MODERN DEVELOPMENTS IN GENETIC MAPPING OF COTTON FOR YIELD, FIBER EXCELLENCE, AND ABIOTIC STRESS RESISTANCE

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Abstract

Cotton (Gossypium spp.) is one of the world's most important cash crops, providing natural fiber and sustaining both agricultural production and the textile industry. However, its productivity is frequently constrained by insect pests, diseases, and diverse abiotic stresses, challenges that conventional breeding alone has struggled to address effectively. In recent years, advances in genome sequencing and molecular breeding have created new opportunities to enhance fiber quality and stress tolerance.

This review summarizes recent developments in genetic mapping, quantitative trait locus (QTL) analysis, and marker-assisted selection (MAS) for the identification of genes associated with key agronomic traits. The emergence of high-throughput sequencing technologies and genome-editing tools, particularly CRISPR/Cas9, has enabled precise modification of target genes to improve cotton performance. Moreover, the integration of high-density molecular markers with genomic selection approaches has shortened breeding cycles by facilitating early and accurate prediction of desirable traits.

The combination of conventional breeding strategies with genomic tools has also helped address challenges related to polyploidy and limited genetic diversity, contributing to improved yield stability under stress conditions. Looking ahead, broader application of genome-assisted breeding, functional genomics, and high-throughput phenotyping will be critical for enhancing cotton's adaptability to climate variability and biotic stresses. Overall, genomics-integrated breeding represents a powerful and sustainable approach to improving cotton yield, fiber quality, and resilience.

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INTRODUCTION

Cotton, the world's largest fibre and oilseed crop in the world (Shahzad et al., 2022). It grows in over 100 countries, with an area of around 33M hectares. As a major cash crop, it produces around 31% of the world's natural fibre. Furthermore, it makes a significant contribution to global production(Nabi et al., 2015). Cotton is a globally important natural fibre and oilseed crop with significant economic implications(HE et al., 2019).

The Gossypium genus contains approximately fifty species with ploidy levels of diploid (2n=26) and tetraploid (2n=52). Diploid species contain genomes A, B, C, D, E, F, G, or K. These are found in both tropical and subtropical regions and are geographically connected (Mei et al., 2004a). Plant height ranges up to 120 cm, has a boll with separate branches. It is a tap- rooted plant with a zone depth of 90cm that may be grown under warm and irrigated

circumstances(Aydoğdu et al., n.d.).

Despite the opportunities of cotton breeding, it is devastated by a high frequency of pests and insect attacks, weeds and herbicide resistance due to climatic insecurities such as drought, floods, and heat waves (Mollaee et al., 2019). The huge and complex genome of the Gossypium species is an assembly of high-quality genomes is challenging. The major goal of genome research is to utilize genomic tools to develop crops with great genetic improvement(H. Bin Zhang et al., 2008a). Functional genomics has accelerated cotton breeding to genomic breeding (Z. Yang et al., 2020).

QTL mapping is primarily a discovery tool that assists researchers in understanding the genetic architecture of complex traits and identifying possible target genes. It is not directly utilized for selection but rather informs other methods such as MAS(Pan et al., 2024). MAS is especially beneficial for features influenced by a few significant QTLs. It enables more efficient selection than traditional approaches, particularly for features that are difficult or expensive to quantify phenotypically. Genomic selection can forecast individuals' breeding value more accurately and sooner in their life cycle than traditional approaches, particularly for traits with many small-effect QTLs(Lübberstedt et al., n.d.).

Even though new sequencing methods have substantially decreased prices, complex polyploid genomes continue to pose a difficulty in terms of short-read assembly. Polyploidy creates genetic and gene expression novelty, but it also provides repetition, making sequence annotation and assembly more difficult. We developed an integrated technique for sequencing and assembling an allopolyploid cotton genome, which might be used to sequence difficult genomes

from other polyploid crops (T. Zhang et al., 2015). One of the key reasons for cotton cultivar diversity is the use of wild genetic resources, which causes linkage dragging of undesirable traits. Another factor is a lack of creative strategies for incorporating genetic differences from exotic cotton plants of the Gossypium genus into breeding cultivars. All these causes contributed to the genetic bottleneck in evolution(Iqbal et al., 2001). This review paper discusses the potential method of genome sequencing that can improve cotton resistance through genetic mapping.

Cotton Genomic Sequencing

Cotton has been domesticated as Gossypium hirsutum and G. barbadense (Tetraploid species), G. arboreum and G. herbaceum (Diploid species)(Wendel & Cronn, 2003). Moreover, 95% of the world's cotton crop is G. hirsutum, which is also known as Upland cotton, with extra-long staple (Z. J. Chen et al., 2007).

G. hirsutum L. is an allotetraploid, as well as a polyploid.Assembly of allopolyploid plant genomes is a difficult process due to the genomes' extremely complex structure(Saski et al., 2017). To exploit this complexity, researchers applied advanced sequencing and genetic mapping techniques on cotton(P. Wang et al., 2024). For this, it is sequenced and assembled withtheallotetraploid genome ofG. hirsutum L. using DNA from the TM-1 pure strain, which isa homozygous species. They compared the G. hirsutum L. assembly to the hypothesized ancestral species, G. raimondii and G. arboreum, to study sub-genome evolution and gene function, including genes involved in fibre biology(F. Li et al., 2015; Z. MA, 2020).

Table no 1
This table explains the specific and common genes located in the species:

Species 1	Specific genes	References	Species 2	Specific genes	Common genes	References
G. arbor etum	16,9 18	(Du et al., 2018)	G. arbor etum	19,2 36	24,0 42	(Hua ng et al., 2020)

G. raim ondii	25,964	(Pate rson et al., 2012)	G. raim ondii	29,202	11,541	(Uda ll et al., 2019)

G. barb aden se	6,504	(Z. J. Chen et al., 2020)	G. barb aden se	3,240	68,057	(M. Wang et al., 2019)
G. barb aden se	27,304	(Hu et al., 2019)	G. barb aden se	23,534	47,763	(J. Wang et al., 2019)
G. barb aden se	25,093	(Hu et al., 2019)	G. barb aden se	24,573	49,988	(Z. J. Chen et al., 2020)

This table lists Gossypium species as well as the specific genes found in each. In the context of species 2, common genes were given alongside specific genes.

