Triticeae Genomics and Genetics, 2024, Vol.15, No.2, 88-99
http://cropscipublisher.com/index.php/lgg

Research Report **Open Access**

Quantitative Trait Loci (QTL) Mapping in Wheat: Success Stories and Lessons Learned

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Triticeae Genomics and Genetics, 2024, Vol.15, No.2 doi: 10.5376/tgg.2024.15.0009
Received: 15 Feb., 2024
Accepted: 20 Mar., 2024
Published: 30 Mar., 2024

Preferred citation for this article:
Zhu J.H., 2024, Quantitative Trait loci (QTL) mapping in wheat: success stories and lessons learned, Triticeae Genomics and Genetics, 15(2): 88-99 (doi: 10.5376/tgg.2024.15.0009)

Abstract Quantitative Trait Loci (QTL) mapping has revolutionized the field of wheat genetics and breeding, enabling the identification of genomic regions associated with key agronomic traits. This study provides a comprehensive overview of the advancements and achievements in QTL mapping for wheat (*Triticum aestivum* L.), discussing successful cases and lessons learned, with a particular focus on its applications in improving grain yield, quality, and stress resistance. The study delves into methodological advancements, including traditional methods and modern technologies such as high-resolution genetic mapping, advanced statistical methods, and multi-parent cross designs. These advancements have significantly enhanced the precision and accuracy of QTL detection. It also addresses the challenges encountered in QTL mapping, such as environmental interactions and genetic background effects, and introduces strategies to overcome these obstacles, including integrated approaches and the use of high-density maps. Future directions for QTL mapping are explored, emphasizing the integration with genomic selection, improving precision and efficiency through new technologies, and applying these methods to other crops. QTL mapping has profoundly impacted wheat breeding programs, providing tools and insights that facilitate the development of high-yielding, high-quality, and stress-resistant wheat varieties. These findings underscore the importance of continued research and technological integration in advancing global food security and agricultural sustainability.

Keywords Wheat; Quantitative trait loci (QTL); Genetic mapping; Grain quality; Yield potential

1 Introducion

Quantitative Trait Loci (QTL) mapping is a pivotal tool in the field of plant genetics and breeding, particularly for complex traits influenced by multiple genes and environmental factors. QTL mapping facilitates the identification of genomic regions associated with specific phenotypic traits, enabling breeders to improve crop performance through marker-assisted selection. In wheat (*Triticum aestivum* L.), QTL mapping has been instrumental in enhancing various agronomic traits such as yield, disease resistance, drought tolerance, and grain quality (Hu et al., 2020; Wang et al., 2022; Xu et al., 2023). As one of the world's most important staple crops, wheat's genetic improvement is crucial for ensuring food security and meeting the demands of a growing global population. The advancements in QTL mapping technologies have significantly accelerated the pace of genetic discoveries and breeding programs, making it a cornerstone of modern wheat breeding strategies (Su et al., 2018).

Numerous studies have demonstrated the efficacy of QTL mapping in wheat. For instance, high-density genetic maps have been constructed to identify QTLs for quality traits such as grain protein content, grain hardness, and starch pasting properties, with significant phenotypic variance explained (PVE) by these QTLs (Li et al., 2021). Comparative genomics and meta-QTL analysis have further refined these QTLs, reducing confidence intervals and identifying stable QTLs across different genetic backgrounds (Shariatipour et al., 2021). Additionally, QTL mapping under specific stress conditions, such as salt stress, has revealed key genomic regions contributing to stress tolerance, which are crucial for breeding resilient wheat varieties (Ilyas et al., 2019).

This study aims to integrate and synthesize successful cases and lessons learned from QTL mapping studies in wheat, providing a comprehensive summary of key QTL identified for yield potential, quality traits, and stress resistance. The research will explore the latest advancements in QTL mapping technologies, including the use of high-density genetic maps and meta-QTL analysis, and how these technologies enhance the precision and reliability of QTL identification. Additionally, common challenges in QTL mapping, such as environmental interactions and genetic complexity, will be identified, and strategies to overcome these challenges will be discussed. The study will also address future research directions and potential applications of QTL mapping in wheat breeding programs, with a particular emphasis on integrating QTL data with genomic selection and other modern breeding techniques. By providing these valuable insights, the study aims to assist researchers and breeders in developing high-yielding, high-quality, and stress-resistant wheat varieties.

2 Methodological Advances in QTL Mapping

2.1 Traditional approaches

Traditional QTL mapping approaches in wheat have primarily relied on bi-parental populations, such as recombinant inbred lines (RILs) and doubled haploids (DHs). These methods typically use molecular markers like restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), and simple sequence repeats (SSRs) to construct genetic maps and identify QTLs associated with phenotypic traits. While effective in identifying major QTLs, these traditional methods have limitations, including low resolution due to limited recombination events and a narrow genetic base, which restricts the detection of QTLs with small effects and the exploration of genetic diversity (Guo et al., 2020). For instance, early studies utilized recombinant inbred lines (RILs) and SSR markers to map QTLs for various traits under specific environmental conditions, but the low marker density restricted the precision of QTL localization (Ilyas et al., 2019). Despite these limitations, traditional approaches laid the groundwork for understanding the genetic basis of complex traits in wheat and highlighted the importance of developing more refined mapping techniques.

