GenBreed Publisher®

Molecular Plant Breeding 2025, Vol.16, No.1, 24-34
http://genbreedpublisher.com/index.php/mpb

Research Insight **Open Access**

Gene Mapping of Mechanization-Friendly Traits in Maize Based on SNP Markers and Breeding for Mechanical Adaptation

Yimiao Zhao, Yan Bao ✉, Lan Zhou, Baihe Zhang, Xiangjun Wang
College of Agriculture, Jilin Agricultural Science and Technology University, Jilin, 132101, Jilin, China
✉ Corresponding email: baoyan0302@126.com

Molecular Plant Breeding, 2024, Vol.16, No.1 doi: 10.5376/mpb.2025.16.0003
Received: 15 Dec., 2024
Accepted: 20 Jan., 2025
Published: 29 Jan., 2025

Preferred citation for this article:
Zhao Y.M., Bao Y., Zhou L., Zhang B.H., and Wang W.J., 2025, Gene mapping of mechanization-friendly traits in maize based on snp markers and breeding for mechanical adaptation, Molecular Plant Breeding, 16(1): 24-34 (doi: 10.5376/mpb.2025.16.0003)

Abstract This study focused on the use of SNP markers for gene mapping of maize mechanization-friendly traits to enhance its mechanized adaptability in agricultural practices, as well as identifying and characterizing quantitative trait loci (QTLS), such as plant height, ear position, and stem strength lamps, that are associated with improving maize compatibility with mechanized agriculture. The findings reveal important QTLS associated with these traits, providing a basis for marker-assisted selection, and also highlight the potential for integrating these markers into breeding programs to improve yield and efficiency in mechanized environments.

Keywords Mechanization-friendly traits; Maize breeding; SNP markers; Gene mapping; Marker-assisted selection

1 Introduction

Mechanization in maize cultivation has become increasingly important as it offers numerous benefits, including increased efficiency, reduced labor costs, and improved crop management. The adoption of mechanized farming practices is essential to meet the growing demand for maize, driven by its significance as a staple food and industrial crop. Mechanization encompasses various aspects such as planting, irrigation, pest control, and harvesting, all of which contribute to higher productivity and sustainability in maize farming (Su et al., 2017; Tomkowiak et al., 2021).

Mechanization-friendly traits in maize are crucial for optimizing the efficiency of mechanized farming operations. Traits such as uniform plant height, sturdy stalks, and synchronized flowering times are essential for the effective use of machinery in planting and harvesting. These traits not only facilitate the use of mechanical equipment but also enhance the overall yield and quality of the maize crop. The identification and incorporation of such traits through advanced breeding techniques, including the use of single-nucleotide polymorphisms (SNPs) and quantitative trait loci (QTL) mapping, can significantly improve the adaptability of maize to mechanized farming systems (Zhang et al., 2020; Chen et al., 2021; Shikha et al., 2021).

In this study, SNP markers were used to locate genes associated with mechanization-friendly traits, and high-throughput genotyping techniques such as DArTseq and genotyping sequencing (GBS) were used to identify key genetic loci affecting traits conducive to mechanical adaptation. This study focuses on traits such as plant structure, grain size and root structure that are critical to efficient mechanized farming. This study aims to provide valuable insights into developing marker-assisted selection and breeding programs for corn varieties suitable for mechanized cultivation, improving mechanized compatibility of corn through precise gene mapping and breeding strategies, and ultimately helping to improve agricultural productivity and sustainability.

2 Mechanization-Friendly Traits in Maize

2.1 Definition and significance of mechanization-friendly traits

Mechanization-friendly traits in maize refer to specific plant characteristics that facilitate the use of mechanical equipment for planting, cultivation, and harvesting. These traits are crucial for improving the efficiency and effectiveness of agricultural practices, reducing labor costs, and increasing overall productivity.

Mechanization-friendly traits are particularly significant in large-scale farming operations where manual labor is impractical and costly. They also contribute to uniformity in crop management and can enhance the resilience of maize plants to environmental stresses.

2.2 Key traits associated with mechanical adaptation

Several key traits are associated with mechanical adaptation in maize, including plant height, ear height, and ear architecture. Plant height is a critical trait that influences lodging resistance and planting density. Lower plant height is generally preferred for mechanized farming as it reduces the risk of lodging and allows for higher planting densities, which can lead to increased yields (Yang et al., 2014). Ear height, the position of the ear on the plant, is another important trait. Lower ear height is advantageous for mechanical harvesting as it reduces the likelihood of ear loss and ensures more efficient harvesting (Zhou et al., 2016; Longmei et al., 2021; Yin et al., 2022). The structure and orientation of the ear can affect how easily it can be harvested by machines. Traits such as ear angle and husk cover are important for ensuring that ears are easily accessible and can be cleanly removed by harvesting equipment (Wallace et al., 2016; Ledesma et al., 2023).