Genetic Mapping using Molecular Markers
Genetic mapping identifies the gene and markers with specific traits to improve breeding. In cotton breeding, markers are the main source to locate desirable genes(Malik et al., 2014). In breeding, these markers are highly valuable in detecting, characterizing, and identifying genetic variants, as well as removing linkage drag in breeding programs to find desirable features that are difficult to measure by visual observation(Kalia et al., 2011). SNPs are mostly and widely used molecular markers with a high level of polymorphism. SNPs are found in coding and non-coding regions of the genome, which allows detection variation (Agarwal et al., 2008). In the past decade, an extensive collection of QTL- mapping tools has been introduced for incorporating a variety of methodologies to locate genes. These methods are based on concepts of parametric and nonparametric linkage analysis, as well as innovative methodologies utilizing the study of dispersion components association analysis and multipoint mapping(JIA et al., 2014; Liu & Muse, 2005; Y.-M. Zhang & Gai, 2009; Z.-S. Zhang et al., 2009).
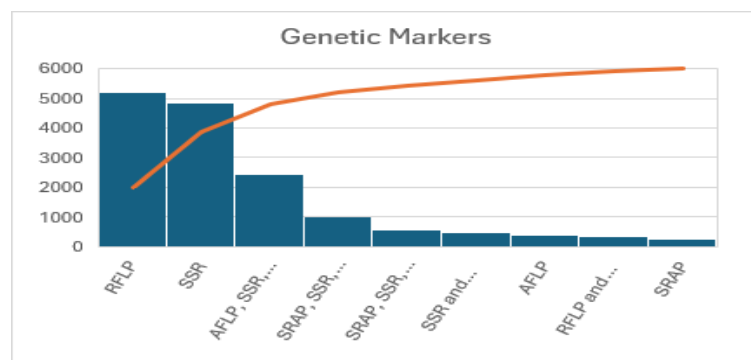

Figure 1

These are the markers widely used in genomics (H. Bin Zhang et al., 2008b)

AFLP: Amplified Fragment Length Polymorphism

SSR: Simple Sequence Repeats

SRAP: Sequence-Related Amplified Polymorphism

RFLP: Restriction Fragment Length Polymorphism

This indicates the uses of different genetic markers along with their usage over different amplifications.

Genetic Mapping using QTL Mapping

The cotton QTL study was conducted on 392 genetic loci, comprising 333 AFLP,

47 SSR, and 12 RFLP(X.-Y. Wang et al., 2012). A genetic map of cotton was constructed for QTL using composite interval mapping and permutation tests. This study discovered that seven QTLs for six fibre-related traits, of which five are found on the A-subgenome chromosomes, are responsible for fibre traits(Syed & Gao, 2010). Prior study also found that QTLs in both the A and D sub-genomes are responsible for fibre-related phenotypes, which are influenced by homoeologous genes(Razzaq et al., 2022). QTL clusters on certain chromosomes are likely to contribute to the high phenotypic diversity in fibre-related characteristics(Mei et al., 2004b; Tan et al., 2018).

Another study uses the high-density cotton molecular marker linkage map based on PCR (Kushanov et al., 2021). An F2 population of a hybrid between "Handan208" and "Pima90" examined the use of SSR, sequence-related amplified polymorphism, RAPD , and retrotransposon microsatellite amplified polymorphism(D. He et al., 2007). Fifty-two distinct QTLs were identified for lint index, seed index, lint yield, seed cotton yield, number of seeds per boll, fibre strength, fibre length, and micronaire. The current map and QTL analysis are a useful tool for breeders to transfer advantageous traits from G. barbadense to the most farmed species, G. hirsutum(D.-H. He et al., 2007). Furthermore, gene expression analysis using RNAseq data identified 40 possible genes, including 23 stable and 17 novel genes. These genes are transcriptionally active at different stages of fibre, ovule, and seed development. These studies have revealed a rich tapestry of genetic elements, including SNPs, QTLs,and candidate genes, and have a high potential for increasing fibre yield in future breeding initiatives for cotton(Joshi et al., 2023).

Genetic Mapping using Marker-Assisted Breeding

Molecular markers provided a significant opportunity in increasing the precision of crop development operations through MAS breeding technology(Collard & Mackill, 2008a). MAS technology enables selection at any stage of plant growth and development. In short, the development of MAS technology has enabled advanced selection resulting in genomics, which has since become an essential component of agricultural science(Kushanov et al., 2021b).

Figure 2

(Kushanov et al., 2021c)This figure implies the types of markers, including morphological and molecular markers.
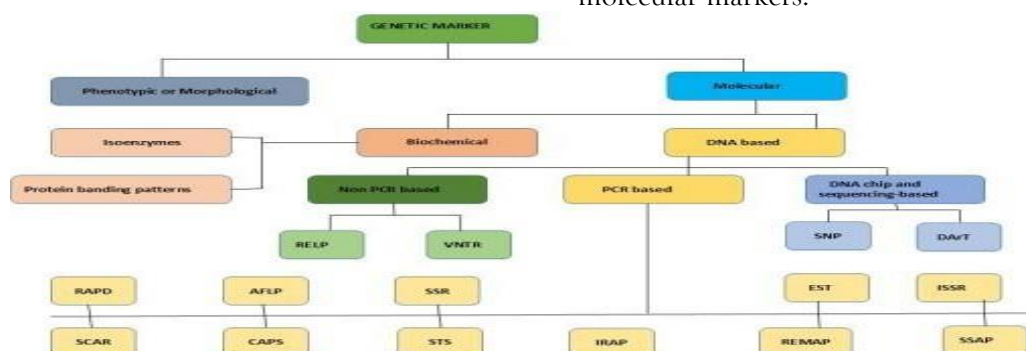
This figure represents the phylogenetic tree of molecular markers at the morphological and molecular levels.

Genetic Mapping for improved fibre quality
Cotton is the leading natural fibre crop because of

its increasing demand in the agricultural market.

Fibre length, consistency, strength, elongation, and micronaire value are some of the most common fibre quality characteristics (Wendel et al., 2010). Fibre length and strength both have an impact on yarn quality. In the textile industry, fibre strength is an important aspect. The micronaire value has a direct effect on fibre processing(Ijaz et al., 2019; Rodgers et al., 2017; X. Yang et al., 2016).

Yield is a complex feature; the lint fraction is the percentage of lint extracted from seed cotton that is positively connected with yield. It has given an indirect and cost-effective method of breeding for increased yield potential, resulting in around 10% increases over the last 60 years. However, lint fraction can be inversely associated with seed size, thereby lowering seedling vigour (Constable et al., 2015).

For improved fibre development, Marker-assisted breeding technology has gained importance because it can locate specific genes with greater efficiency(Tan et al., 2015). Recent advances in molecular breeding have enabled the combination of traditional breeding and biotechnology procedures with the desired output. However, integration of cotton traditional breeding with marker-assisted breeding helped in accelerating breeding with potential results(Morales-Aranibar et al., 2024). Recent investigations revealed that the paternal BC population investigates the genetic mechanism of fibre quality, detecting 19 and 8 QTLs in the BC/P and
populations shared three QTLs for fibre strength and elongation: qFS-Chr21-2, qFE- Chr2-3, and qFE-Chr3-1. This demonstrates isolating novel elite alleles of the male father for fibre quality(L. MA et al., 2020).

Another study identified ninety-one QTL loci associated with fibre quality indicators in a BC5S5 upland population of 107 lines. Their PEV ranged from 4.53% to
20.92. Among them, the favourable alleles of QTLs qFS-A02-1 and qSCI-A02-1 discovered in stable detection were all from
G. tomentosum, with PVE ranging from 9.8-

16.71% and 14.78-20.92%, respectively. This shows that the G. tomentosum significantly improved the fibre quality in upland cotton. Fourteen genes were discovered in the candidate interval, includingGhir_A02G012730, Ghir_A02G012790, and Ghir_A02G012830, which are involved in cellulose and cell wall production and have a reasonably high expression during fibre formation (Chang et al., 2023). Furthermore, Crisper/CAS can also be used to validate the results and alleles. Cotton fibre quality has been successfully improved through the introduction of foreign genes pertinent to fibre manufacturing. However, more research is needed in addition to the advanced methodologies previously stated(Ahmed et al., 2020). Discovering and integrating more distant fibre-related genes into cotton can increase fibre characteristics even further. Understanding the molecular foundation of diverse fibre creation mechanisms necessitates additional research to improve fibre features(Baghyalakshmi et al., 2024).

