

Research Insight

Open Access

Meta-Analysis of Yield-Related Genetic Markers in Cotton

Shanjun Zhu, Mengting Luo ► Institute of Life Science, Jiyang College of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China Corresponding email: mengting.luo@jicat.org Field Crop, 2024, Vol.7, No.6 doi: 10.5376/fc.2024.07.0033 Received: 08 Nov., 2024 Accepted: 12 Dec., 2024 Published: 25 Dec., 2024 Copyright © 2024 Zhu and Luo, This is an open access article published under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. Preferred citation for this article:

Zhu S.J., and Luo M.T., 2024, Meta-analysis of yield-related genetic markers in cotton, Field Crop, 7(6): 325-333 (doi: 10.5376/fc.2024.07.0033)

Abstract This study presents a meta-analysis of yield-related genetic markers in cotton, focusing on their historical development, current applications, and future prospects. Advances in genetic marker technologies, including the use of SSRs, SNPs, and high-throughput sequencing, are explored, alongside their association with key yield traits such as boll size, lint weight, and plant height. Marker-assisted selection (MAS) and genomic selection (GS) are evaluated for their roles in improving breeding efficiency. A case study highlights the successful implementation of MAS in cotton breeding programs and the associated challenges. This analysis identifies significant markers and consistent quantitative trait loci (QTLs) across diverse studies, providing insights into emerging trends and practical applications. The study concludes by emphasizing the integration of advanced technologies, the importance of collaborative research, and actionable recommendations to enhance the role of genetic markers in sustainable cotton breeding. These findings offer valuable guidance for researchers and breeders aiming to address future challenges in cotton productivity. **Keywords** Cotton breeding; Genetic markers; Marker-assisted selection; Yield improvement; Quantitative trait loci (QTLs)

1 Introduction

Cotton (*Gossypium* spp.) is a crucial crop globally, serving as a primary source of natural fiber for the textile industry and contributing significantly to the economies of many countries (Hussain et al., 2019; Zhang et al., 2019). It is cultivated extensively worldwide, with India being one of the largest areas for cotton cultivation, although it faces challenges in productivity (Joshi et al., 2023). The economic importance of cotton is underscored by its role in providing employment and supporting industries related to textiles and agriculture (Gu et al., 2020).

Enhancing cotton yield is fraught with challenges, particularly due to environmental stresses such as drought, which significantly impact production. The genetic erosion of cotton due to a narrow genetic base further complicates breeding efforts aimed at improving yield (Hussain et al., 2019). Additionally, the variability in environmental conditions across different regions necessitates the development of cotton varieties that can maintain high yields under diverse conditions (Baytar et al., 2018; Gu et al., 2020).

Genetic markers, particularly quantitative trait loci (QTLs), play a pivotal role in understanding the genetic basis of yield-related traits in cotton. These markers help in identifying genes associated with fiber quality and yield, facilitating marker-assisted selection (MAS) in breeding programs (Said et al., 2013; Li et al., 2016; Liu et al., 2022). Recent studies have identified numerous QTLs linked to yield and fiber quality traits, providing insights into the genetic architecture of these traits and aiding in the development of improved cotton varieties (Xia et al., 2014; Qin et al., 2015; Zhang et al., 2019).

This study attempts to consolidate existing research on yield-related genetic markers in cotton to identify consistent QTLs that can be utilized in breeding programs, discuss the integration of data from multiple studies to provide a comprehensive understanding of the genetic factors influencing yield traits, and provide an overview of strategies to enhance the efficiency of breeding aimed at improving cotton yield and quality. The findings are expected to offer valuable insights for cotton breeders and contribute to the development of high-yielding, resilient cotton varieties.



2 Advances in Genetic Marker Research in Cotton

2.1 Historical development of genetic marker technologies

The development of genetic marker technologies in cotton has evolved significantly over the years. Initially, traditional breeding methods were the primary approach for cotton improvement, but these methods were limited by their time-consuming nature and the need for extensive field trials (Figure 1) (Kushanov et al., 2021). The introduction of molecular markers revolutionized cotton breeding by enabling the identification and utilization of DNA polymorphisms. Early marker systems included Restriction Fragment Length Polymorphism (RFLP) and Random Amplified Polymorphic DNA (RAPD), which laid the groundwork for more advanced techniques (Shehzad et al., 2017). The sequencing of cotton genomes, such as *G. raimondii* and *G. hirsutum*, further propelled the development of genetic markers by providing a comprehensive understanding of the cotton genome (Sabev et al., 2020).