2.2 Modern techniques and tools

Recent advances in molecular biology, genomics, and bioinformatics have significantly enhanced QTL mapping methodologies. These modern techniques offer higher resolution, greater accuracy, and the ability to explore complex traits influenced by multiple genetic and environmental factors.

2.2.1 High-resolution genetic maps

The development of high-density genetic maps using single nucleotide polymorphism (SNP) arrays and genotyping-by-sequencing (GBS) has revolutionized QTL mapping. These maps provide a more detailed representation of the wheat genome, enabling the precise localization of QTLs and the identification of closely linked markers for marker-assisted selection (MAS). High-density SNP arrays, such as the Wheat55K and Wheat660K, have been widely used to construct genetic maps with thousands of markers distributed across all wheat chromosomes (Liu et al., 2018; Ren et al., 2021). These high-resolution maps have significantly improved the power to detect QTLs and have facilitated the fine-mapping of important agronomic traits. Techniques such as specific-locus amplified fragment sequencing (SLAF-seq) and single nucleotide polymorphism (SNP) arrays have enabled the construction of high-density maps with thousands of markers. For example, a study utilizing the Wheat55K SNP array constructed a genetic map with 11 583 markers, facilitating the identification of stable QTLs for kernel-related traits across multiple environments (Ren et al., 2021). Similarly, SLAF-seq was employed to create a high-density map with 193 RILs, leading to the identification of 30 QTLs for quality traits such as grain protein content and grain hardness (Li et al., 2021). These high-resolution maps allow for more precise localization of QTLs and the identification of candidate genes.

2.2.2 Statistical and computational tools

Advancements in statistical and computational tools have also played a crucial role in modern QTL mapping. Meta-QTL analysis, for instance, consolidates QTL data from multiple studies to identify stable and reliable QTLs. A meta-analysis of 735 QTLs from 27 mapping populations condensed these into 100 meta-QTLs, significantly reducing the confidence intervals and improving the reliability of QTL identification (Shariatipour et al., 2021). The use of advanced statistical methods such as inclusive composite interval mapping (ICIM) and multi-environment trial (MET) analysis has enabled the detection of QTLs with greater accuracy and consistency across different environments (Ren et al., 2021). Additionally, software tools like QTL Cartographer, MapQTL, and R/qtl have been developed to handle large datasets and perform complex analyses, enhancing the efficiency and precision of QTL mapping studies (Su et al., 2018; Yang et al., 2019).

2.2.3 Multi-parental cross designs

Multi-parental cross designs, such as nested association mapping (NAM) and multi-parent advanced generation inter-cross (MAGIC) populations, have emerged as powerful tools for QTL mapping. These designs incorporate genetic diversity from multiple parents, creating populations with a higher level of recombination and genetic variation. This allows for the dissection of complex traits and the identification of novel QTLs that are not detectable in traditional bi-parental populations. Studies using these designs have successfully identified QTLs for various traits, including yield, disease resistance, and quality traits in wheat (Hu et al., 2020; Li et al., 2020). The increased recombination in these populations enhances the resolution of QTL mapping, facilitating the identification of candidate genes and the understanding of genetic mechanisms underlying important traits. For example, a study on a double haploid population derived from a cross between two wheat lines identified nine QTLs for thousand-grain weight, with some QTLs showing strong and stable effects across multiple environments (Liu et al., 2020). These multi-parental designs facilitate the identification of novel QTLs and the dissection of complex genetic interactions.

The integration of high-resolution genetic maps, advanced statistical tools, and multi-parental cross designs has revolutionized QTL mapping in wheat. These methodological advances have not only improved the precision and reliability of QTL identification but also provided valuable insights into the genetic mechanisms underlying important agronomic traits.

3 Success Stories in Wheat QTL Mapping

3.1 QTL mapping for grain yield

Quantitative Trait Loci (QTL) mapping has significantly advanced our understanding of the genetic basis of grain yield in wheat. Numerous studies have successfully mapped QTLs that contribute to yield and its components, such as thousand kernel weight (TKW), grain number per spike, and grain weight. Shariatipour et al. (2021) by meta-analysis identified 735 QTLs for grain yield (GY) and related traits, consolidating them into 100 meta-QTLs (MQTLs) with reduced confidence intervals, thus enhancing the precision of QTL mapping. Yang et al. (2019) evaluated 266 recombinant inbred lines derived from two wheat lines, Zhongmai 871 and Zhongmai 895, across various environments. Key traits analyzed included thousand grain weight (TGW), grain length (GL), grain width (GW), grain number per spike (GNS), and grain filling rate (GFR). The researchers used a high-density SNP array to perform initial QTL mapping, identifying four major genetic regions on chromosomes 1AL, 2BS, 3AL, and 5B that significantly influence TGW-related traits (Figure 1). This was followed by using Kompetitive Allele Specific PCR (KASP) markers to validate these QTLs in a larger set of lines, confirming their influence across multiple environments and explaining a significant proportion of the phenotypic variance. These findings suggest that the identified QTLs, especially those on chromosomes 1AL and 5B, could be critical targets for marker-assisted selection in wheat breeding programs aimed at improving yield and other agronomically important traits. Additionally, a genome-wide QTL mapping study by Dhakal et al. (2021) in wheat identified 51 QTLs for grain yield and agronomic traits across 28 diverse environments, highlighting the robustness of these QTLs in different conditions.