Genetic Mapping for stress resistance
Extensive research has been conducted in cotton production and quality over the last few years using traditional breeding. However, this has increased susceptibility
BC/M populations, respectively. Both BC against stresses(Maqbool et al., 2010). Stress
tolerance is influenced by genetic as well as environmental factors, which are lacking in conventional breeding due to genetic diversity(H. Sun et al., 2019). Abiotic stress typically includes drought, heat, salinity and cold stress. In addition to enhancing yield, quality, and resistance to diseases and insects, it also pays more attention to tolerance to stresses and efficient use of soil resources(Abdelraheem et al., 2021; Diouf et al., 2017). Besides abiotic stress, cotton is highly susceptible to Cotton leaf curl virus, which is a biotic stress.

To address these issues, the meta- analysis program Biomercator was used by researchers to examine 661 stress resistance QTLs. This included QTL for drought tolerance in a greenhouse and field conditions, salt tolerance in a greenhouse, resistance to Verticillium wilt, resistance to

Fusarium wilt, and resistance to uniform nematodes and root-knot nematodes(Abdelraheem et al., 2017). Recent breakthroughs in functional genomics, genetic and analytical methods, particularly complete gene expression profiling of cotton fibre cells, along with the availability of a sequenced genome, have opened new avenues for improving cotton fibre properties through genetic manipulation. Several fibre-specific genes involved in fibre cell initiation, elongation, or cell wall biosynthesis have been identified as possibilities for genetic manipulation to improve fibre yield and/or quality(Walford et al., 2011).

Another study on the investigation on drought stress uses a total of 1,116 SNPs and 782 SSRs. In which nineteen QTLs were found in one chromosome 3, 4, 5, 7, 8, 12,

13, 15, and 26 for plant morphological features. This mapping approach identified one QTL hotspot on chromosome 8 using public domain mapping data. These findings suggest candidate alleles for

drought tolerance in upland cotton, which can be used to produce cotton varieties with stress resilience through marker- assisted selection (MAS) breeding programs(Shukla et al., 2021).

In agriculture, biotic factors are a major cause of large output losses up to 84% for insects and up to 30% for pathogens(Jans et al., 2021). At the same time, attempts to reduce infestations include increasing the internal defensive mechanisms of plants or introducing pathogen-targeted constructs into the genome(Kamburova & Abdurakhmonov, 2018). Classical breeding methods increase the plant's internal defence mechanisms and use cotton germplasm reserves to produce new resistant varieties over time, whereas MAS and QTL mapping have been widely used in the development of cotton varieties resistant to Verticillium and Fusarium wilt. More than 400 QTL indicating resistance to both types of wilt have been found(Kamburova & Abdurakhmonov, 2018; C. Wang et al., 2018a; J. Zhang et al., 2014). These results were achieved by mapping chromosome-substituted and RIL populations using different markers and GWAS. The same meta-analysis

showed 74 QTLs for nematode resistance(Kushanov et al., 2021d). Thus, 71 QTLs relate to resistance to root-knot nematode, while three remain associated with resistance to reniform nematodes. Furthermore, this study found two QTLs for resistance to Xanthomonascampestrispv. Malvacearum(C. Wang et al., 2018b). CLcV is one of the most devastating biotic stresses, but we used quantitative trait loci (QTL) mapping in four crosses with different sources of resistance to identify single-nucleotide polymorphism (SNP) markers associated with the resistance trait, allowing for the development of varieties without the need for field screening every

generation. To aid in the analysis of many populations, a new publicly available R/Shiny App was built to simplify genetic mapping utilizing SNP arrays as well as give an easy method to convert and deposit genetic data into the CottonGen database(Schoonmaker et al., 2023).

In comparison to the advancement in cotton resistance is largely sluggish, and there is still a gap in resistance breeding. Future study will be undertaken based on the investigation and evaluation of good resources, the major effect of resistance QTL, and the cloning of excellent key resistance genes, employing marker- assisted selection (MAS) and transgenic technology to polymerize resistance genes(Saud & Wang, 2022).

Future Direction
Genome Editing through CRISPR/Cas
Genome editing plays a crucial role in functional gene studies and crop improvement. The CRISPR/Cas9 uses single guide RNA molecules to control double-strand breaks in the genome sequence, has the potential to revolutionize agriculture (Gao et al., 2017a). The CRISPR/Cas9 technique uses a guide RNA (gRNA) to lead the Cas9 nuclease to a specific genomic sequence, causing a double-strand break (DSB). This break can then be repaired using the cell's natural repair mechanisms, non-homologous end joining (NHEJ) or homology-directed repair (HDR), resulting in specific gene changes. The capacity to construct gRNAs to target almost any sequence in the genome has

made CRISPR/Cas9 a very versatile tool for diverse genetic changes in cotton (Thangaraj et al., 2025).

The successful use of the CRISPR/Cas9 system for crop improvement or functional investigation can generate transformed mutants and undertake phenotypic characterization of homozygous stable

contained in the sgRNA is a critical component influencing the overall mutagenesis efficacy of the CRISPR/Cas9 system(Ma et al., 2015). In cotton, CRISPR/Cas9 has been used to improve a variety of agronomically significant properties. For example, researchers employed this technology to improve fibre quality by targeting genes involved in fibre growth, resulting in longer and stronger fibres (C. Li et al., 2017). CRISPR/Cas9 has also been used to improve resistance to biotic stressors like pests and diseases by removing susceptibility genes or increasing defence-related genes(Gao et al., 2017b). Furthermore, CRISPR/Cas9 has been used to improve abiotic stress tolerance, such as drought and salinity, by editing genes that regulate stress responses, increasing cotton's endurance to harsh environmental conditions(X. Chen et al., 2017).

The successful implementation of the CRISPR/Cas9 system for crop improvement or functional analysis is dependent on the creation of stably transformed mutants in order to characterization of homozygous stable mutants. The sequence of the target site contained in the sgRNA is an important factor affecting the overall mutagenic efficiency of the CRISPR/Cas9 system, as different sgRNAs can result in very different efficiencies when targeting the same gene (Ma et al., 2016).
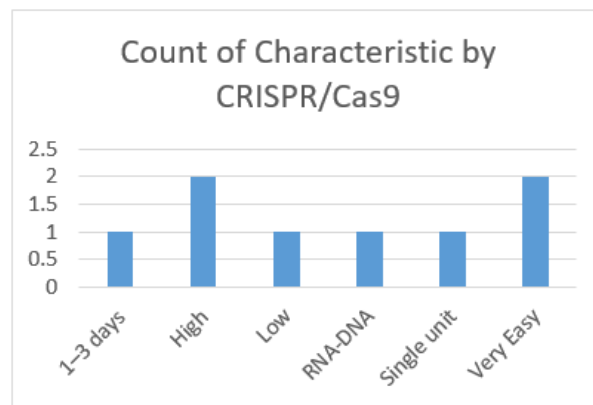
Figure 3

mutants. The sequence of the target site (Khan et al., 2023) This diagram depicts the three gene- editing technologies. CRISPR/Cas9 is the simplest and quickest to design and construct, whereas ZFNs are the most complicated and expensive. CRISPR/Cas9, on the other hand, works as a single unit.

