because of their codominant inheritance and relatively high

polymorphism [12–14]. The development of cotton reference genomes and high-throughput sequencing has greatly expanded the availability of single nucleotide polymorphism markers. SNP arrays and genotyping-by-sequencing technologies permit high-density genome-wide genotyping, improving mapping resolution and facilitating the detection of smaller-effect loci. High-density markers also facilitate fine mapping, in which a broad QTL interval is progressively narrowed using additional markers and larger or specially designed populations. Fine mapping is important because a broad QTL interval may contain hundreds of genes, whereas a smaller interval can facilitate candidate-gene identification and functional validation.

7. QTL Meta-Analysis and Stable QTL Identification

Individual QTL mapping experiments frequently identify different genomic regions because of differences in genetic backgrounds, mapping populations, marker systems and environments. QTL meta-analysis provides an approach for integrating results from multiple studies and identifying consensus genomic regions. Recent meta-analysis of cotton fibre-quality QTLs combined 379 original QTLs from 21 independent studies and identified 74 meta-QTLs across the 26 chromosomes [15–16]. These meta-QTLs contained thousands of genes, and integration with RNA sequencing, functional annotation and expression analysis helped narrow the list of potential candidate genes. Meta-QTL analysis is therefore particularly valuable for distinguishing stable genomic regions from QTLs that are specific to individual populations or environments. Stable meta-QTLs can serve as priorities for fine mapping, functional characterization and marker-assisted selection.

8. Genome-Wide Association Studies for Fibre Quality

Genome-wide association studies have complemented conventional linkage mapping by exploiting historical recombination in diverse germplasm. Instead of relying on a single segregating population, GWAS evaluates marker-trait associations across a collection of genetically diverse cotton accessions. GWAS can provide higher mapping resolution than conventional QTL mapping because historical recombination can narrow association intervals. However, population structure and genetic relatedness must be carefully controlled to reduce false-positive associations [17–18]. Recent cotton research has increasingly combined GWAS with genomic selection and selective-sweep analysis and

Table 1. Major cotton fibre quality traits and their genetic and breeding significance

Fibre quality trait	Major characteristic	Genetic nature	Breeding importance
Fibre length	Length of individual fibres	Quantitative, polygenic	Important for spinning and yarn quality
Fibre strength	Resistance to fibre breakage	Quantitative	Determines yarn strength and durability
Micronaire	Indicator of fibre fineness and maturity	Quantitative	Influences processing and dyeing
Fibre elongation	Ability to extend before breaking	Quantitative	Affects processing performance
Fibre uniformity	Consistency of fibre length	Quantitative	Important for uniform yarn formation
Short fibre index	Proportion of short fibres	Quantitative	Higher levels can reduce processing efficiency
Fibre maturity	Degree of secondary wall development	Quantitative	Influences dye uptake and processing quality

identification of significant associations for fibre elongation, length and uniformity and reported stable QTL regions across environments, illustrating the growing integration of multiple genomic approaches in fibre-quality improvement.

9. Candidate Genes Underlying Fibre Quality QTLs

Identification of a QTL is an important first step, but determining the gene responsible for the phenotype provides greater biological and breeding value. Candidate-gene analysis integrates QTL intervals with genome annotation, gene-expression profiles, functional genomics and sequence variation. Several classes of genes have been associated with cotton fibre development, including transcription factors, hormone-related genes, genes involved in cell-wall biosynthesis and genes controlling carbohydrate metabolism. Transcription-factor families such as MYB, HD-ZIP IV, bHLH and ERF have received considerable attention because of their roles in fibre initiation and elongation. Recent research has further integrated QTL and GWAS signals with transcriptomic information to identify candidate genes controlling fibre quality. Functional validation is increasingly important for confirming candidate genes [19-20]. Gene-editing approaches such as CRISPR/Cas can be used to determine whether disruption or modification of a candidate gene changes fibre characteristics. For example, recent work has demonstrated the use of CRISPR validation for candidate genes associated with fibre length.

10. Marker-Assisted Selection for Fibre Quality

Marker-assisted selection enables breeders to select plants carrying favourable alleles using molecular markers rather than relying exclusively on phenotypic measurements. This approach is particularly useful for traits that are expensive or time-consuming to evaluate and for QTLs whose effects are difficult to distinguish

under field conditions. For fibre quality, markers linked to stable QTLs can be incorporated into breeding populations. Individuals carrying favourable alleles can be selected at early developmental stages, thereby reducing the number of plants requiring extensive field evaluation. However, MAS is most effective when QTL effects are stable and markers are sufficiently close to the causal gene. Therefore, validation across multiple genetic backgrounds and environments is essential before widespread deployment [20-21]. The integration of QTL mapping, high-density markers and MAS has already been recognized as an important strategy for cotton fibre-quality improvement.

11. Integration of QTL Mapping with Genomic Selection

Genomic selection differs from conventional MAS because it uses genome-wide marker information to predict the breeding value of individuals. Instead of selecting only for a limited number of major QTLs, genomic selection captures contributions from numerous loci, including small-effect genes. This approach is particularly attractive for cotton fibre quality because the traits are highly quantitative and controlled by many loci. A training population with both genotypic and phenotypic information is developed, and genomic prediction models are subsequently used to estimate breeding values for untested individuals [23]. Combining stable QTL information with genomic prediction may improve selection accuracy. QTLs with large and reproducible effects can be explicitly incorporated into prediction models, while genome-wide markers capture additional small-effect variation.