3.2 QTL Mapping for grain quality

Grain quality traits, such as grain protein content (GPC), grain hardness (GH), and starch pasting properties, are crucial for wheat's end-use quality. Li et al. (2020) used Specific-Locus Amplified Fragment Sequencing (SLAF-seq) and Bulked Segregant RNA Sequencing (BSR-Seq) techniques to construct a high-density genetic map of wheat. Based on this map, they identified quantitative trait loci (QTL) associated with wheat quality traits (Figure 2). In 193 recombinant inbred lines derived from two wheat varieties, Chuanmai 42 and Chuanmai 39, the researchers identified 30 QTLs that could explain up to 47.99% of the phenotypic variation. The traits involved included falling number (FN), grain protein content (GPC), grain hardness (GH), and starch pasting characteristics. Notably, a major QTL for GH on chromosome 5D was found to be closely linked to the pina-D1 and pinb-D1 genes, exhibiting a high phenotypic variance explanation rate. Additionally, a QTL on chromosome 3D showed stable expression across different environments and significantly improved FN, with its effects validated in a doubled haploid population. Guo et al. (2020) study mapped 106 QTLs for protein- and starch-related quality traits, identifying 26 relatively high-frequency QTLs (RHF-QTLs) that were consistent across multiple environments. These findings underscore the potential of QTL mapping in improving wheat quality through targeted breeding programs.

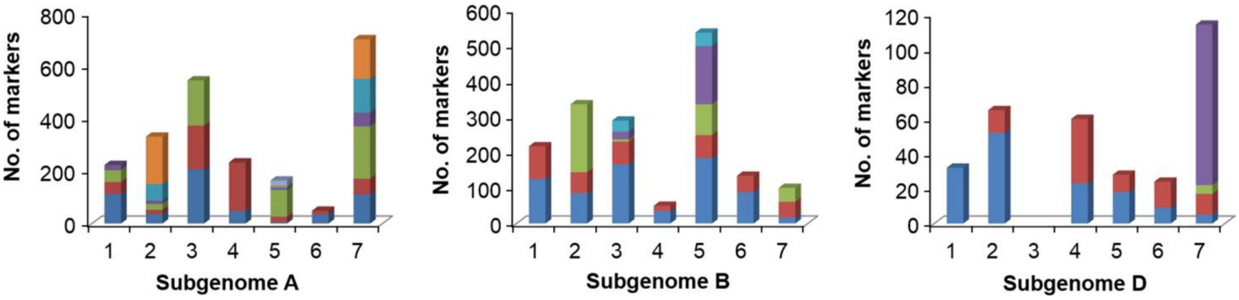

Figure 1 A distribution map of QTLs located on wheat chromosomes (Adapteded from Yang et al., 2019)

Image caption: The map depicts the specific locations of QTLs associated with thousand grain weight (TGW), grain length (GL), grain width (GW), and grain filling rate (GFR) on different wheat chromosomes; QTLs are represented by bar charts in different colors, showing their coverage on the chromosomes and their overlaps; This visual representation helps breeders understand the genetic control regions of these traits and their potential genetic interactions, thereby enabling more effective use of this information for marker-assisted selection (Adapted from Yang et al., 2019)

3.3 QTL mapping for stress tolerance

3.3.1 Abiotic stress tolerance

Abiotic stresses, such as salinity and drought, pose significant challenges to wheat production. A study on salt stress identified 60 QTLs for physiological and biochemical traits, with the B genome contributing the highest number of QTLs under salt stress conditions (Ilyas et al., 2019). This study highlighted the potential of these QTLs for developing salinity-tolerant wheat varieties through MAS. Additionally, a meta-analysis of QTLs for drought tolerance in rice, which shares genomic collinearity with wheat, identified stable QTLs that could be leveraged for improving drought tolerance in wheat (Selamat and Nadarajah, 2021).

3.3.2 Biotic stress tolerance

Biotic stress tolerance, including resistance to diseases and pests, is critical for maintaining wheat yield and quality. While the provided data does not include specific studies on biotic stress tolerance in wheat, the principles of QTL mapping and the identification of stable QTLs in other crops, such as rice, can be applied to wheat. For instance, the identification of QTLs for salinity tolerance in rice (Islam et al., 2019) and their potential role in epigenetic modifications (Mazumder et al., 2020) can inform similar approaches in wheat for biotic stress tolerance.

In summary, QTL mapping has provided valuable insights into the genetic basis of grain yield, quality, and stress tolerance in wheat. These success stories highlight the potential of QTL mapping to enhance wheat breeding programs and improve crop performance under various environmental conditions.

4 Case Studies

4.1 Recombinant inbred line (RIL) populations

Recombinant Inbred Line (RIL) populations have been extensively used in QTL mapping studies to identify genetic loci associated with various traits in wheat. In the study by Goel et al. (2019), 206 recombinant inbred lines (RILs) derived from the wheat varieties WL711 and C306 were cultivated across three different locations in India to evaluate various quality-related traits under different environmental conditions. This research aimed to investigate the genetic control of wheat grain quality traits and map quantitative trait loci (QTLs) to gain a deeper understanding of how genetic factors influence wheat performance in diverse environments (Figure 3) (Hussain et al., 2018).