High-Throughput Markers

The high-quality phenotypic data are crucial for enhanced cotton yield. This study reveals that HTP offers a lot of potential for data collection and analysis while assessing phenotypic traits in cotton in the form of cheaper input costs and resources(Bolouri et al., 2024). Imaging and sensor technologies based on spectral, thermal, fluorescence, and 3D sensors are the most useful and powerful tools for evaluating crop characteristics, tracking crop growth and development, and assessing cotton health. With the emergence of HTP technologies, several ground and aerial-based platform systems for phenotypic and agronomic research in cotton have been built(Pabuayon et al., 2019).

The high-throughput phenotyping technology developed in the field reconstructed precise 3D surface models. Multiple morphological parameters at the plot level, such as plant height, projected canopy area, and plant volume, were retrieved concurrently. Because of its relatively large data collection and processing capacity, the device aids in the repetitive scanning of the field. The measured morphological features had the highest correlation with eventual yield between 67 and 109 DAP. Further research will focus on using additional sensor data to derive more phenotypic features from the 3D point cloud. Although this method was only tested on cotton plants, it has proven to be a successful application(S. Sun et al., 2018).

Genomic Breeding

Cotton genomic sequencing has made significant advancements in recent years, with multiple high-quality reference genomes for G. hirsutum and G. barbadense. This research has enabled the researchers to identify crucial genes involved in fibre growth, insect resistance, and stress tolerance in cotton(Collard & Mackill, 2008b). Furthermore, genomic approaches such as molecular markers and gene editing technologies are becoming more common for accurate cotton breeding. However, in the face of several challenges, including ongoing global growth, complex environmental conditions, and decreasing genetic gain effects of breeding new cotton varieties, the cotton research community must urgently rethink and design the future of cotton breeding(Kun et al., 2025). Also, genomic selection, another tool for estimating GEBV, has proven application in testing individuals because it is not dependent on the late measurement phenotype, which significantly reduces the generation interval. It estimates GEBV using marker information from the entire genome, which considerably enhances its accuracy. Furthermore, genomic selection can estimate some features that are difficult to quantify phenotypically (Zhai, 2023).

Digital Technologies

Cotton must continue its fibre market leadership as the most abundant and natural fibre of choice for a wide range of industrial and commercial applications. To do this, cotton production, which has traditionally been input-intensive and has an indelible negative environmental impact, must be continuously refined to use the fewest inputs while optimizing yield, fibre quality, and profit using existing and developing technology. To fully benefit from new advanced techniques and technologies as they are developed globally, these enabling tools

 (such as variety breeding, improved irrigation systems/biodegradable mulching, autonomous aerial systems, computer vision/agricultural remote sensing techniques, robotic harvesters and multipurpose platforms, HDPT, and chemical topping) for cotton agronomy optimization must be continuously improved upon. Some of these tools have been thoroughly studied and commercialized in the global cotton industry (Adeleke, 2024).

Conclusion

Cotton is an important cash crop which plays a pivotal role in textile production, and agriculture is subject to many external factors. Changing climatic conditions worsen the situation of cotton development. Both biotic and abiotic stress negatively affected the increasing demand for high-quality cotton. Traditional breeding methods have less genetic diversity, thus leading to a decline in cotton innovation. Integration of marker-assisted breeding and genetic mapping techniques can revolutionize cotton breeding by identifying QTLs which can improve desired traits. Recent studies have also found genes and markers which can directly locate the desired trait. However, integrating conventional breeding through genome editing, high-throughput markers, and molecular breeding designs, many of the constraints of traditional breeding may be overcome for the new era of cotton assisted with cotton.

REFERENCE

Abdelraheem, A., Liu, F., Song, M., & Zhang, J. F. (2017). A meta-analysis of quantitative trait loci for abiotic and biotic stress resistance in tetraploid cotton. *Molecular Genetics and Genomics,292*(6), 1221–1235. https://doi.org/10.1007/s00438-017-1342-0 Abdelraheem, A., Thyssen, G. N., Fang, D. D.,

Jenkins, J. N., McCarty, J. C., Wedegaertner, T., & Zhang, J. (2021). GWAS reveals consistent QTL for drought and salt tolerance in a MAGIC

population of 550 lines derived from intermating of 11 Upland cotton (Gossypium hirsutum) parents. *Molecular Genetics and Genomics, 296*(1), 119–129. https://doi.org/10.1007/s00438-020-01733-2 Adeleke, A. A. (2024). Technological advancements

in cotton agronomy: a review and prospects. *Technology in Agronomy, 4*(1), 0–0. https://doi.org/10.48130/tia-0024-0005

Agarwal, M., Shrivastava, N., & Padh, H. (2008). Advances in molecular marker techniques and their applications in plant sciences. *Plant Cell Reports, 27*(4), 617–631. https://doi.org/10.1007/s00299-008-0507-z Ahmed, M., Iqbal, A., Latif, A., Din, S. Ud, Sarwar,

M. B., Wang, X., Rao, A. Q., Husnain, T., & Ali Shahid, A. (2020). Overexpression of a Sucrose Synthase Gene Indirectly Improves Cotton Fibre Quality Through Sucrose Cleavage. *Frontiers in Plant Science, 11*. https://doi.org/10.3389/fpls.2020.476251 Aydoğdu, M. H., Doğan, H. P., & Küçük, N. (n.d.).

Economic Analysis of Agricultural Water Usage Efficiency in the GAP-Harran Plain: Cotton Production Sampling, Sanliurfa-Turkey. www.kibanresearchpublications.com

Baghyalakshmi, K., Priyanka, R. A., Sarathapriya, G., Ramchander, S., & Prakash, A. H. (2024). Genetic improvement of fibre quality in tetraploid cotton: an overview of major QTLs and genes involved in and edited for the quality of cotton fibres. *Journal of Cotton Research*, 7(1), 33. https://doi.org/10.1186/s42397-024-00196-9

Bolouri, F., Kocoglu, Y., Pabuayon, I. L., Ritchie, G., & Sari-Sarraf, H. (2024). CottonSense: A high- throughput field phenotyping system for cotton fruit segmentation and enumeration on edge devices. *Computers and Electronics in Agriculture*, 216,108531. https://doi.org/10.1016/j.compag.2023.10853 1 Chang, X., Guo, C., Pan, Z., Wu, Y., Shen, C., Chao,

L., Shui, G., You, C., Xu, J., Lin, Z., & Nie, X.