2.3 Impact of these traits on agricultural practices and yield

The mechanization-friendly traits of plant height, ear height, and ear architecture have significant impacts on agricultural practices and yield. Lower plant height and ear height contribute to better lodging resistance, which is crucial for maintaining plant stability and reducing crop losses due to plants falling over (Zhou et al., 2016). Traits that allow for higher planting densities can lead to increased yields per unit area. This is particularly important in mechanized farming systems where maximizing land use efficiency is a key goal (Yang et al., 2014; Yin et al., 2022). Optimized ear height and architecture facilitate more efficient mechanical harvesting, reducing the time and labor required for this process. This can lead to cost savings and higher overall productivity (Wallace et al., 2016; Longmei et al., 2021). Mechanization-friendly traits contribute to uniformity in crop management practices, making it easier to apply inputs such as fertilizers and pesticides uniformly across the field, which can enhance crop health and yield (Karnatam et al., 2023; Ledesma et al., 2023).

3 Genetic Basis of Mechanization-Friendly Traits

3.1 Identification of candidate genes linked to mechanization-friendly traits

The identification of candidate genes linked to mechanization-friendly traits in maize has been significantly advanced through various mapping techniques. For instance, in silico mapping has proven effective in detecting associations that are repeatable across different populations, identifying significant marker loci for traits such as plant height and grain moisture (Parisseaux and Bernardo, 2004). Additionally, the use of ultra-high density linkage maps and genome-wide composite interval mapping (GCIM) has led to the identification of stable QTLs and differentially expressed genes (DEGs) associated with yield-related traits, including grain weight (Zhao and Su, 2019). Furthermore, combined linkage and association mapping have revealed numerous candidate genes regulating kernel size traits, which are directly correlated with grain yield (Liu et al., 2019).

3.2 Role of quantitative trait loci (QTL) in trait expression

Quantitative trait loci (QTL) play a crucial role in the expression of mechanization-friendly traits in maize. QTL mapping has identified multiple loci associated with key traits such as grain yield, plant height, and ear height. For example, a study using a population of 400 F2:3 lines identified 13 distinct QTLs for grain yield, plant height, and ear height, explaining a significant portion of the phenotypic variance (Sibov et al., 2004). Another study combining QTL mapping and genome-wide association studies (GWAS) identified 100 QTLs and 138 SNPs controlling yield-related traits, with several QTLs showing pleiotropic effects across different environments (Zhang et al., 2020). These findings underscore the importance of QTLs in understanding the genetic architecture of mechanization-friendly traits and their potential for marker-assisted selection in breeding programs.

3.3 Genetic diversity and its importance in trait enhancement

Genetic diversity is paramount for the enhancement of mechanization-friendly traits in maize. The use of diverse genetic populations in QTL mapping studies has revealed a wide range of loci associated with important agronomic traits. For instance, a study on tropical maize identified QTLs for grain yield, plant height, and ear height across multiple environments, highlighting the genetic variation present in tropical maize populations (Sibov et al., 2004). Additionally, the integration of high-density SNP markers through genotyping-by-sequencing (GBS) has facilitated the construction of detailed genetic linkage maps, enabling the identification of numerous QTLs associated with yield traits (Su et al., 2017). This genetic diversity is crucial for the development of robust maize varieties that can adapt to mechanized farming practices, ultimately leading to improved crop performance and yield stability.

4 SNP Markers and Their Application in Gene Mapping

4.1 Overview of single nucleotide polymorphisms (SNPs) as genetic markers

Single nucleotide polymorphisms (SNPs) are the most frequent type of genetic variation found within genomes. They occur when a single nucleotide in the genome sequence is altered. SNPs are abundant and evenly distributed across the genomes of most plant species, making them ideal markers for genetic research. Their high frequency and distribution allow for detailed genetic mapping and association studies, which are crucial for understanding the genetic basis of complex traits in crops like maize (Rafalski, 2002; Jones et al., 2009; Yan et al., 2010).