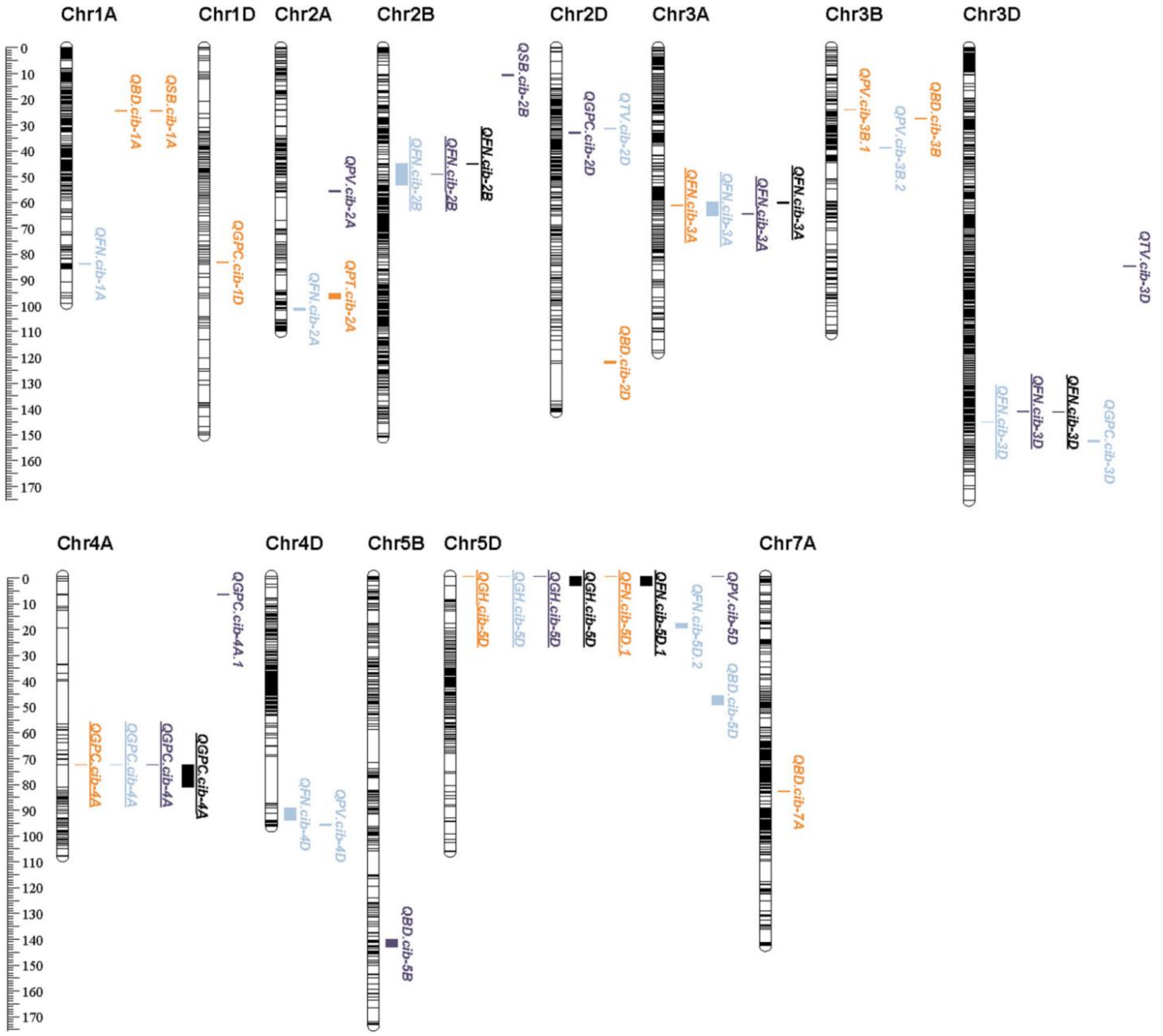

Figure 2 Distribution of QTLs on wheat chromosomes across different environments (Adapted from Li et al., 2020)

Image caption: These QTLs are associated with quality traits such as grain protein content (GPC), grain hardness (GH), falling number (FN), and starch pasting characteristics; The orange, blue, purple, and black markers represent QTLs detected in different environments (E1, E2, E3) and those identified using the BLUP method; The discovery of these QTLs aids breeders in understanding the genetic basis of wheat quality formation under various environmental conditions. For instance, the figure shows that certain QTLs are consistently detected across multiple environments, indicating that the genetic factors in these regions may play significant roles in improving and stabilizing wheat quality; By identifying and utilizing these QTLs, targeted molecular marker-assisted selection can be employed to enhance the quality traits of wheat (Adapted from Li et al., 2020)

Using phenotypic and genotypic analysis, the study identified 38 putative QTLs for 13 quality-related traits, such as grain protein content (GPC), kernel hardness, and thousand-kernel weight (TKW). These QTLs were spread across 14 chromosomes, explaining 7.9% to 16.8% of the phenotypic variation, highlighting the complex genetic basis of these traits. The study particularly noted significant QTLs on chromosomes like 1B, 1D, 5D, and 7A, which were involved in controlling GPC, a critical quality trait for bread-making.