(2023). QTL Mapping for Fibre Quality Based on Introgression Lines Population from G. hirsutum × G. tomentosum. *Agriculture (Switzerland)*,13(3). https://doi.org/10.3390/agriculture13030579 Chen, X., Lu, X., Shu, N., Wang, S., Wang, J., Wang,

D., Guo, L., & Ye, W. (2017). Targeted mutagenesis in cotton (Gossypium hirsutum L.) using the CRISPR/Cas9 system. *Scientific Reports*, 7(1), 44304. https://doi.org/10.1038/srep44304

Chen, Z. J., Scheffler, B. E., Dennis, E., Triplett, B. A.,

Zhang, T., Guo, W., Chen, X., Stelly, D. M.,

Rabinowicz, P. D., Town, C. D., Arioli, T., Brubaker, C., Cantrell, R. G., Lacape, J. M., Ulloa, M., Chee, P., Gingle, A. R., Haigler, C. H., Percy, R., … Paterson, A. H. (2007). Toward sequencing cotton (Gossypium) genomes. In *Plant Physiology* (Vol. 145, Issue 4, pp. 1303– 1310). American Society of Plant Biologists. https://doi.org/10.1104/pp.107.107 672

Chen, Z. J., Sreedasyam, A., Ando, A., Song, Q., De

Santiago, L. M., Hulse-Kemp, A. M., Ding, M.,

Ye, W., Kirkbride, R. C., Jenkins, J., Plott, C.,

Lovell, J., Lin, Y. M., Vaughn, R., Liu, B., Simpson, S., Scheffler, B. E., Wen, L., Saski, C. A., … Schmutz, J. (2020). Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. *Nature Genetics*, 52(5), 525–533. https://doi.org/10.1038/s41588-020-0614-5

Collard, B. C. Y., & Mackill, D. J. (2008a). Marker- assisted selection: An approach for precision plant breeding in the twenty-first century. In *Philosophical Transactions of the Royal Society B: Biological Sciences* (Vol. 363, Issue 1491, pp. 557– 572). Royal Society. https://doi.org/10.1098/rstb.2007.217 0

Collard, B. C. Y., & Mackill, D. J. (2008b). Marker- assisted selection: An approach for precision plant breeding in the twenty-first century. In *Philosophical Transactions of the Royal Society B: Biological Sciences* (Vol. 363, Issue 1491, pp. 557– 572). RoyalSociety. https://doi.org/10.1098/rstb.2007.217 0

Constable, Greg, Clement Koebernick, J., Llewelyn, Danny, & Walford, S. (2015). Cotton Breeding for Fibre Quality Improvement. In *Industrial Crops: Breeding for Bioenergy and Bioproducts* (pp. 191–232). https://doi.org/10.1007/978-1-4939-1447-0_10

Diouf, L., Pan, Z., He, S. P., Gong, W. F., Jia, Y. H.,

Magwanga, R. O., Romy, K. R. E., Rashid, H. O., Kirungu, J. N., & Du, X. (2017). High-density linkage map construction and mapping of salt-tolerant QTLs at the seedling stage in upland cotton using genotyping by sequencing (GBS). *International Journal of Molecular Sciences*, *18*(12). https://doi.org/10.3390/ijms181226 22

Du, X., Huang, G., He, S., Yang, Z., Sun, G., Ma, X.,

Li, N., Zhang, X., Sun, J., Liu, M., Jia, Y., Pan, Z.,

Gong, W., Liu, Z., Zhu, H., Ma, L., Liu, F., Yang, D., Wang, F., … Li, F. (2018). Resequencing of

243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. *Nature Genetics*, *50*(6),

796–802. https://doi.org/10.1038/s41588-018-0116-x

Gao, W., Long, L., Tian, X., Xu, F., Liu, J., Singh, P. K., Botella, J. R., & Song, C. (2017a). Genome editing in cotton with the CRISPR/Cas9 system. *Frontiers in Plant Science*, *8*.

https://doi.org/10.3389/fpls.2017.01364

Gao, W., Long, L., Tian, X., Xu, F., Liu, J., Singh, P. K., Botella, J. R., & Song, C. (2017b). Genome editing in cotton with the CRISPR/Cas9 system. *Frontiers in Plant Science*, *8*.

https://doi.org/10.3389/fpls.2017.01364

He, D., Lin, Z.-X., Zhang, X., Nie, Y.-C., Guo, X.-P.,

Zhang, Y.-X., & Li, W. (2007). QTL mapping for economic traits based on a dense genetic map of cotton with PCR-based markers using the interspecific cross of Gossypium hirsutum × Gossypium barbadense. *Euphytica*, *153*, 181–

197. https://doi.org/10.1007/s10681-006-9254-9

He, D.-H., Lin, Z.-X., Zhang, X.-L., Nie, Y.-C., Guo, X.-P., Zhang, Y.-X., & Li, W. (2007). QTL

mapping for economic traits based on a dense genetic map of cotton with PCR-based markers using the interspecific cross of Gossypium hirsutum × Gossypium barbadense. *Euphytica*, *153*(1),181–197.

https://doi.org/10.1007/s10681-006-9254-9

HE, W., ZHAO, H., YANG, X., ZHANG, R., &

WANG, J. (2019). Patent analysis provides insights into the history of cotton molecular breeding worldwide over the last 50 years. *Journal of Integrative Agriculture*, *18*(3), 539–552. https://doi.org/https://doi.org/10.10 16/S209 5-3119(18)62012-X

Hu, Y., Chen, J., Fang, L., Zhang, Z., Ma, W., Niu, Y.,

Ju, L., Deng, J., Zhao, T., Lian, J., Baruch, K.,

Fang, D., Liu, X., Ruan, Y. ling, Rahman, M. ur,

Han, J., Wang, K., Wang, Q., Wu, H., … Zhang,

T. (2019). Gossypium barbadense and Gossypium hirsutum genomes provide insights into the origin and evolution of allotetraploid cotton. *Nature Genetics*, *51*(4), 739–748. https://doi.org/10.1038/s41588-019-0371-5

Huang, G., Wu, Z., Percy, R. G., Bai, M., Li, Y.,

Frelichowski, J. E., Hu, J., Wang, K., Yu, J. Z., & Zhu, Y. (2020). Genome sequence of Gossypium herbaceum and genome updates of Gossypium arboreum and Gossypium hirsutum provide insights into cotton A-genome evolution. *Nature Genetics*,*52*(5),516–524. https://doi.org/10.1038/s41588-020-0607-4

Ijaz, B., Zhao, N., Kong, J., & Hua, J. (2019). Fibre Quality Improvement in Upland Cotton (Gossypium hirsutum L.): Quantitative Trait

Loci Mapping and Marker-Assisted Selection Application. In *Frontiers in Plant Science* (Vol. 10). Frontiers Media S.A. https://doi.org/10.3389/fpls.2019.01585

Iqbal, M. J., Reddy, O. U. K., El-Zik, K. M., & Pepper,

A. E. (2001). A genetic bottleneck in the "evolution under domestication" of upland cotton Gossypium hirsutum L. was examined using DNA fingerprinting. *Theoretical and Applied Genetics*, *103*(4), 547–554. https://doi.org/10.1007/PL00002908

Jans, Y., Von Bloh, W., Schaphoff, S., & Müller, C. (2021). Global cotton production under climate change – Implications for yield and water consumption. *Hydrology and Earth System Sciences*, *25*, 2027–2044. https://doi.org/10.5194/hess-25-2027-2021

JIA, Y., SUN, J., WANG, X., ZHOU, Z., PAN, Z., HE,

S., PANG, B., WANG, L., & DU, X. (2014).