Figure 1 Marker-assisted selection in comparison with conventional breeding (Adopted from Kushanov et al., 2021) Image caption: P1 and P2, parental genotypes, F1, first generation hybrid, Fn, hybrid progeny obtained from first generation by self-pollination, and BCn, backcross generations (Adopted from Kushanov et al., 2021)

2.2 Commonly used genetic markers in cotton breeding

In cotton breeding, several types of genetic markers are commonly used, including simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs). SSR markers are valued for their high polymorphism and ease of use in genetic diversity studies and DNA fingerprinting (Wu et al., 2020; Kuang et al., 2022). They have been instrumental in constructing linkage maps and conducting QTL analysis for traits such as fiber quality and yield (Sabev et al., 2020). SNP markers, on the other hand, offer high-throughput genotyping capabilities and are increasingly used for genome-wide association studies and genomic selection (Ashrafi et al., 2015; Hulse-Kemp et al., 2015). The development of SNP arrays, such as the CottonSNP63K, has provided a standardized resource for high-density genetic mapping and trait dissection.

2.3 Advances in high-throughput sequencing and marker discovery

Recent advances in high-throughput sequencing technologies have significantly enhanced marker discovery in cotton. Techniques such as genotyping-by-sequencing (GBS) and specific locus amplified fragment sequencing (SLAF-seq) have enabled the rapid identification of SNP markers across the cotton genome (Fan et al., 2018). These technologies facilitate the construction of high-density genetic maps, which are crucial for precise QTL mapping and marker-assisted selection (Wang et al., 2015; Zhang et al., 2016). The use of transcriptome



sequencing has also been explored to reduce sequencing costs while still providing valuable SNP data for breeding programs (Ashrafi et al., 2015). These advancements have accelerated the breeding process by allowing for the selection of desirable traits at the DNA level, thus improving the efficiency and effectiveness of cotton breeding programs (Kushanov et al., 2021).

In summary, the evolution of genetic marker technologies in cotton has transitioned from traditional methods to sophisticated molecular techniques, with SSRs and SNPs being the most commonly used markers. High-throughput sequencing has further advanced marker discovery, enabling more efficient breeding strategies and the development of high-yielding, high-quality cotton cultivars.

3 Yield-Related Traits in Cotton and Their Genetic Basis

3.1 Key traits influencing cotton yield

Cotton yield is influenced by several key traits, including boll size, lint weight, and plant height. Boll size is a critical determinant of yield as it directly affects the number of seeds and the amount of fiber produced per plant. Larger bolls generally contribute to higher yields (Hussain et al., 2019). Lint weight, which refers to the weight of the fiber after ginning, is another crucial trait, as it determines the quantity of usable fiber obtained from the cotton plant (Zhang et al., 2020). Plant height can also influence yield, as it affects the plant's ability to capture sunlight and its overall biomass production (Baytar et al., 2018).

3.2 Quantitative trait loci (QTLs) associated with yield components

Numerous QTLs have been identified that are associated with yield components in cotton. For instance, a study identified 983 QTLs related to fiber quality and yield, with 198 being stable across different environments (Zhang et al., 2019). Another research effort mapped 73 yield-related QTLs, with 10 being stable across multiple environments, highlighting the genetic complexity of yield traits (Liu et al., 2022). Additionally, 134 QTLs were associated with fiber yield traits, with 39 being novel discoveries, indicating ongoing advancements in understanding the genetic basis of yield (Joshi et al., 2023). These QTLs are distributed across various chromosomes, with some clusters showing significant correlations with yield traits (Gu et al., 2020).

3.3 The relationship between marker-assisted breeding and yield traits

Marker-assisted breeding (MAB) has become an essential tool in improving yield traits in cotton. By utilizing genetic markers linked to desirable traits, breeders can more efficiently select for high-yielding varieties. For example, the identification of stable QTLs and candidate genes through genome-wide association studies (GWAS) and other mapping techniques has facilitated the development of cotton lines with enhanced yield potential (Su et al., 2020). The integration of MAB in breeding programs has allowed for the precise selection of traits such as boll weight and lint percentage, leading to improved cotton varieties with higher yields (Diouf et al., 2018). This approach not only accelerates the breeding process but also increases the accuracy of selecting for complex traits like yield (Fan et al., 2018).