Moreover, the study revealed the potential of using marker-assisted selection (MAS) to improve wheat grain and bread-making quality, based on the identified QTLs. This genetic insight provides a valuable foundation for breeding strategies aimed at enhancing the quality of wheat according to specific consumer and industrial needs, thereby addressing the growing demands for high-quality wheat products.

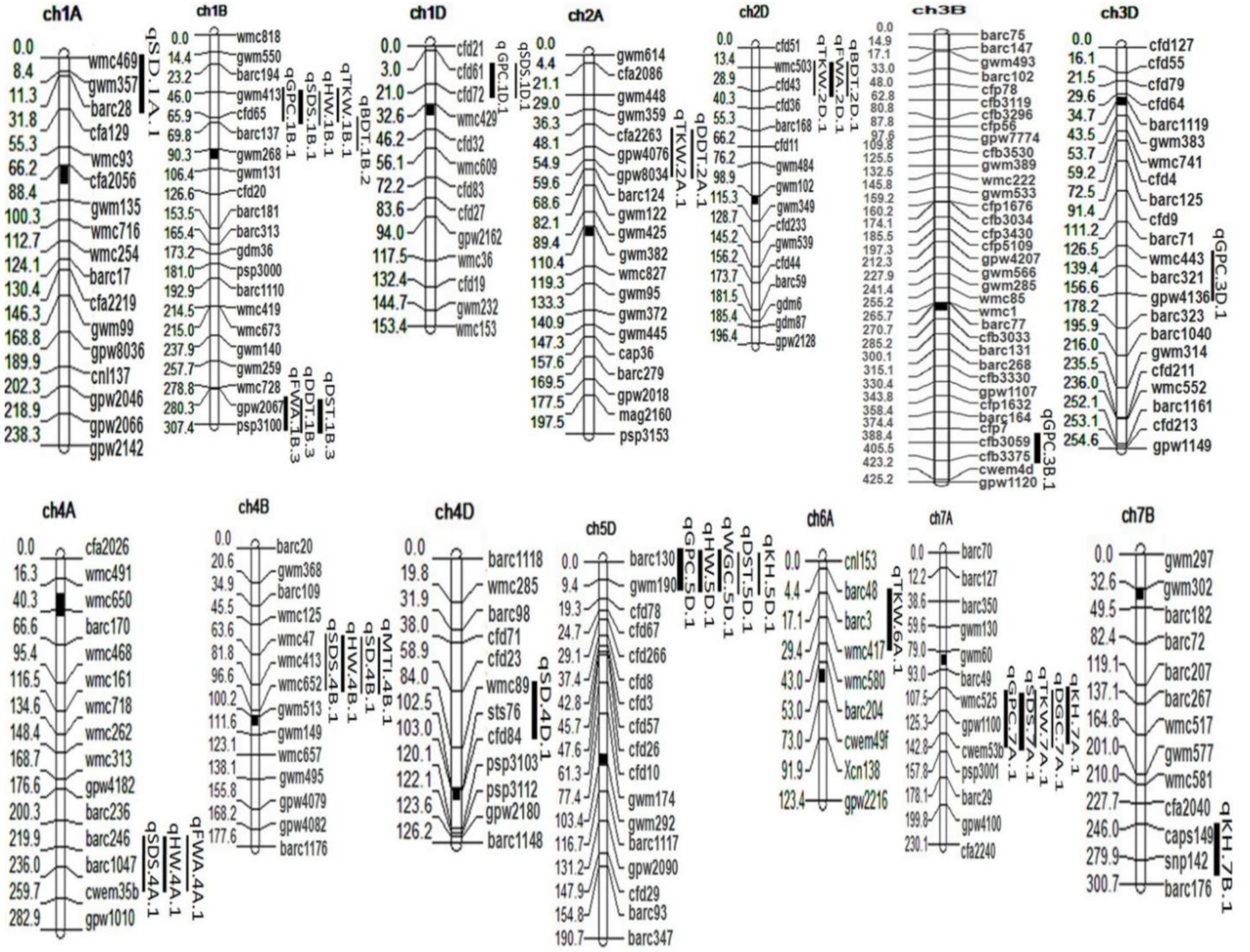

Figure 3 The distribution of quantitative trait loci (QTLs) associated with grain quality traits in the wheat recombinant inbred line (RIL) population (Adapted from Goel et al., 2019)

Image caption: The vertical bars represent the confidence intervals of QTLs on different chromosomes, with chromosome numbers indicated on the left side of the figure; The color bands on each chromosome denote different QTLs, with color variations potentially indicating QTL differences under various traits or environmental conditions; This distribution map provides visual information for understanding the relative positions of each QTL within the genome and their potential interactions, aiding further genetic analysis and variety improvement efforts (Adapted from Goel et al., 2019)

Another study utilized a RIL population from the cross between Taejoong and Keumkang, identifying eight QTLs for yield potential traits such as days to heading date, spike length, tiller number, and length of center rachis (Kang et al., 2020). These studies highlight the effectiveness of RIL populations in uncovering genetic loci that contribute to important agronomic traits in wheat.