4.2 Methods for SNP marker identification and validation

The identification and validation of SNP markers involve several steps, starting from sequencing and SNP discovery to marker design and validation. Various high-throughput platforms and technologies have been developed to facilitate this process. Sequencing-by-synthesis technologies, such as Illumina sequencing, enable efficient genome-wide SNP discovery by reducing genome complexity and focusing on informative regions. Complexity reduction of polymorphic sequences (CRoPS) reduces the complexity of the genome, allowing for the identification of informative SNPs between genetically distinct lines (Mammadov et al., 2010). GoldenGate assay allows for the rapid and simultaneous genotyping of up to a million SNP markers, providing high accuracy and low error rates (Yan et al., 2010). KASP SNP markers developed from RNA-Seq data, these markers are used for automatic genotyping and are highly polymorphic, making them valuable for map-based cloning and marker-assisted selection (Chen et al., 2021). Validation of SNP markers typically involves in silico analysis and experimental validation using platforms like the Illumina GoldenGate assay, which ensures the accuracy and polymorphism of the identified SNPs (Mammadov et al., 2010; Chen et al., 2021).

4.3 Case studies of successful SNP mapping in maize

Several studies have demonstrated the successful application of SNP markers in maize gene mapping. Researchers mined 1 088 loci sequenced across 60 public inbreds used in maize breeding, identifying SNPs that were amenable to marker design. These SNPs were mapped on the IBM2 high-resolution genetic map, showing high colinearity with the genetic nested association map (Jones et al., 2009). A custom GoldenGate assay containing 1 536 SNPs was developed and used to genotype two recombinant inbred line populations and a panel of diverse inbred lines. This study successfully integrated SNP markers with previously mapped simple sequence repeat markers to construct a high-density linkage map (Yan et al., 2010). Using the DArTseq method, researchers identified 49 911 polymorphisms, including 16 459 SNP markers, which were associated with various morphological traits in maize. This method allowed for the identification of markers linked to important agronomic traits, facilitating marker-assisted selection (Tomkowiak et al., 2021). These case studies highlight the effectiveness of SNP markers in genetic mapping and their potential to enhance maize breeding programs by enabling the precise identification of genes associated with desirable traits.

5 Breeding Strategies for Mechanical Adaptation

5.1 Traditional breeding methods for enhancing mechanization-friendly traits

Traditional breeding methods have long been employed to enhance mechanization-friendly traits in maize. These methods primarily rely on phenotypic selection, where plants exhibiting desirable traits are selected and bred over multiple generations. This approach, while effective, is often time-consuming and labor-intensive. Traditional breeding has been successful in improving traits such as plant height, ear placement, and stalk strength, which are crucial for mechanical harvesting. However, the process is limited by the genetic variability present in the breeding population and the environmental influence on phenotypic expression.

5.2 Marker-assisted selection (MAS) and its application in breeding programs

Marker-assisted selection (MAS) has revolutionized plant breeding by integrating molecular markers with traditional breeding techniques. MAS allows for the selection of plants carrying desirable traits based on their genetic makeup rather than solely on phenotypic expression. This method significantly accelerates the breeding process and increases the precision of selecting for complex traits.

MAS has been particularly effective in improving traits that are difficult to score phenotypically, such as disease resistance and abiotic stress tolerance (Zhou and Xu, 2024). For instance, MAS has been used to enhance drought adaptation in maize through marker-assisted backcrossing (MABC), which involves the introgression of favorable alleles at specific target regions (Ribaut and Ragot, 2006). Additionally, the development of high-throughput genotyping technologies, such as genotyping-by-sequencing (GBS), has further enhanced the efficiency of MAS by enabling the simultaneous discovery and genotyping of single nucleotide polymorphisms (SNPs) in large crop genomes (He et al., 2014).

The application of MAS in maize breeding has led to significant improvements in yield, stress tolerance, and other agronomically important traits. For example, the use of MAS in wheat breeding has shown promise in improving complex polygenic traits through advanced strategies like marker-assisted recurrent selection and genome-wide selection (Gupta et al., 2010).

5.3 Genomic selection as a modern approach to breeding

Genomic selection (GS) represents a modern approach to plant breeding that leverages genome-wide marker data to predict the breeding value of individuals. Unlike MAS, which focuses on specific markers linked to target traits, GS uses a large number of markers distributed across the entire genome to capture the genetic variance associated with complex traits.

GS has the potential to further accelerate the breeding process by enabling the selection of superior genotypes at an early stage, even before phenotypic traits are expressed. This approach has been facilitated by advancements in next-generation sequencing technologies and the development of dense SNP marker panels. For instance, the use of kompetitive allele specific PCR (KASP) SNP markers developed from RNA-Seq data has provided a valuable resource for map-based cloning and GS in maize (Chen et al., 2021).

The integration of GS into breeding programs has shown promising results in improving traits such as kernel size, yield, and stress tolerance. By combining linkage and association mapping, researchers have identified numerous SNPs and quantitative trait loci (QTLs) associated with key agronomic traits, providing a robust foundation for GS (Figure 1) (Liu et al., 2019). The continuous improvement of genomic prediction models and the increasing availability of high-quality genomic data are expected to further enhance the efficiency and accuracy of GS in maize breeding.