In summary, understanding the genetic basis of key yield-related traits and leveraging marker-assisted breeding techniques are crucial for enhancing cotton yield. The identification of QTLs and their integration into breeding programs can significantly improve the efficiency and effectiveness of developing high-yielding cotton varieties.

4 Integration of Genetic Markers in Breeding Programs

4.1 Marker-assisted selection (MAS) for yield improvement

Marker-assisted selection (MAS) has become a pivotal tool in cotton breeding, allowing for the precise selection of desirable traits at the DNA level, thereby accelerating the breeding process. MAS facilitates the identification and incorporation of quantitative trait loci (QTLs) associated with yield and fiber quality into breeding programs. This approach has been successfully used to develop high-yielding cotton cultivars with superior fiber quality and resistance to biotic and abiotic stresses (Sabev et al., 2020; Kushanov et al., 2021). For instance, the development of the 'Ravnaq' cotton cultivar series exemplifies the successful application of MAS, where specific SSR markers were used to transfer QTLs associated with fiber quality traits into elite cultivars (Darmanov et al., 2022).



Field Crop 2024, Vol.7, No.6, 325-333 http://cropscipublisher.com/index.php/fc

4.2 Use of genomic selection (GS) in breeding pipelines

Genomic selection (GS) is an emerging approach that leverages genome-wide marker data to predict the breeding value of individuals, thus enhancing the efficiency of selection in breeding programs. GS has shown promise in capturing the genetic variation for complex traits such as yield and fiber quality in cotton. By integrating GWAS hits into prediction models, GS can improve the accuracy of trait predictions, although careful consideration of significance thresholds is necessary (Billings et al., 2022). The development of high-density SNP arrays, such as the CottonSNP63K, provides a robust resource for implementing GS in cotton breeding, enabling the dissection of complex traits and enhancing the genetic gain (Hulse-Kemp et al., 2015).

4.3 Challenges and opportunities in translating marker data to breeding success

While the integration of genetic markers into breeding programs offers significant advantages, several challenges remain. One major challenge is the environment-specific nature of many alleles, which can limit their utility across different breeding contexts (Billings et al., 2022). Additionally, the narrow genetic diversity in cotton breeding programs can hinder the effective use of marker data (Aydın et al., 2023). However, opportunities exist in expanding the genetic base by incorporating wild alleles and utilizing advanced genome editing technologies like CRISPR/Cas9 to enhance yield-related traits (Figure 2) (Mubarik et al., 2020). Furthermore, the development of comprehensive genetic maps and the use of diverse molecular markers can facilitate the effective translation of marker data into breeding success (Qin et al., 2015; Sabev et al., 2020).

In summary, the integration of genetic markers through MAS and GS offers substantial potential for improving cotton yield and quality. However, addressing challenges such as allele specificity and genetic diversity is crucial for maximizing the benefits of these technologies in breeding programs.



Figure 2 Proposed revamped cotton breeding program (Adopted from Mubarik et al., 2020)

Image caption: Fine-tune the already present traits and add new traits to cultivated cotton varieties through plant breeding, genetic engineering, and genome editing tools. Pyramiding of useful traits by crossing between genetically altered and elite cultivars to develop climate resilient cotton cultivars (Adopted from Mubarik et al., 2020)

5 Case Study: Marker-Assisted Selection for Cotton Yield Improvement 5.1 Description of a breeding program implementing MAS

Marker-assisted selection (MAS) has been effectively implemented in various cotton breeding programs to enhance fiber quality and yield. One notable program targeted the improvement of fiber quality traits such as fiber length, strength, micronaire, and uniformity by utilizing SSR markers associated with specific QTLs. In this program, donor genotypes possessing desirable fiber quality traits were crossed with local elite cultivars, and the resulting populations were backcrossed over multiple generations. The transfer of targeted QTLs was monitored



using polymorphic SSR markers, leading to the development of new cotton cultivars with superior fiber quality (Darmanov et al., 2022).

5.2 Success stories and quantitative impact on yield improvement

The application of MAS in cotton breeding has led to significant improvements in fiber quality and yield. For instance, the development of the 'Ravnaq' cultivar series demonstrated the successful transfer of QTLs associated with superior fiber traits, resulting in cultivars with stronger, longer, and more uniform fibers compared to their parent lines (Figure 3) (Darmanov et al., 2022). Additionally, the identification of novel marker-trait associations has provided new insights into the genetic basis of yield and fiber quality, facilitating the development of high-yielding cotton varieties (Li et al., 2016; Kumar et al., 2021). These advancements underscore the potential of MAS to accelerate breeding processes and achieve substantial genetic gains in cotton (Kushanov et al., 2021).