4.2 Use of advanced statistical methods

The application of advanced statistical methods in QTL mapping has significantly enhanced the precision and accuracy of detecting QTLs. These methods have evolved to handle the complexity of genetic data and the multifaceted nature of traits controlled by multiple genes. These methods include Interval Mapping, Composite Interval Mapping, and Multiple-trait Composite Interval Mapping.

4.2.1 Interval mapping

Interval Mapping (IM) is a method that estimates the position and effect of QTLs within a defined interval between genetic markers. Interval mapping is one of the foundational techniques in QTL analysis. This method scans the genome at regular intervals to identify regions associated with phenotypic variation. This method was employed in a study that mapped QTLs for root traits in a RIL population of hexaploid wheat. In the study by Li et al. (2023), the interval mapping (IM) method was used to physically locate quantitative trait loci (QTLs) related to root traits in hexaploid wheat. By crossing two wheat varieties, Spica and Maringa, which exhibit significantly different root morphologies, a recombinant inbred line (RIL) population was generated and evaluated under controlled conditions. Using the 90K SNP chip for genotyping these lines, an average of 7.5 QTLs per trait were identified. The detected QTLs were then compared with the Chinese Spring wheat reference genome to determine specific genes and genomic regions associated with root traits such as root dry weight and root diameter (Li et al. 2023). The use of IM allowed for the precise localization of QTLs associated with root architecture, which is crucial for nutrient and water absorption.

4.2.2 Composite interval mapping

Composite interval mapping (CIM) is an advanced genetic mapping technique frequently used for the precise localization of quantitative trait loci (QTL). CIM combines the fundamental principles of interval mapping (IM) with multiple regression analysis, which allows it to effectively control for genetic background noise, thereby enhancing the accuracy and power of QTL detection. In the study by Li et al. (2020), composite interval mapping (CIM) was employed by utilizing a high-density genetic map in conjunction with bulked segregant RNA sequencing (BSR-Seq) to identify quantitative trait loci (QTL) related to wheat quality traits. The CIM method allows researchers to more precisely locate and validate QTL by leveraging the increased marker density. Through this approach, 30 QTLs were discovered, explaining up to 47.99% of the phenotypic variation for traits such as falling number (FN), grain protein content (GPC), grain hardness (GH), and starch pasting characteristics.This composite interval mapping technique, by narrowing confidence intervals and improving the precision of QTL detection, is of significant importance for the genetic improvement of wheat quality traits. It allows researchers to validate the stability and effects of QTL across multiple environments, thereby enabling more effective molecular marker-assisted selection in wheat breeding.

4.2.3 Multiple-trait composite interval mapping

Multiple-trait Composite Interval Mapping (MCIM) extends CIM by simultaneously analyzing multiple traits, which can increase the power to detect QTLs and provide insights into the genetic correlations between traits. The study by Ilyas et al. (2020) focused on identifying quantitative trait loci (QTL) for physiological and biochemical traits of wheat under salt stress conditions (Figure 4). The research utilized a recombinant inbred line (RIL) population derived from a cross between the salt-tolerant variety Pasban90 and the salt-sensitive variety Frontana. The aim was to identify specific genomic regions associated with the plant's response to salinity, including traits such as relative water content, membrane stability index, chlorophyll content, and ion concentrations (sodium, potassium, chloride).

In this study, the multi-trait composite interval mapping (MCIM) method was applied to locate QTLs for wheat physiological and biochemical traits under salt stress conditions. This method allows researchers to consider the genetic correlations and interactions among multiple traits simultaneously, leading to more precise identification of QTLs controlling these traits. Using a linkage map constructed with 202 polymorphic SSR markers, the study identified a total of 60 QTLs. The MCIM approach helped uncover both major and minor QTLs associated with wheat's response to salt stress.

Applying this method is crucial for understanding how plants respond to environmental stress at the genomic level, particularly in identifying key genomic regions that enhance crop tolerance to salt stress. By using MCIM, the study not only mapped individual QTLs but also analyzed the genetic interactions between different QTLs, providing practical insights for future marker-assisted selection to breed salt-tolerant wheat varieties. This integrated multi-trait analysis approach offers a powerful tool for crop improvement, enhancing the environmental Adaptedability and yield of essential crops like wheat.

These case studies and the application of advanced statistical methods underscore the progress and challenges in QTL mapping in wheat. The identification of QTLs through these approaches provides valuable insights for marker-assisted selection and the development of superior wheat cultivars.