Molecular Diversity and Association Analysis of Drought and Salt Tolerance in Gossypium hirsutum L. Germplasm. *Journal of Integrative Agriculture*, *13*(9),1845–1853. https://doi.org/https://doi.org/10.1016/S209 5-3119(13)60668-1

Joshi, B., Singh, S., Tiwari, G. J., Kumar, H., Boopathi, N. M., Jaiswal, S., Adhikari, D., Kumar, D., Sawant, S. V., Iquebal, M. A., & Jena,

S. N. (2023). Genome-wide association study of fibre yield-related traits uncovers the novel genomic regions and candidate genes in Indian upland cotton (Gossypium hirsutum L.). *Frontiers in Plant Science*, *14*.

https://doi.org/10.3389/fpls.2023.1252746 Kalia, R. K., Rai, M. K., Kalia, S., Singh, R., &

Dhawan, A. K. (2011). Microsatellite markers: an overview of the recent progress in plants. *Euphytica*, *177*(3),309–334. https://doi.org/10.1007/s10681-010-0286-9

Kamburova, V., & Abdurakhmonov, I. (2018). *Overview of the Biosafety and Risk Assessment Steps for Insect-Resistant Biotech Crops*. https://doi.org/10.1201/9781315119571-9

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., & Azhar, M. T. (2023). Genome editing in cotton: challenges and opportunities. In *Journal of Cotton Research* (Vol. 6, Issue 1). BioMed Central Ltd. https://doi.org/10.1186/s42397-023-00140-3

Kun, W., Shoupu, H., & Yuxian, Z. (2025). Cotton2035: From genomics research to optimized breeding. *Molecular Plant*, *18*(2), 298–312.

https://doi.org/https://doi.org/10.1016/j.molp.2025.01.010

Kushanov, F. N., Turaev, O. S., Ernazarova, D. K., Gapparov, B. M., Oripova, B. B., Kudratova, M. K., Rafieva, F. U., Khalikov, K. K., Erjigitov, D. S., Khidirov, M. T., Kholova, M. D., Khusenov,

N. N., Amanboyeva, R. S., Saha, S., Yu, J. Z., & Abdurakhmonov, I. Y. (2021a). Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (Gossypium spp.). In *Frontiers in Plant Science* (Vol. 12). Frontiers MediaS.A. https://doi.org/10.3389/fpls.2021.779386

Kushanov, F. N., Turaev, O. S., Ernazarova, D. K., Gapparov, B. M., Oripova, B. B., Kudratova, M. K., Rafieva, F. U., Khalikov, K. K., Erjigitov, D. S., Khidirov, M. T., Kholova, M. D., Khusenov,

N. N., Amanboyeva, R. S., Saha, S., Yu, J. Z., & Abdurakhmonov, I. Y. (2021b). Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (Gossypium spp.). In *Frontiers in Plant Science* (Vol. 12). Frontiers MediaS.A. https://doi.org/10.3389/fpls.2021.779386

Kushanov, F. N., Turaev, O. S., Ernazarova, D. K., Gapparov, B. M., Oripova, B. B., Kudratova, M. K., Rafieva, F. U., Khalikov, K. K., Erjigitov, D. S., Khidirov, M. T., Kholova, M. D., Khusenov,

N. N., Amanboyeva, R. S., Saha, S., Yu, J. Z., & Abdurakhmonov, I. Y. (2021c). Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (Gossypium spp.). In *Frontiers in Plant Science* (Vol. 12). Frontiers Media S.A. https://doi.org/10.3389/fpls.2021.779386

Kushanov, F. N., Turaev, O. S., Ernazarova, D. K., Gapparov, B. M., Oripova, B. B., Kudratova, M. K., Rafieva, F. U., Khalikov, K. K., Erjigitov, D. S., Khidirov, M. T., Kholova, M. D., Khusenov,

N. N., Amanboyeva, R. S., Saha, S., Yu, J. Z., & Abdurakhmonov, I. Y. (2021d). Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (Gossypium spp.). In *Frontiers in Plant Science* (Vol. 12). Frontiers Media S.A. https://doi.org/10.3389/fpls.2021.779386

Li, C., Unver, T., & Zhang, B. (2017). A high- efficiency CRISPR/Cas9 system for targeted mutagenesis in Cotton (Gossypium hirsutum L.). *Scientific Reports*, 7(1), 43902. https://doi.org/10.1038/srep43902

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(524–530.

https://doi.org/10.1038/nbt.3208

Liu, K., & Muse, S. V. (2005). PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics*, 21(9), 2128– 2129.

https://doi.org/10.1093/bioinformatics/bti2 8 2

Lübberstedt, T., Beavis, W., & Suza, W. (n.d.). *Chapter 7: Marker-Assisted Selection and Genomic Selection.* https://iastate.pressbooks.pub/molecularplan tbreeding/chapter/marker-assisted-selection- and-genomic-selection/

MA, L., SU, Y., NIE, H., CUI, Y., CHENG, C., IJAZ,

B., & HUA, J. (2020). QTL and genetic analysis controlling fibre quality traits using paternal backcross population in upland cotton. *Journal of Cotton Research*, 3(1), 22.

https://doi.org/10.1186/s42397-020-00060-6 Ma, X., Zhang, Q., Zhu, Q., Liu, W., Chen, Y., Qiu,

R., Wang, B., Yang, Z., Li, H., Lin, Y., Xie, Y.,

Shen, R., Chen, S., Wang, Z., Chen, Y., Guo, J.,

Chen, L., Zhao, X., Dong, Z., & Liu, Y.-G. (2015).

A Robust CRISPR/Cas9 System for Convenient, High-Efficiency Multiplex Genome Editing in Monocot and Dicot Plants. *Molecular Plant*, 8(8), 1274–1284.

https://doi.org/10.1016/j.molp.2015.04.007 Ma, X., Zhu, Q., Chen, Y., & Liu, Y.-G. (2016).