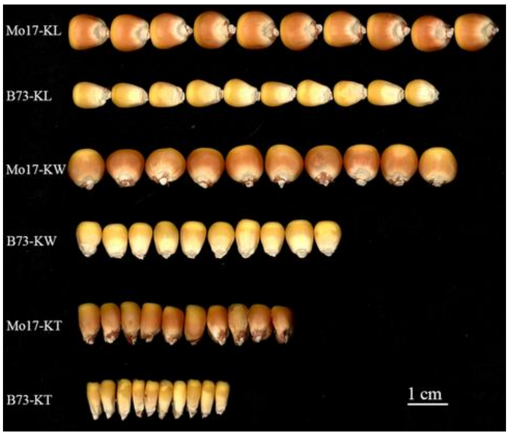

Figure 1 Phenotypes of kernel size traits and variations of kernel size between two parental lines of the IBM Syn 10 DH population (Adopted from Liu et al., 2019)

Image caption: Phenotypes of KL, KW and KT illustrated with 10 kernels of the two parental lines in IBM Syn 10 DH population. Bar = 1 cm (Adopted from Liu et al., 2019)

In conclusion, the adoption of modern breeding strategies, including MAS and GS, has significantly advanced the development of mechanization-friendly traits in maize. These approaches offer a more efficient and precise means of selecting for complex traits, ultimately contributing to the improvement of maize varieties suited for mechanical adaptation.

6 Challenges in Breeding for Mechanization-Friendly Traits

6.1 Limitations of current breeding practices

Current breeding practices in maize often focus on yield and disease resistance, with less emphasis on traits that facilitate mechanization. Traditional breeding methods are time-consuming and labor-intensive, making it difficult to rapidly develop varieties that meet the specific needs of mechanized farming. Additionally, the reliance on phenotypic selection can be inefficient due to the complex nature of mechanization-friendly traits, which are often influenced by multiple genes and environmental factors (Su et al., 2017; Liu et al., 2019).

6.2 Genetic complexities and trait interactions

Mechanization-friendly traits in maize, such as uniform plant height, ear placement, and stalk strength, are controlled by complex genetic interactions. These traits often exhibit pleiotropy, where a single gene affects multiple traits, complicating the breeding process (Hou et al., 2024). For instance, the genetic basis of yield-related traits involves numerous quantitative trait loci (QTL) and single nucleotide polymorphisms (SNPs), which interact in intricate ways (Romay et al., 2013; Yang et al., 2014; Zhang et al., 2020). The identification and manipulation of these genetic components require advanced genomic tools and techniques, such as genome-wide association studies (GWAS) and genomic prediction, to unravel the underlying genetic architecture (Ertiro et al., 2020; Sethi et al., 2023).

6.3 Environmental factors affecting trait expression

Environmental factors play a significant role in the expression of mechanization-friendly traits. Variability in soil type, climate, and management practices can lead to inconsistent trait expression, making it challenging to select and stabilize these traits across different environments. Studies have shown that traits like kernel size and nitrogen use efficiency are highly influenced by environmental conditions, which can mask the genetic potential of the plants (Liu et al., 2019; Ertiro et al., 2020; Chen et al., 2021). This environmental dependency necessitates multi-environment trials and sophisticated statistical models to accurately assess and select for mechanization-friendly traits (Yuan et al., 2019). By addressing these challenges through the integration of advanced genomic tools and multi-environment testing, breeding programs can more effectively develop maize varieties that are well-suited for mechanized agriculture.

7 Advanced Genomic Techniques in Trait Mapping

7.1 Use of genome-wide association studies (GWAS) in trait identification

Genome-wide association studies (GWAS) have become a cornerstone in identifying genetic loci associated with complex traits in maize. By leveraging high-density SNP markers, GWAS can dissect the genetic architecture of various agronomic traits. For instance, a study expanded an association panel to 513 inbred lines and identified numerous loci for traits such as plant height using both mixed linear models (MLM) and the Anderson-Darling (A-D) test, highlighting the utility of GWAS in maize genetics and breeding (Yang et al., 2014).

Another study utilized a large maize SNP array for diversity analysis and high-density linkage mapping, demonstrating the array's effectiveness in genetic mapping and validating the B73 reference genome (Ganal et al., 2011). Additionally, GWAS has been instrumental in understanding the genetic basis of yield-related traits, as evidenced by the identification of 138 SNPs associated with these traits in maize (Zhang et al., 2020). These examples underscore the power of GWAS in linking genotypic variations to phenotypic differences, thereby facilitating the identification of candidate genes for breeding programs (Figure 2) (Xiao et al., 2017; Shikha et al., 2021).