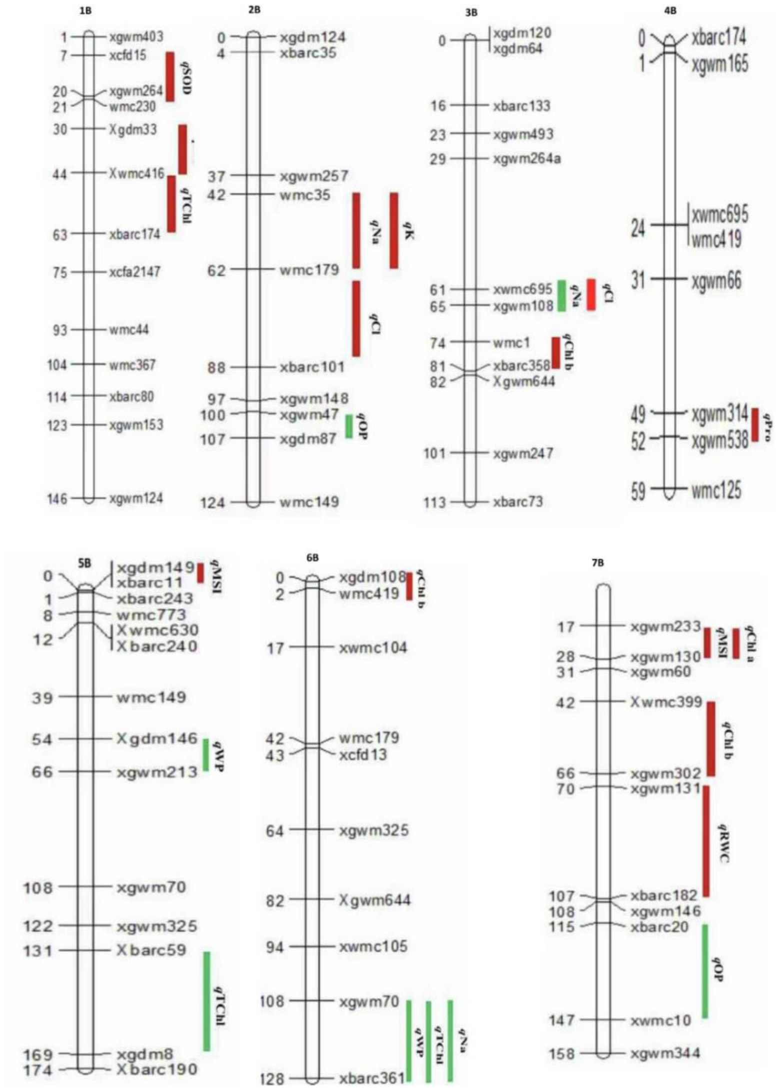

Figure 4 The distribution of quantitative trait loci (QTL) for physiological and biochemical traits on the B genome of the Pasban90/Frontana recombinant inbred lines (RILs) of wheat (Adapted from Ilyas et al., 2020)

Image caption: The horizontal axis represents the different chromosomes of the B genome, ranging from 1B to 7B, while the vertical axis indicates the relative positions of the QTLs; Each QTL is marked by colored segments or points, with different colors representing various physiological and biochemical traits, such as chlorophyll content, water potential, and ion concentrations; The localization of these QTLs helps to identify genomic regions that play crucial roles in regulating responses to salt stress, providing valuable insights for breeding salt-tolerant wheat varieties (Adapted from Ilyas et al., 2020)

5 Lessons Learned

5.1 Challenges in QTL mapping

5.1.1 Environmental interactions

One of the major challenges in QTL mapping is the interaction between genetic loci and environmental conditions. Environmental factors such as temperature, soil type, and moisture levels can significantly influence the expression of traits, leading to variations in QTL effects across different environments. This genotype-by-environment interaction makes it difficult to identify QTLs that are consistently expressed, which is essential for their effective use in breeding programs. For instance, protein- and starch-related quality traits in wheat are heavily influenced by environmental conditions, making it difficult to consistently identify QTLs across different environments (Guo et al., 2020). Similarly, the phenotypic variance explained (PVE) by QTLs for traits such as falling number, grain protein content, and grain hardness can vary significantly across different environmental conditions (Li et al., 2020). This variability necessitates the need for multi-environment trials to ensure the stability and reliability of identified QTLs.

5.1.2 Genetic background effects

The genetic background of the mapping population also poses a significant challenge in QTL mapping. The genetic background refers to the overall genetic makeup of an organism, which can modulate the effects of individual QTLs. QTLs identified in one genetic background may not have the same effect in another due to differences in genetic interactions. This phenomenon complicates the transfer of QTLs across different wheat varieties and can limit the applicability of QTLs identified in specific mapping populations (Xu et al., 2023). The effects of QTLs can be masked or modified by the genetic background, leading to difficulties in detecting and validating QTLs. For example, in a study mapping QTLs for salt stress tolerance, it was found that the B and D genomes of wheat contributed more significantly to salinity tolerance, indicating that the genetic background plays a crucial role in the expression of these traits (Ilyas et al., 2019). Additionally, the co-localization of QTLs for different traits, such as grain yield and micronutrient content, further complicates the identification of specific QTLs due to the pleiotropic effects of certain genomic regions (Shariatipour et al., 2021).

5.2 Strategies for overcoming challenges

To address these challenges, researchers have developed several strategies that enhance the reliability and applicability of QTL mapping in wheat.

5.2.1 Integrative approaches

To overcome the challenges posed by environmental interactions and genetic background effects, integrative approaches that combine multiple mapping techniques and data sources are essential. For instance, the use of meta-QTL analysis allows for the consolidation of QTLs from multiple studies, leading to the identification of more stable and reliable QTLs (Shariatipour et al., 2021). This approach reduces the confidence interval of QTLs and helps in pinpointing candidate genes with greater accuracy. Additionally, combining QTL mapping with transcriptomic data, such as bulked segregant RNA-seq (BSR-Seq), can provide insights into the underlying genetic mechanisms and validate the effects of identified QTLs (Li et al., 2020).