CRISPR/Cas9 Platforms for Genome Editing in Plants: Developments and Applications. *Molecular Plant*, 9(7), 961–974. https://doi.org/10.1016/j.molp.2016.04.009

MA, Z. (2020). Unravelling the puzzle of the origin and evolution of cotton A-genome. *Journal of Cotton Research*, 3(1), 17. https://doi.org/10.1186/s42397-020-00056-2 Malik, W., Ashraf, J., Iqbal, M. Z., Ali Khan, A.,

Qayyum, A., Ali Abid, M., Noor, E., Qadir Ahmad, M., & Hasan Abbasi, G. (2014). Molecular markers and cotton genetic improvement: Current status and prospects. In *Scientific World Journal* (Vol. 2014). Hindawi PublishingCorporation. https://doi.org/10.1155/2014/607091 Maqbool, A., Abbas, W., Rao, A. Q., Irfan, M.,

Zahur, M., Bakhsh, A., Riazuddin, S., & Husnain, T. (2010). Gossypium arboreum GHSP26 enhances drought tolerance in Gossypium hirsutum. *Biotechnology Progress*, 26(1), 21–25. https://doi.org/10.1002/btpr.306

Mei, M., Syed, N. H., Gao, W., Thaxton, P. M., Smith,

C. W., Stelly, D. M., & Chen, Z. J. (2004a).

Genetic mapping and QTL analysis of fibre-related traits in cotton (Gossypium). *Theoretical and Applied Genetics*, 108(2), 280–291. https://doi.org/10.1007/s00122-003-1433-7

Mei, M., Syed, N. H., Gao, W., Thaxton, P. M., Smith,

C. W., Stelly, D. M., & Chen, Z. J. (2004b).

Genetic mapping and QTL analysis of fibre-related traits in cotton (Gossypium). *Theoretical and Applied Genetics*, 108(2), 280–291. https://doi.org/10.1007/s00122-003-1433-7

Mollaee, M., Mobli, A., Mutti, N. K., Manalil, S., & Chauhan, B. S. (2019). Challenges and Opportunities in Cotton Production. In *Cotton Production* (pp. 371–390). Wiley. https://doi.org/10.1002/9781119385523.ch18

Morales-Aranibar, L., Rivera, M. Y. N., Gonzales, H.

H. S., Aranibar, C. G. M., Gutiérrez, N. L.,

Gomez, F. G., Zuffo, A. M., Aguilera, J. G., & Steiner, F. (2024). Comparative analysis of key fibre characteristics in white Pima cotton (Gossypium barbadense L.): Native accessions from the Peruvian Amazon. *Agrosystems, Geosciences andEnvironment*, 7(2). https://doi.org/10.1002/agg2.20517

Nabi, G., Shokat, S., Azhar, M. T., & Azhar, F. M. (2015). GENETIC BASIS OF ION UPTAKE AND PROLINE ACCUMULATION IN

GOSSYPIUM HIRSUTUM L. of relative frequency of dominance and recessive alleles in the parents; (H 1 /D) 0.5-average degree of dominance; H 1 and H 2-dominance effects of genes; H 2 /4H 1-proportion of gene with positive and negative effects in the parents; h2- overall dominance effect; h 2-heritability in narrow sense; NaCl-sodium chloride; K- Potassium; TSS-total soluble salts.842 Agricultural Academy. In *Bulgarian Journal of Agricultural Science* (Vol. 21, Issue 4).

Pabuayon, I. L. B., Sun, Y., Guo, W., & Ritchie, G. L. (2019). High-throughput phenotyping in cotton: a review. In *Journal of Cotton Research* (Vol. 2, Issue 1). BioMed Central Ltd. https://doi.org/10.1186/s42397-019-0035-0

Pan, Y., Jiang, F., Shaw, R. K., Sun, J., Li, L., Yin, X.,

Bi, Y., Kong, J., Zong, H., Gong, X., Ijaz, B., & Fan, X. (2024). QTL mapping and genome-wide association analysis reveal genetic loci and candidate genes for resistance to gray leaf spot in tropical and subtropical maize germplasm. *Theoretical and Applied Genetics*, *137*(12). https://doi.org/10.1007/s00122-024-04764-0

Paterson, A. H., Wendel, J. F., Gundlach, H., Guo, H., Jenkins, J., Jin, D., Llewellyn, D.,

Showmaker, K. C., Shu, S., Udall, J., Yoo, M. J., Byers, R., Chen, W., Doron-Faigenboim, A., Duke, M. V., Gong, L., Grimwood, J., Grover, C., Grupp, K., … Schmutz, J. (2012). Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. *Nature*, *492*(7429), 423–427.

https://doi.org/10.1038/nature11798

Razzaq, A., Zafar, M. M., Ali, A., Hafeez, A., Sharif,

F., Guan, X., Deng, X., Pengtao, L., Shi, Y.,

Haroon, M., Gong, W., Ren, M., & Yuan, Y. (2022). The Pivotal Role of Major Chromosomes of Sub-Genomes A and D in Fibre Quality Traits of Cotton. In *Frontiers in Genetics* (Vol. 12). Frontiers MediaS.A. https://doi.org/10.3389/fgene.2021.642595

Rodgers, J., Zumba, J., & Fortier, C. (2017). Measurement comparison of cotton fibre micronaire and its components by portable near infrared spectroscopy instruments. *Textile Research Journal*, *87*(1), 57–69. https://doi.org/10.1177/00405175156 22153

Saski, C. A., Scheffler, B. E., Hulse-Kemp, A. M., Liu,

B., Song, Q., Ando, A., Stelly, D. M., Scheffler, J.

A., Grimwood, J., Jones, D. C., Peterson, D. G., Schmutz, J., & Chen, Z. J. (2017). Sub-genome anchored physical frameworks of the allotetraploid Upland cotton (Gossypium hirsutum L.) genome, and an approach toward reference-grade assemblies of polyploids. *ScientificReports*, 7(1).

https://doi.org/10.1038/s41598-017-14885-w

Saud, S., & Wang, L. (2022). Mechanism of cotton resistance to abiotic stress, and recent research advances in the osmoregulation-related genes. In *Frontiers in Plant Science* (Vol. 13). Frontiers MediaS.A.

https://doi.org/10.3389/fpls.2022.972635 Schoonmaker, A. N., Hulse-Kemp, A. M.,

Youngblood, R. C., Rahmat, Z., Atif Iqbal, M., Rahman, M. U., Kochan, K. J., Scheffler, B. E., & Scheffler, J. A. (2023). Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in Gossypium hirsutum and iCottonQTL: a New R/Shiny App to Streamline Genetic Mapping. *Plants*,*12*(5).

https://doi.org/10.3390/plants12051153 Shahzad, K., Mubeen, I., Zhang, M., Zhang, X., Wu,

J., & Xing, C. (2022). Progress and perspective on cotton breeding in Pakistan. *Journal of Cotton Research*,*5*(1),29.

https://doi.org/10.1186/s42397-022-00137-4 Shukla, R. P., Tiwari, G. J., Joshi, B., Song-Beng, K.,

Tamta, S., Boopathi, N. M., & Jena, S. N. (2021). GBS-SNP and SSR-based genetic mapping and

QTL analysis for drought tolerance in upland cotton. *Physiology and Molecular Biology of Plants*, *27*(8), 1731–1745.

https://doi.org/10.1007/s12298-021-01041-y Sun, H., Meng, M., Yan, Z., Lin, Z., Nie, X., & Yang,

X. (2019). Genome-wide association mapping of stress-tolerance traits in cotton. *The Crop Journal*, 7(1),77–88. https://doi.org/https://doi.org/10.1016/j.cj.2018.11.002

Sun, S., Li, C., Paterson, A. H., Jiang, Y., Xu, R., Robertson, J. S., Snider, J. L., & Chee, P. W. (2018). In-field high-throughput phenotyping and cotton plant growth analysis using LiDAR. *Frontiers in Plant Science* 9. https://doi.org/10.3389/fpls.2018.00016