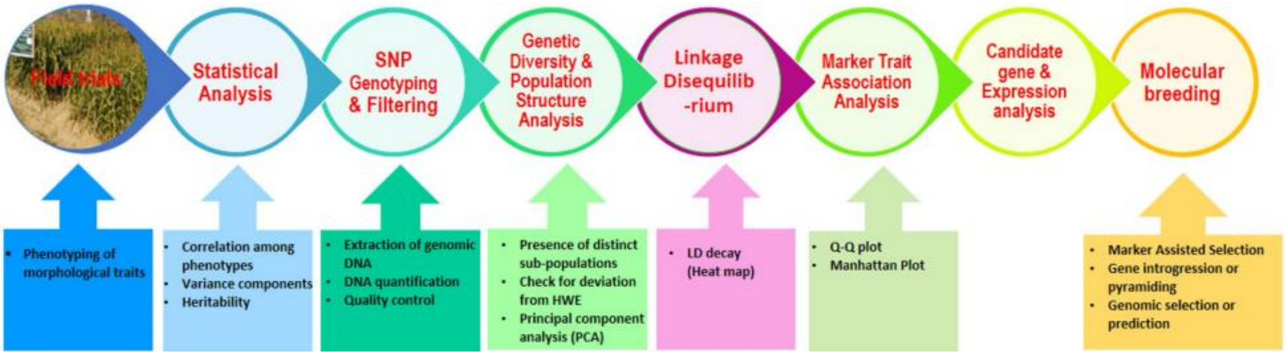

Figure 2 A generalized procedure of genome-wide association study (Adopted from Shikha et al., 2021)

7.2 Integration of multi-omics approaches for comprehensive trait analysis

The integration of multi-omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, offers a comprehensive framework for trait analysis in maize. By combining data from various omics layers, researchers can gain a holistic understanding of the molecular mechanisms underlying complex traits. For example, the use of RNA, protein, and metabolite-based omics studies in GWAS has been discussed as a means to uncover hidden causes of phenotypic variation (Xiao et al., 2017). This integrative approach allows for the identification of key regulatory networks and pathways that contribute to trait expression. Moreover, the combination of QTL mapping and GWAS has been shown to enhance the resolution of trait mapping, as demonstrated by the identification of significant SNPs and candidate genes for yield-related traits in maize (Zhang et al., 2020). Such integrative strategies are crucial for advancing our understanding of trait architecture and improving the efficiency of molecular breeding.

7.3 Future prospects of genomic technologies in maize breeding

The future of genomic technologies in maize breeding looks promising, with several advancements on the horizon. The continuous development of high-density SNP arrays and next-generation sequencing technologies will further enhance the resolution and accuracy of GWAS, enabling the identification of novel loci associated with important agronomic traits (Ganal et al., 2011; Xiao et al., 2017). Additionally, the adoption of machine learning methods for dimensionality reduction and the use of advanced statistical models will improve the prediction accuracy of genomic selection (Susmitha et al., 2023).

The integration of multi-omics data will also play a pivotal role in elucidating the complex genetic networks that govern trait expression, paving the way for more targeted and efficient breeding strategies. Furthermore, the use of joint-GWAS approaches, which combine data from multiple populations, will increase the statistical power of trait mapping and facilitate the discovery of rare and common genetic variants (Müller et al., 2018). These advancements will ultimately contribute to the development of maize varieties with enhanced yield, quality, and stress tolerance, addressing the global challenges of food security and climate change (Huang et al., 2010; Shikha et al., 2021).

8 Case Study: Breeding Mechanization-Friendly Maize Varieties

8.1 Overview of a successful breeding program focused on mechanization

A successful breeding program aimed at developing mechanization-friendly maize varieties involves the integration of advanced genetic mapping techniques and marker-assisted selection (MAS). One such program utilized high-density linkage maps and genome-wide association studies (GWAS) to identify quantitative trait loci (QTL) associated with key traits such as kernel size, yield, and root architecture. For instance, the use of genotyping-by-sequencing (GBS) technology enabled the discovery of over 29 000 high-quality SNPs, which were instrumental in constructing a detailed genetic linkage map and identifying 28 QTLs associated with yield traits (Su et al., 2017). Additionally, the program focused on root architectural traits, which are crucial for improving water and nutrient use efficiency, thereby enhancing plant adaptation under suboptimal conditions (Figure 3) (Moussa et al., 2021).