5.2.2 Use of high-density maps

The use of high-density genetic maps significantly enhances the resolution and accuracy of QTL mapping. High-density maps constructed using advanced genotyping technologies, such as SNP arrays and specific-locus amplified fragment sequencing (SLAF-seq), enable the identification of QTLs with higher precision (Li et al., 2020; Ren et al., 2021). For example, a high-density genetic map with 11,583 markers was used to map QTLs for kernel-related traits, resulting in the identification of stable QTLs across multiple environments (Ren et al., 2021). Similarly, the use of a Wheat50K SNP array-derived map facilitated the mapping of QTLs for plant height and grain traits, highlighting the importance of high-density maps in QTL studies (Lv et al., 2021).

While challenges such as environmental interactions and genetic background effects complicate QTL mapping, strategies like integrative approaches and the use of high-density maps provide effective solutions. These advancements have enhanced the reliability and applicability of QTL mapping, contributing to the ongoing improvement of wheat varieties.

6 Future Directions in QTL Mapping

6.1 Integration with genomic selection

The integration of QTL mapping with genomic selection (GS) represents a promising future direction for enhancing wheat breeding programs. Genomic selection leverages genome-wide markers to predict the genetic value of individuals, thereby accelerating the breeding cycle. By combining QTL mapping with GS, breeders can more accurately identify and select for desirable traits. For instance, the high-density genetic maps and identified QTLs for traits such as grain protein content, grain hardness, and starch pasting properties (Li et al., 2020) can be incorporated into GS models to improve the precision of selection. Additionally, the meta-QTLs identified through comparative genomics (Shariatipour et al., 2021) provide stable targets that can be integrated into GS frameworks, enhancing the reliability of trait prediction across different environments.

6.2 Enhancing precision and efficiency

Advancements in high-throughput sequencing and genotyping technologies have significantly improved the precision and efficiency of QTL mapping. High-resolution genome-wide association studies (GWAS) have identified numerous QTLs with narrow confidence intervals, facilitating the discovery of candidate genes (Pang et al., 2020). For example, the identification of 395 QTLs for various agronomic traits in wheat (Pang et al., 2020) underscores the potential of GWAS to enhance mapping resolution. Furthermore, the development of high-density genetic maps, such as those containing over 10,000 loci (Guo et al., 2020), allows for more precise localization of QTLs. These technological advancements enable the fine-mapping of QTLs and the identification of causal genes, which can be directly targeted in breeding programs to improve trait performance.

6.3 Expanding to other crops

While significant progress has been made in QTL mapping for wheat, expanding these methodologies to other crops can provide broader agricultural benefits. The genetic and genomic tools developed for wheat can be Adapteded for use in other cereal crops, such as rice and maize, which share genomic collinearity with wheat (Shariatipour et al., 2021). For instance, the identification of orthologous MQTLs in wheat, rice, and maize (Shariatipour et al., 2021) highlights the potential for cross-species application of QTL mapping results. Additionally, the domestication and improvement of perennial crops like intermediate wheatgrass (Larson et al., 2019) can benefit from the QTL mapping techniques refined in wheat research. By applying these methods to a wider range of crops, researchers can accelerate the breeding of high-yielding, stress-tolerant varieties, thereby enhancing global food security.

7 Concluding Remarks

Quantitative Trait Loci (QTL) mapping has revolutionized wheat breeding by providing a detailed understanding of the genetic basis of important agronomic traits. Over the past few decades, significant strides have been made in identifying and utilizing QTLs for grain yield, quality, and stress tolerance. These advancements have been underpinned by methodological improvements, such as the development of high-density genetic maps, the application of advanced statistical methods, and the use of recombinant inbred line (RIL) populations.

Despite the successes, QTL mapping in wheat faces challenges such as environmental interactions and genetic background effects, which can complicate the identification and application of QTLs. However, integrative approaches that combine QTL mapping with other genomic tools, such as genomic selection, and the use of advanced technologies, like machine learning and AI, offer promising solutions to these challenges.

The future of QTL mapping in wheat looks bright, with opportunities to enhance precision and efficiency in identifying key genetic loci. Moreover, the lessons learned from wheat can be extended to other crops, broadening the impact of these genetic tools on global agriculture. By continuing to refine and apply QTL mapping techniques, researchers can develop more resilient and high-performing wheat varieties, ultimately contributing to global food security.

In conclusion, QTL mapping has proven to be a powerful tool in wheat genetics and breeding. The integration of QTL mapping with advanced genomic technologies holds great promise for the future of wheat improvement, enabling the development of high-yielding, high-quality, and stress-tolerant wheat varieties. As the field continues to evolve, the integration of cutting-edge technologies and collaborative efforts across crops will further unlock the genetic potential of wheat, paving the way for a new era of crop improvement.

Acknowledgments

Thank you to the two anonymous peer reviewers for reviewing the paper.

Conflict of Interest Disclosure

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

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