Syed, M. M. , & Gao, N. (2010). *Publication Overview Title: Genetic mapping and QTL analysis of fibre-related traits in cotton (Gossypium).* https://www.cottongen.org/pub/10143

Tan, Z., Fang, X., Tang, S., Zhang, J., Liu, D., Teng, Z., Li, L., Ni, H., Zheng, F., Liu, D., Zhang, T., Paterson, A. H., & Zhang, Z. (2015). Genetic map and QTL controlling fibre quality traits in upland cotton (Gossypium hirsutum L.). *Euphytica*, 203(3), 615–628. https://doi.org/10.1007/s10681-014-1288-9

Tan, Z., Zhang, Z., Sun, X., Li, Q., Sun, Y., Yang, P., Wang, W., Liu, X., Chen, C., Liu, D., Teng, Z., Guo, K., Zhang, J., Liu, D., & Zhang, Z. (2018). Genetic map construction and fibre quality QTL mapping using the cottonSNP80K array in upland cotton. *Frontiers in Plant Science*, 9. https://doi.org/10.3389/fpls.2018.00225

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, 151084. https://doi.org/https://doi.org/10.1016/j.bbrc.2024.151084

Udall, J. A., Long, E., Hanson, C., Yuan, D., Ramaraj, T., Conover, J. L., Gong, L., Arick, M. A., Grover, C. E., Peterson, D. G., & Wendel, J. F. (2019). De Novo Genome Sequence Assemblies of Gossypium raimondii and Gossypium turneri. *G3: Genes, Genomes, Genetics*, 9(10), 3079–3085. https://doi.org/10.1534/g3.119.400392

Walford, S. A., Wu, Y., Llewellyn, D. J., & Dennis, E. S. (2011). GhMYB25-like: A key factor in early cotton fibre development. *Plant Journal*, 65(5), 785–797.https://doi.org/10.1111/j.1365-313X.2010.04464.x

Wang, C., Ulloa, M., Duong, T., & Roberts, P. A. (2018a). Quantitative trait loci mapping of multiple independent loci for resistance to Fusarium oxysporum f. sp. vasinfectum Races 1 and 4 in an interspecific cotton population. *Phytopathology*, 108(6), 759–767. https://doi.org/10.1094/PHYTO-06-17-0208-R Wang, C., Ulloa, M., Duong, T., & Roberts, P. A. (2018b). Quantitative trait loci mapping of multiple independent loci for resistance to Fusarium oxysporum f. sp. vasinfectum Races 1 and 4 in an interspecific cotton population. *Phytopathology*,108(6), 759–767. https://doi.org/10.1094/PHYTO-06-17-0208-R Wang, J., Yuan, J., Yu, J., Meng, F., Sun, P., Li, Y., Yang, N., Wang, Z., Pan, Y., Ge, W., Wang, L., Li, J., Liu, C., Zhao, Y., Luo, S., Ge, D., Cui, X., Feng, G., Wang, Z., ... Xi, Z. (2019). Recursive paleohexaploidization shaped the durian genome. *Plant Physiology*, 179(1), 209–219. https://doi.org/10.1104/pp.18.00921

Wang, M., Tu, L., Yuan, D., Zhu, D., Shen, C., Li, J.,

Liu, F., Pei, L., Wang, P., Zhao, G., Ye, Z.,

Huang, H., Yan, F., Ma, Y., Zhang, L., Liu, M.,

You, J., Yang, Y., Liu, Z., … Zhang, X. (2019). Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense. *Nature Genetics*, *51*(2),224–229. https://doi.org/10.1038/s41588-018-0282-x
Wang, P., Abbas, M., He, J., Zhou, L., Cheng, H., &

Guo, H. (2024). Advances in genome sequencing and artificially induced mutation provide new avenues for cotton breeding. In *Frontiers in Plant Science* (Vol. 15). Frontiers Media SA. https://doi.org/10.3389/fpls.2024.140020 1 Wang, X.-Y., Li, C.-Q., Xia, Z., Dong, N., & Wang,

Q.-L. (2012). [QTL mapping for "pre-summer boll, summer boll and autumn boll" traits in cotton]. *Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji*, *34*, 757–764. https://doi.org/10.3724/SP.J.1005.201 2.00757

Wendel, J. F., Brubaker, C. L., & Seelanan, T. (2010). The Origin and Evolution of Gossypium. In J. McD. Stewart, D. M., Oosterhuis, J. J., Heitholt, & J. R. Mauney (Eds.), *Physiology of Cotton* (pp. 1–18). Springer Netherlands. https://doi.org/10.1007/978-90-481-3195-2_1

Wendel, J. F., & Cronn, R. C. (2003). *POLYPLOIDY AND THE EVOLUTIONARY HISTORY OF COTTON*.

Yang, X., Wang, Y., Zhang, G., Wang, X., Wu, L., Ke, H., Liu, H., & Ma, Z. (2016). Detection and validation of one stable fibre strength QTL on c9

in tetraploid cotton. *Molecular Genetics and Genomics*, *291*(4),1625–1638. https://doi.org/10.1007/s00438-016-1206-z
Yang, Z., Qanmber, G., Wang, Z., Yang, Z., & Li, F.

(2020). Gossypium Genomics: Trends, Scope, and Utilization for Cotton Improvement. *Trends in Plant Science*, *25*(5), 488– 500. https://doi.org/10.1016/j.tplants.2019.12.011
Zhai, D. (2023). *Application of Various Genomic*

Selection Models in Cotton Fibre Quality. https://doi.org/10.20944/preprints20 2311.067 7.v1

Zhang, H. Bin, Li, Y., Wang, B., & Chee, P. W. (2008a). Recent advances in cotton genomics. In *International Journal of Plant Genomics* (Vol. 2008). https://doi.org/10.1155/2008/74230 4

Zhang, H. Bin, Li, Y., Wang, B., & Chee, P. W. (2008b). Recent advances in cotton genomics. In *International Journal of Plant Genomics* (Vol. 2008). https://doi.org/10.1155/2008/74230 4

Zhang, J., Fang, H., Zhou, H., Sanogo, S., & Ma, Z. (2014). Genetics, Breeding, and Marker-Assisted Selection for Verticillium Wilt Resistance in Cotton. *Crop Science*, *54*, 1289–1303. https://doi.org/10.2135/cropsci2013. 08.0550

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., … Chen, Z. J. (2015). Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fibre improvement. *Nature Biotechnology*, *33*(5), 531–

537. https://doi.org/10.1038/nbt.3207

Zhang, Y.-M., & Gai, J. (2009). Methodologies for segregation analysis and QTL mapping in plants.*Genetica*, *136*(2),311–318. https://doi.org/10.1007/s10709-008-9313-3

Zhang, Z.-S., Hu, M.-C., Zhang, J., Liu, D.-J., Zheng, J., Zhang, K., Wang, W., & Wan, Q. (2009).

Construction of a comprehensive PCR-based marker linkage map and QTL mapping for fibre quality traits in upland cotton (Gossypium hirsutum L.). *Molecular Breeding*, *24*(1), 49–61. https://doi.org/10.1007/s11032-009-9271-1