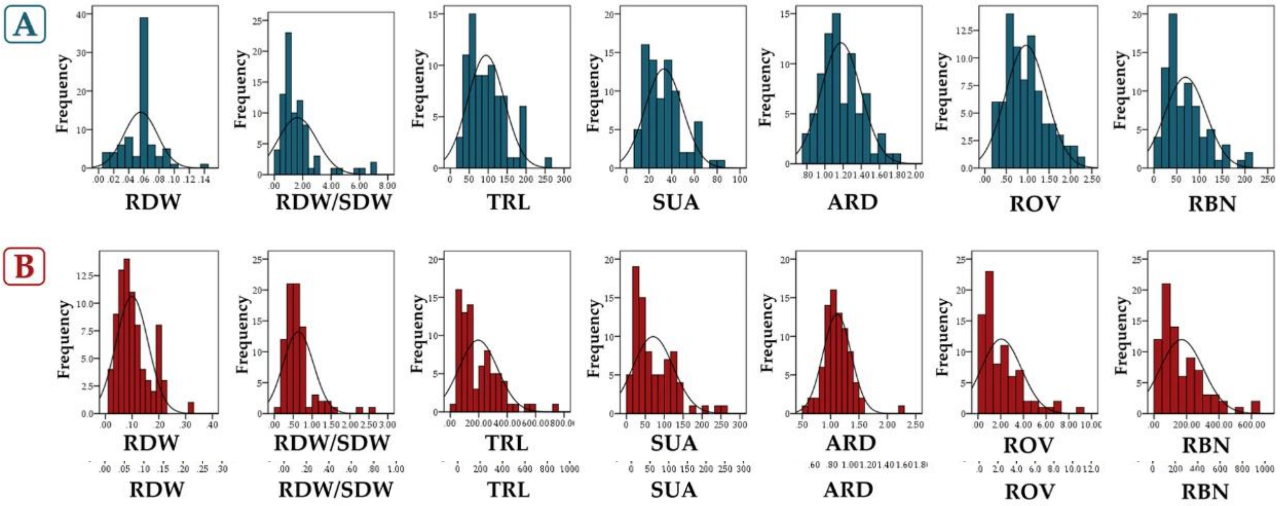

Figure 3 Distribution frequencies of the seven seedling root traits in the GWAS population across three stages (Adopted from Moussa et al., 2021)

Image caption: A, B, and C represent the results from V1 (in turquoise color), V2 (in red color), and V3 (in blue color) stages, respectively). RDW = root dry weight; RDW/SDW = root per shoot dry weight; TRL = total root length; SUA = surface area; ARD = average root diameter; ROV = root volume; RBN = root branching number (Adopted from Moussa et al., 2021)

8.2 Key outcomes and benefits of the developed varieties

The breeding program led to the development of maize varieties with several mechanization-friendly traits. The identification of QTLs associated with yield traits such as kernel weight, ear length, and grain weight per plant facilitated the development of high-yielding maize varieties. For example, QTLs identified by the composite interval mapping (CIM) method accounted for 6.4% to 19.7% of the phenotypic variation in yield traits (Su et al., 2017). The program successfully identified significant SNPs associated with root traits, which are essential for efficient water and nutrient uptake. This led to the development of maize varieties with robust root systems, enhancing their adaptability to mechanized farming practices (Moussa et al., 2021). The integration of meta-QTL analysis revealed breeding-friendly MQTLs that were associated with both quality and yield traits. These MQTLs were further validated and recommended for use in future breeding programs to develop biofortified, high-yielding maize varieties (Sethi et al., 2023).

8.3 Lessons learned and implications for future research

Several lessons were learned from this breeding program, which have important implications for future research. The use of high-resolution genetic mapping and GWAS proved to be highly effective in identifying key QTLs and SNPs associated with mechanization-friendly traits. Future research should continue to leverage these advanced tools to uncover the genetic basis of other important traits (Su et al., 2017; Liu et al., 2019). The coordination of multiple targets within a single breeding program is complex but essential. The successful identification of MQTLs that influence both yield and quality traits highlights the importance of multi-trait breeding approaches (Sethi et al., 2023). The functional verification of candidate genes associated with key traits is crucial for ensuring their effectiveness in breeding programs. Future research should prioritize the validation of identified genes through various approaches such as marker-assisted breeding, genetic engineering, and genome editing (Moussa et al., 2021). By incorporating these lessons, future breeding programs can continue to develop maize varieties that are well-suited for mechanized farming, ultimately contributing to increased agricultural productivity and sustainability.