Figure 3 Fibre staple lengths (mm) of 'Ravnaq-1' and 'Ravnaq-2' cultivar compared to controls lines (Adopted from Darmanov et al., 2022)

5.3 Challenges and lessons learned from real-world applications of MAS

Despite the successes, implementing MAS in cotton breeding presents several challenges. One major issue is the negative correlation between yield and fiber quality, which complicates the simultaneous improvement of both traits (Constable et al., 2015; Shang et al., 2015). Additionally, the complexity of cotton's genetic architecture, with multiple QTLs influencing key traits, requires precise mapping and validation of markers to ensure effective selection (Deng et al., 2019). Lessons learned from these challenges highlight the importance of integrating MAS with traditional breeding methods and utilizing comprehensive genomic tools to overcome limitations and enhance breeding efficiency (Rafiq et al., 2016).

In summary, while MAS has proven to be a powerful tool in cotton breeding, its success depends on careful planning, integration with conventional methods, and continuous refinement of genomic resources.

6 Key Insights from the Meta-Analysis

6.1 Compilation of significant markers linked to yield traits

The meta-analysis compiled a comprehensive list of significant markers associated with yield traits in cotton. For instance, a study identified 983 QTLs related to fiber yield and quality, with 198 being stable across multiple environments (Zhang et al., 2019). Another research identified 53, 70, and 68 significant SNPLDB loci associated with boll number, boll weight, and lint percentage, respectively (Su et al., 2020). Additionally, 71 QTLs for fiber quality and yield traits were detected, with 16 being stable across different environments (Li et al., 2016).

6.2 Identification of consistent QTLs across different studies and environments

Consistent QTLs were identified across various studies and environments, highlighting their stability and potential utility in breeding programs. For example, 24 stable QTLs for fiber quality and 12 for yield traits were identified in one study (Gu et al., 2020). Another study found 62 stable QTLs for fiber quality and 10 for yield-related traits across multiple environments (Liu et al., 2022). Furthermore, 30 QTLs were consistent in at least two environments, indicating their reliability (Diouf et al., 2018).

6.3 Emerging trends in marker development and application

Emerging trends in marker development and application include the use of high-density SNP markers and genome-wide association studies (GWAS) to enhance the precision of QTL mapping. For instance, a high-density



genetic map with 6187 bin markers was used to identify novel QTLs for fiber quality and yield traits (Gu et al., 2020). The use of 5178 SNP markers in another study facilitated the identification of 110 QTLs for various traits (Diouf et al., 2018). These advancements in marker technology are crucial for improving the efficiency of marker-assisted selection (MAS) in cotton breeding programs (Zhang et al., 2019).

In summary, the meta-analysis highlights the identification of significant markers and consistent QTLs across different studies, emphasizing their potential in improving cotton yield traits. The advancements in marker development and application are paving the way for more efficient breeding strategies.

7 Implications for Future Cotton Breeding

7.1 Integration of advanced technologies like CRISPR and genomic selection

The integration of advanced technologies such as CRISPR and genomic selection holds significant promise for the future of cotton breeding. CRISPR/Cas9 technology can be utilized to edit genes associated with disease susceptibility and negative regulators of yield-related traits, thereby enhancing cotton's resilience and productivity (Rauf et al., 2019; Mubarik et al., 2020). Genomic selection, which leverages high-throughput genotyping and phenotyping data, can accelerate the breeding process by predicting the performance of breeding lines before field trials, thus improving the efficiency of developing high-yielding and high-quality cotton cultivars (Bolek et al., 2016; Billings et al., 2022). These technologies, when combined, can significantly enhance the precision and speed of breeding programs, leading to the development of superior cotton varieties that meet the demands of changing climates and market needs (Sabev et al., 2020; Yang et al., 2022).

7.2 Role of collaborative research and data sharing in accelerating marker utility

Collaborative research and data sharing are crucial for maximizing the utility of genetic markers in cotton breeding. Programs like the CSIRO cotton breeding initiative demonstrate the benefits of partnerships between research institutions and commercial entities, which facilitate access to diverse genetic resources and advanced technologies (Conaty et al., 2022). By sharing genomic data and breeding outcomes, researchers can build comprehensive databases that enhance the understanding of marker-trait associations, thus improving the accuracy of marker-assisted selection (MAS) (Kushanov et al., 2021). Such collaborations can also help in standardizing methodologies and tools across different breeding programs, thereby accelerating the development and deployment of improved cotton varieties globally (Billings et al., 2022).