12. QTL × Environment Interactions

Environmental conditions can substantially influence the expression of fibre-quality traits. Temperature, water availability, soil conditions and crop-management practices can affect fibre development. Consequently, a QTL identified in one environment may have

a smaller effect or fail to be detected in another environment. Multi-environment trials are therefore essential for identifying stable QTLs. Stable QTLs are particularly valuable for breeding because they are less dependent on environmental conditions. Conversely, environment-specific QTLs may still be useful when breeding for specific production regions [24-25]. Understanding QTL $\times$ environment interactions can also contribute to climate-resilient cotton breeding. Future studies should combine genomic information with detailed environmental measurements to identify alleles that maintain fibre quality under variable temperature and water conditions.

13. Relationship Between Fibre Quality and Yield

One of the major challenges in cotton breeding is achieving simultaneous improvement of fibre quality and yield. Selection for higher yield may sometimes result in undesirable changes in fibre characteristics, while selection for superior fibre quality may negatively affect productivity. QTL mapping provides an opportunity to identify genomic regions controlling fibre quality independently of yield [21]. It can also reveal genomic regions affecting multiple traits, allowing breeders to determine whether associations are caused by linkage or pleiotropy. Modern breeding programmes should therefore consider fibre quality, yield, maturity, plant architecture and stress adaptation as interconnected traits. Multi-trait genomic selection and strategic QTL pyramiding may help overcome undesirable genetic correlations.

14. Challenges in QTL Mapping of Fibre Quality Traits

Despite considerable progress, several challenges remain. First, fibre quality is controlled by numerous loci with variable effects, making it difficult to distinguish major genes from minor-effect QTLs. Second, QTL expression can be strongly influenced by environmental conditions. Third, different studies often identify different genomic regions because of variation in parental genotypes and experimental populations. Another challenge is the polyploid nature of cultivated cotton [22]. Homoeologous genes in the A and D subgenomes may have overlapping or distinct functions, making functional validation more complicated. In addition, linkage between favourable fibre-quality alleles and undesirable agronomic traits can limit the direct use of some QTLs. The translation of QTL discoveries into breeding gains also requires rigorous validation. A marker associated with a trait in one population may not have the

same predictive value in another genetic background. Therefore, validation across populations and environments should precede large-scale deployment.

15. Future Perspectives

The future of cotton fibre-quality improvement will depend increasingly on the integration of genetic mapping, genomics, phenomics and precision breeding. High-density SNP genotyping, pan-genome resources and long-read sequencing will improve the ability to detect structural variants and rare favourable alleles. Combining QTL mapping with GWAS and meta-analysis can identify robust genomic regions, while transcriptomics and proteomics can help reveal biological mechanisms underlying these loci. Recent studies have already demonstrated the value of integrating QTL data with RNA sequencing and functional annotation to identify candidate genes. Genome editing provides another important opportunity. Once candidate genes are validated, CRISPR/Cas technologies can potentially modify favourable alleles or remove undesirable gene functions. Recent reviews indicate that several genes involved in cotton fibre quality are now being investigated or edited for improvement of fibre characteristics. Future breeding programmes should move toward integrated genomic strategies in which stable QTLs, GWAS signals, candidate genes and genomic prediction are combined with high-throughput phenotyping. Such approaches could accelerate the development of cotton cultivars that combine superior fibre quality, high yield and resistance to environmental stresses.

16. Conclusion

QTL mapping has significantly advanced understanding of the genetic architecture of cotton fibre quality. Numerous genomic regions controlling fibre length, strength, micronaire, elongation and uniformity have been identified through linkage mapping, association studies and meta-analysis. The increasing availability of high-density molecular markers and cotton genome resources has improved the resolution of QTL detection and facilitated the identification of candidate genes. Stable QTLs identified across multiple environments are particularly valuable for marker-assisted breeding, while GWAS and meta-QTL analysis provide complementary approaches for discovering robust genomic regions. Integration of QTL mapping with transcriptomics, genomic selection and genome editing is creating new opportunities for precise improvement of cotton fibre quality. Future research should focus on validating stable loci, identifying causal genes and developing breeding

Table 2. Major molecular approaches used for cotton fibre-quality improvement

Approach	Main application	Major advantage	Main limitation
SSR markers	Linkage mapping and QTL detection	Codominant and informative	Lower density than SNP systems
SNP markers	High-density genetic mapping	Genome-wide coverage	Genotyping infrastructure required
QTL mapping	Identification of genomic regions	Effective in segregating populations	Resolution depends on population size
QTL fine mapping	Narrowing QTL intervals	Facilitates candidate-gene identification	Requires large populations and dense markers
QTL meta-analysis	Integration of independent QTL studies	Identifies stable consensus loci	Requires comparable QTL information
GWAS	Association mapping in diverse germplasm	High mapping resolution	Population structure can create false associations
RNA sequencing	Identification of differentially expressed genes	Provides functional information	Expression does not always indicate causality
Genomic selection	Prediction of breeding values	Captures many small-effect loci	Requires suitable training populations
Marker-assisted selection	Selection of favourable QTL alleles	Accelerates breeding	Less effective for highly polygenic traits
CRISPR/Cas	Functional validation and targeted modification	Precise genetic manipulation	Technical and regulatory challenges

strategies that simultaneously improve fibre quality, yield and environmental adaptability. Such integrated approaches will contribute to the development of next-generation cotton cultivars capable of meeting the changing requirements of the textile industry and sustainable cotton production.

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