9 Future Directions for Research and Breeding

9.1 Emerging trends in mechanization-friendly trait research

Recent advancements in high-throughput sequencing technologies and SNP marker development have significantly enhanced our ability to fine-map quantitative trait loci (QTL) and understand the genetic basis of mechanization-friendly traits in maize. The development of high-density polymorphic KASP SNP markers, as demonstrated by the identification of 71 311 KASP SNP markers from RNA-Seq data, provides a valuable resource for map-based cloning and marker-assisted selection (MAS) in maize breeding (Chen et al., 2021). Additionally, the use of genotyping-by-sequencing (GBS) technology has facilitated the construction of high-resolution linkage maps and the identification of numerous QTLs associated with yield traits, which are crucial for mechanization (Su et al., 2017). The integration of genome-wide association studies (GWAS) with advanced statistical models, such as the Anderson-Darling test, has further refined our understanding of the genetic architecture of complex traits, including those relevant to mechanization (Yang et al., 2014).

9.2 Potential for collaboration between breeders and technologists

The intersection of plant breeding and technological innovation presents a unique opportunity for enhancing mechanization in maize production. Collaboration between breeders and technologists can lead to the development of automated genotyping platforms, such as the KASP SNP markers, which enable high-throughput and accurate genotyping (Chen et al., 2021). Furthermore, the comprehensive genotyping of large maize germplasm collections using GBS technology underscores the potential for integrating diverse genetic resources into breeding programs (Romay et al., 2013). By leveraging the expertise of technologists in next-generation sequencing and data analysis, breeders can more effectively identify and select for traits that improve mechanization, such as plant architecture traits that facilitate high-density planting and mechanical harvesting (Ledesma et al., 2023).

9.3 Recommendations for enhancing mechanization in maize production

To enhance mechanization in maize production, several key recommendations can be made based on recent research findings. Utilize high-density SNP markers, such as those developed through KASP and GBS technologies, to fine-map QTLs and identify candidate genes associated with mechanization-friendly traits (Su et al., 2017; Chen et al., 2021). Employ GWAS combined with advanced statistical models, like the Anderson-Darling test, to dissect the genetic architecture of complex traits and improve the accuracy of trait selection (Yang et al., 2014). Incorporate diverse genetic resources from global germplasm collections into breeding programs to enhance genetic diversity and identify novel alleles that contribute to mechanization-friendly traits (Romay et al., 2013). Prioritize the selection of plant architecture traits that facilitate mechanization, such as reduced ear height, upright leaf angles, and optimized tassel branch number, which have been shown to improve adaptation to high planting density and mechanical harvesting (Ledesma et al., 2023). Encourage collaboration between plant breeders, geneticists, and technologists to develop and implement innovative breeding strategies and automated genotyping platforms that streamline the selection process for mechanization-friendly traits (Romay et al., 2013; Chen et al., 2021). By following these recommendations, maize breeding programs can more effectively develop varieties that are well-suited for mechanized agriculture, ultimately improving efficiency and productivity in maize production.

10 Concluding Remarks

This study has highlighted significant advancements in the genetic mapping of mechanization-friendly traits in maize using SNP markers. Key findings include the identification of numerous quantitative trait loci (QTLs) and single nucleotide polymorphisms (SNPs) associated with yield-related traits, kernel size, and other agronomic characteristics. For instance, meta-QTL analysis revealed 68 MQTLs across different genetic backgrounds and environments, with ten breeding-friendly MQTLs (BF-MQTLs) showing significant phenotypic variation and potential for future breeding programs. Additionally, combined linkage and association mapping identified 73 candidate genes regulating seed development, providing insights into the genetic architecture of kernel size traits. High-density linkage maps constructed using genotyping-by-sequencing (GBS) technology have further facilitated the identification of QTLs associated with yield traits, enhancing our understanding of the molecular basis of phenotypic variation. Genome-wide association studies (GWAS) have also been instrumental in identifying genomic regions associated with abiotic and biotic stress tolerance, improving the efficiency of marker-assisted selection in maize breeding.

Mechanization-friendly traits are crucial for sustainable maize production as they directly impact the efficiency and effectiveness of agricultural practices. Traits such as kernel size, plant architecture, and stress tolerance are essential for optimizing mechanical harvesting and reducing labor costs. For example, the identification of SNP markers related to morphological features such as plant height and ear position can aid in developing maize varieties that are better suited for mechanical harvesting. Moreover, understanding the genetic basis of these traits allows for the development of maize varieties that can withstand environmental stresses, thereby ensuring stable yields and food security. The integration of advanced breeding techniques, such as marker-assisted selection and genome editing, can accelerate the development of high-yielding, stress-tolerant maize varieties, contributing to sustainable agricultural practices.

While significant progress has been made in mapping mechanization-friendly traits in maize, several challenges and opportunities remain. One of the primary challenges is the complexity of polygenic traits and the need for high-resolution mapping to accurately identify and utilize beneficial alleles. The integration of multi-omics approaches, including transcriptomics and proteomics, can provide a more comprehensive understanding of the genetic and molecular mechanisms underlying these traits. Additionally, the development of high-throughput phenotyping platforms and advanced computational tools for data analysis will be essential for accelerating breeding programs. Future research should also focus on the validation and functional characterization of candidate genes to ensure their effectiveness in different environmental conditions. Collaborative efforts between researchers, breeders, and policymakers will be crucial in addressing these challenges and harnessing the full potential of mechanization-friendly traits for sustainable maize production.