7.3 Recommendations for enhancing the practical application of markers in breeding

To enhance the practical application of genetic markers in cotton breeding, several strategies can be recommended. First, the development of high-density genetic maps and the use of next-generation sequencing technologies can improve the identification and validation of quantitative trait loci (QTLs) associated with economically important traits (Constable et al., 2015; Bolek et al., 2016). Second, integrating marker-assisted selection with traditional breeding methods can help overcome the limitations of conventional approaches, such as the time-consuming nature of phenotypic selection (Sabev et al., 2020). Finally, investing in training programs for breeders to effectively use molecular tools and data analytics can ensure that the latest advancements in genomics are fully utilized in breeding programs (Rauf et al., 2019; Kushanov et al., 2021). These steps will facilitate the creation of elite cotton cultivars with enhanced yield, fiber quality, and stress resistance.

In summary, the future of cotton breeding lies in the strategic integration of cutting-edge technologies, collaborative efforts, and the practical application of genetic markers. These approaches will collectively drive the development of cotton varieties that are not only high-yielding and resilient but also tailored to meet the specific needs of different growing environments and market demands.

8 Concluding Remarks

The meta-analysis of yield-related genetic markers in cotton has revealed significant insights into the genetic architecture underlying fiber quality and yield traits. Across multiple studies, a variety of quantitative trait loci (QTLs) have been identified, with some being stable across different environments. For instance, one study identified 983 QTLs related to fiber quality and yield, with 198 being stable across 17 environments. Another



study found 210 fiber quality QTLs and 73 yield-related QTLs, with several being stable across multiple environments. Additionally, novel genomic regions and candidate genes have been uncovered, providing a deeper understanding of the genetic basis for these traits.

Genetic marker research plays a crucial role in achieving sustainable yield improvements in cotton by enabling the identification and utilization of key genetic loci associated with desirable traits. The use of high-density genetic maps and genome-wide association studies (GWAS) has facilitated the discovery of QTLs and candidate genes that can be targeted in breeding programs to enhance fiber quality and yield. This research supports the development of cotton varieties that are more resilient to environmental stresses, such as drought, thereby contributing to sustainable agricultural practices.

To address future challenges in cotton breeding, a multidisciplinary approach is essential. Integrating genomics, phenomics, and environmental data can enhance our understanding of complex traits and improve breeding strategies. Collaboration between geneticists, agronomists, and data scientists can lead to the development of more robust cotton varieties that meet the demands of both productivity and environmental sustainability. By leveraging advances in molecular biology, bioinformatics, and field trials, the cotton industry can continue to innovate and adapt to changing global conditions.

Acknowledgments

We are grateful to Dr. Xie for critically reading the manuscript and providing valuable feedback that improved the clarity of the text. We express our heartfelt gratitude to the two anonymous reviewers for their valuable comments on the manuscript.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Ashrafi H., Hulse-Kemp A., Wang F., Yang S., Guan X., Jones D., Matvienko M., Mockaitis K., Chen Z., Stelly D., and Van Deynze A., 2015, A long-read transcriptome assembly of cotton (*Gossypium hirsutum* L.) and intraspecific single nucleotide polymorphism discovery, The Plant Genome, 8(2): 1-14. https://doi.org/10.3835/plantgenome2014.10.0068
- Aydın A., 2023, Determination of genetic diversity of some upland and sea island cotton genotypes using high-resolution capillary electrophoresis gel, Agronomy, 13(9): 2407.

https://doi.org/10.3390/agronomy13092407

- Baytar A., Peynircioğlu C., Sezener V., Basal H., Frary A., Frary A., and Doğanlar S., 2018, Genome-wide association mapping of yield components and drought tolerance-related traits in cotton, Molecular Breeding, 38: 1-16. https://doi.org/10.1007/s11032-018-0831-0
- Billings G., Jones M., Rustgi S., Bridges W., Holland J., Hulse-Kemp A., and Campbell B., 2022, Outlook for implementation of genomics-based selection in public cotton breeding programs, Plants, 11(11): 1446.

https://doi.org/10.3390/plants11111446

- Bolek Y., Hayat K., Bardak A., and TehseenAzhar M., 2016, Molecular breeding of cotton, Intech Publishers, 2016: 123-166. https://doi.org/10.5772/64593
- Conaty W., Broughton K., Egan L., Li X., Li Z., Liu S., Llewellyn D., MacMillan C., Moncuquet P., Rolland V., Ross B., Sargent D., Zhu Q., Pettolino F., and Stiller W., 2022, Cotton breeding in australia: meeting the challenges of the 21st century, Frontiers in Plant Science, 13: 904131. https://doi.org/10.3389/fpls.2022.904131
- Constable G., Llewellyn D., Walford S., and Clement J., 2015, Cotton breeding for fiber quality improvement, Industrial Crops: Breeding for Bioenergy and Bioproducts, 2015: 191-232.

https://doi.org/10.1007/978-1-4939-1447-0_10

- Darmanov M., Makamov A., Ayubov M., Khusenov N., Buriev Z., Shermatov S., Salakhutdinov I., Ubaydullaeva K., Norbekov J., Kholmuradova M., Narmatov S., Normamatov I., and Abdurakhmonov I., 2022, Development of superior fibre quality upland cotton cultivar series 'Ravnaq' using marker-assisted selection, Frontiers in Plant Science, 13: 906472. https://doi.org/10.3389/fpls.2022.906472
- Deng X., Gong J., Liu A., Shi Y., Gong W., Ge Q., Li J., Shang H., Wu Y., and Yuan Y., 2019, QTL mapping for fiber quality and yield-related traits across multiple generations in segregating population of CCRI 70, Journal of Cotton Research, 2: 1-10. https://doi.org/10.1186/s42397-019-0029-y



- Diouf L., Magwanga R., Gong W., He S., Pan Z., Jia Y., Kirungu J., and Du X., 2018, QTL mapping of fiber quality and yield-related traits in an intra-specific upland cotton using genotype by sequencing (GBS), International Journal of Molecular Sciences, 19(2): 441. https://doi.org/10.3390/iims19020441
- Fan L., Wang L., Wang X., Zhang H., Zhu Y., Guo J., Gao W., Geng H., Chen Q., and Qu Y., 2018, A high-density genetic map of extra-long staple cotton (*Gossypium barbadense*) constructed using genotyping-by-sequencing based single nucleotide polymorphic markers and identification of fiber traits-related QTL in a recombinant inbred line population, BMC Genomics, 19: 1-12. <u>https://doi.org/10.1186/s12864-018-4890-8</u>
- Gu Q., Ke H., Liu Z., Lv X., Sun Z., Zhang M., Chen L., Yang J., Zhang Y., Wu L., Li, Z., Wu J., Wang G., Meng C., Zhang G., Wang X., and Ma Z., 2020, A high-density genetic map and multiple environmental tests reveal novel quantitative trait loci and candidate genes for fibre quality and yield in cotton, Theoretical and Applied Genetics, 133: 3395-3408.

https://doi.org/10.1007/s00122-020-03676-z

- Hulse-Kemp A., Lemm J., Plieske J., Ashrafi H., Buyyarapu R., Fang D., Frelichowski J., Giband M., Hague S., Hinze L., Kochan K., Riggs P., Scheffler J., Udall J., Ulloa M., Wang S., Zhu Q., Bag S., Bhardwaj A., Burke J., Byers R., Claverie M., Gore M., Harker D., Islam M., Jenkins J., Jones D., Lacape J., Llewellyn D., Percy R., Pepper A., Poland J., Rai K., Sawant S., Singh S., Spriggs A., Taylor J., Wang F., Yourstone S., Zheng X., Lawley C., Ganal M., Van Deynze A., Wilson I., and Stelly D., 2015, Development of a 63K SNP array for cotton and high-density mapping of intraspecific and interspecific populations of *Gossypium* spp, G3: Genes/Genomes/Genetics, 5: 1187-1209. <u>https://doi.org/10.1534/g3.115.018416</u>
- Hussain S., Hussain M., Javed M., Sarwar S., and Zubair M., 2019, Mapping of QTLs responsible for yield related traits in advance lines of cotton (*Gossypium hirsutum* L.), Genetics, 3: 15-22.

https://doi.org/10.35841/GENETICS-MOLECULAR-BIOLOGY.3.15-22

Joshi B., Singh S., Tiwari G., Kumar H., Boopathi N., Jaiswal S., Adhikari D., Kumar D., Sawant S., Iquebal M., and Jena S., 2023, Genome-wide association study of fiber yield-related traits uncovers the novel genomic regions and candidate genes in Indian upland cotton (*Gossypium hirsutum* L.), Frontiers in Plant Science, 14: 1252746.

https://doi.org/10.3389/fpls.2023.1252746

Kuang Z., Xiao C., Ilyas M., Ibrar D., Khan S., Guo L., Wang W., Wang B., Huang H., Li Y., Li Y., Zheng J., Saleem S., Tahir A., Ghafoor A., and Chen H., 2022, Use of SSR markers for the exploration of genetic diversity and DNA finger-printing in early-maturing upland cotton (*Gossypium hirsutum* L.) for future breeding program, Agronomy, 12(7): 1513.

https://doi.org/10.3390/agronomy12071513

- Kumar P., Nimbal S., Sangwan R., Budhlakoti N., Singh V., Mishra D.S., and Choudhary R., 2021, Identification of novel marker-trait associations for lint yield contributing traits in upland cotton (*Gossypium hirsutum* L.) using SSRs, Frontiers in Plant Science, 12: 653270. <u>https://doi.org/10.3389/fpls.2021.653270</u>
- Kushanov F., Turaev O., Ernazarova D., Gapparov B., Oripova B., Kudratova M., Rafieva F., Khalikov K., Erjigitov D., Khidirov M., Kholova M., Khusenov N., Amanboyeva R., Saha S., Yu J., and Abdurakhmonov I., 2021, Genetic diversity, QTL mapping, and marker-assisted selection technology in cotton (*Gossypium* spp.), Frontiers in Plant Science, 12: 779386. https://doi.org/10.3389/fpls.2021.779386
- Li C., Dong Y., Zhao T., Li L., Li C., Yu E., Mei L., Daud M., He Q., Chen J., and Zhu S., 2016, Genome-wide SNP linkage mapping and QTL analysis for fiber quality and yield traits in the upland cotton recombinant inbred lines population, Frontiers in Plant Science, 7: 1356. https://doi.org/10.3389/fpls.2016.01356
- Liu X., Yang L., Wang J., Wang Y., Guo Z., Li Q., Yang J., Wu Y., Chen L., Teng Z., Liu D., Liu D., Guo K., and Zhang Z., 2022, Analyzing quantitative trait loci for fiber quality and yield-related traits from a recombinant inbred line population with *Gossypium hirsutum* race palmeri as one parent, Frontiers in Plant Science, 12: 817748.

https://doi.org/10.3389/fpls.2021.817748

Mubarik M.C., Majeed S., Du X., and Azhar M., 2020, Revamping of cotton breeding programs for efficient use of genetic resources under changing climate, Agronomy, 10: 1190.

https://doi.org/10.3390/agronomy10081190

- Qin H., Chen M., Yi X., Bie S., Zhang C., Zhang Y., Lan J., Meng Y., Yuan Y., and Jiao C., 2015, Identification of associated SSR markers for yield component and fiber quality traits based on frame map and upland cotton collections, PLoS One, 10(1): e0118073. <u>https://doi.org/10.1371/journal.pone.0118073</u>
- Rafiq M., Liaqat S., Ahmed R., Najeebullah M., Touqeer R.A., Karim A., and Jabbar A., 2016, An overview of marker assisted selection and QTL mapping in cotton, International Journal of Agronomy and Agricultural Research, 8(1): 71-80.
- Rauf S., Shehzad M., Al-Khayri J., Imran H., and Noorka I., 2019, Cotton (Gossypium hirsutum L.) breeding strategies, Advances in Plant Breeding Strategies: Industrial and Food Crops, 6: 2019: 29-59.

https://doi.org/10.1007/978-3-030-23265-8_2

- Sabev P., Valkova N., and Todorovska E., 2020, Molecular markers and their application in cotton breeding: progress and future perspectives, Bulgarian Journal of Agricultural Science, 26(4): 816-828.
- Said J., Lin Z., Zhang X., Song M., and Zhang J., 2013, A comprehensive meta QTL analysis for fiber quality, yield, yield related and morphological traits, drought tolerance, and disease resistance in tetraploid cotton, BMC Genomics, 14: 776-776. <u>https://doi.org/10.1186/1471-2164-14-776</u>



- Shang L., Liang Q., Wang Y., Wang X., Wang K., Abduweli A.L., Cai S., and Hua J., 2015, Identification of stable QTLs controlling fiber traits properties in multi-environment using recombinant inbred lines in Upland cotton (*Gossypium hirsutum* L.), Euphytica, 205: 877-888. https://doi.org/10.1007/s10681-015-1434-z
- Shehzad M., 2017, Role of molecular markers and importance of snp for the development of cotton programs, Journal of Biology, Agriculture and Healthcare, 7: 61-73.
- Su J., Wang C.Q., Zhang A., Shi C., Liu J., Zhang X., Yang D., and Ma X., 2020, An RTM-GWAS procedure reveals the QTL alleles and candidate genes for three yield-related traits in upland cotton, BMC Plant Biology, 20: 1-15. <u>https://doi.org/10.1186/s12870-020-02613-y</u>
- Wang Y., Ning Z., Hu Y., Chen J., Zhao R., Chen H., Ai N., Guo W., and Zhang T., 2015, Molecular mapping of restriction-site associated DNA markers in allotetraploid upland cotton, PLoS One, 10(4): e0124781. https://doi.org/10.1371/journal.pone.0124781
- Wu Y., Huang L., Zhou D., Fu X., Li C., Wei S., Peng J., and Kuang M., 2020, Development and application of perfect SSR markers in cotton, Journal of Cotton Research, 3: 1-8.

https://doi.org/10.1186/s42397-020-00066-0

- Xia Z., Zhang X., Liu Y., Jia Z., Zhao H., Li C., and Wang Q., 2014, Major gene identification and quantitative trait locus mapping for yield- related traits in upland cotton (*Gossypium hirsutum* L.), Journal of Integrative Agriculture, 13: 299-309. https://doi.org/10.1016/S2095-3119(13)60508-0
- Yang Z., Gao C., Zhang Y., Yan Q., Hu W., Yang L., Wang Z., and Li F., 2022, Recent progression and future perspectives in cotton genomic breeding, Journal of Integrative Plant Biology, 65(2): 548-569. <u>https://doi.org/10.1111/jipb.13388</u>
- Zhang K., Kuraparthy V., Fang H., Zhu L., Sood S., and Jones D., 2019, High-density linkage map construction and QTL analyses for fiber quality, yield and morphological traits using cotton SNP63K array in upland cotton (*Gossypium hirsutum* L.), BMC Genomics, 20: 1-26. https://doi.org/10.1186/s12864-019-6214-z
- Zhang T., Zhang N., Li W., Zhou X., Pei X., Liu Y., Ren Z., He K., Zhang W., Zhou K., Zhang F.X., Yang D., and Li Z., 2020, Genetic structure, gene flow pattern, and association analysis of superior germplasm resources in domesticated upland cotton (*Gossypium hirsutum* L.), Plant Diversity, 42: 189-197. https://doi.org/10.1016/j.pld.2020.03.001
- Zhang Z., Li J., Jamshed M., Shi Y., Liu A., Gong J., Wang S., Zhang J., Sun F., Jia F., Ge Q., Fan L., Zhang Z., Pan J., Fan S., Wang Y., Lu Q., Liu R., Deng X., Zou X., Jiang X., Liu P., Li P., Iqbal M., Zhang C., Zou J., Chen H., Tian Q., Jia X., Wang B., Ai N., Feng G., Wang Y., Hong M., Li S., Lian W., Wu B., Hua J., Zhang C., Huang J., Xu A., Shang H., Gong W., and Yuan Y., 2019, Genome-wide quantitative trait loci reveal the genetic basis of cotton fibre quality and yield-related traits in a *Gossypium hirsutum* recombinant inbred line population, Plant Biotechnology Journal, 18: 239-253. https://doi.org/10.1111/pbi.13191
- Zhang Z., Shang H., Shi Y., Huang L., Li J., Ge Q., Gong J., Liu A., Chen T., Wang D., Wang Y., Palanga K., Muhammad J., Li W., Lu Q., Deng X., Tan Y., Song W., Cai J., Li P., Rashid H., Gong W., and Yuan Y., 2016, Construction of a high-density genetic map by specific locus amplified fragment sequencing (SLAF-seq) and its application to quantitative trait loci (QTL) analysis for boll weight in upland cotton (*Gossypium hirsutum*.), BMC Plant Biology, 16: 1-18.

https://doi.org/10.1186/s12870-016-0741-4



Disclaimer/Publisher's Note

The statements, opinions, and data contained in all publications are solely those of the individual authors and contributors and do not represent the views of the publishing house and/or its editors. The publisher and/or its editors disclaim all responsibility for any harm or damage to persons or property that may result from the application of ideas, methods, instructions, or products discussed in the content. Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.