Acknowledgments

The authors appreciate the two anonymous peer reviewers for their suggestions during the review process, which helped us to identify weaknesses in the study.

Funding

This work was jointly supported by the Science and Technology Development of Jilin Province (QTL) Mapping of Maize Resistance to Ear Rot Based on SNP Markers and Breeding of New High-Yield, Disease-Resistant, and Machine-Harvestable Varieties (#20240303017NC) and College Students’ Innovative Entrepreneurial Training (GJ202211439016).

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

Chen Z., Tang D., Ni J., Li P., Wang L., Zhou J., Li C., Lan H., Li L., and Liu J., 2021, Development of genic KASP SNP markers from RNA-Seq data for map-based cloning and marker-assisted selection in maize, BMC Plant Biology, 21: 157. https://doi.org/10.1186/s12870-021-02932-8

Ertiro B., Labuschagne M., Olsen M., Das B., Prasanna B., and Gowda M., 2020, Genetic dissection of nitrogen use efficiency in tropical maize through genome-wide association and genomic prediction, Frontiers in Plant Science, 11: 474. https://doi.org/10.3389/fpls.2020.00474

Ganal M., Durstewitz G., Polley A., Bérard A., Buckler E., Charcosset A., Clarke J., Graner E., Hansen M., Joets J., Paslier M., McMullen M., Montalent P., Rose M., Schön C., Sun Q., Walter H., Martin O., and Falque M., 2011, A large maize (*Zea mays* L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome, PLoS One, 6(12): e28334. https://doi.org/10.1371/journal.pone.0028334

Gupta P., Langridge P., and Mir R., 2010, Marker-assisted wheat breeding: present status and future possibilities, Molecular Breeding, 26: 145-161. https://doi.org/10.1007/s11032-009-9359-7

He J., Zhao X., Laroche A., Lu Z., Liu H., and Li Z., 2014, Genotyping-by-sequencing (GBS), an ultimate marker-assisted selection (MAS) tool to accelerate plant breeding, Frontiers in Plant Science, 5: 484. https://doi.org/10.3389/fpls.2014.00484

Hou J., Zhang J., Bao F., Zhang P., Han H., Tan H., Chen B., and Zhao F., 2024, The contribution of exotic varieties to maize genetic improvement, Molecular Plant Breeding, 15(4): 198-208.

Huang X., Wei X., Sang T., Zhao Q., Feng Q., Zhao Y., Li C., Zhu C., Lu T., Zhang Z., Li M., Fan D., Guo Y., Wang A., Wang L., Deng L., Li W., Lu Y., Weng Q., Liu K., Huang T., Zhou T., Jing Y., Li W., Lin Z., Buckler E., Qian Q., Zhang Q., Li J., and Han B., 2010, Genome-wide association studies of 14 agronomic traits in rice landraces, Nature Genetics, 42: 961-967.

Jones E., Chu W., Ayele M., Ho J., Bruggeman E., Yourstone K., Rafalski A., Smith O., McMullen M., Bezawada C., Warren J., Babayev J., Basu S., and Smith S., 2009, Development of single nucleotide polymorphism (SNP) markers for use in commercial maize (*Zea mays* L.) germplasm, Molecular Breeding, 24: 165-176.
https://doi.org/10.1007/s11032-009-9281-z

Karnatam K., Chhabra G., Saini D., Singh R., Kaur G., Praba U., Kumar P., Goyal S., Sharma P., Ranjan R., Sandhu S., Kumar R., and Vikal Y., 2023, Genome-wide meta-analysis of QTLs associated with root traits and implications for maize breeding, International Journal of Molecular Sciences, 24(7): 6135.
https://doi.org/10.3390/ijms24076135

Ledesma A., Santana A., Ribeiro F., Aguilar F., Edwards J., Frei U., and Lübberstedt T., 2023, Genome-wide association analysis of plant architecture traits using doubled haploid lines derived from different cycles of the Iowa Stiff Stalk Synthetic maize population, Frontiers in Plant Science, 14: 1294507.
https://doi.org/10.3389/fpls.2023.1294507

Liu M., Tan X., Yang Y., Liu P., Zhang X., Zhang Y., Wang L., Hu Y., Ma L., Li Z., Zhang Y., Zou C., Lin H., Gao S., Lee M., Lübberstedt T., Pan G., and Shen Y., 2019, Analysis of the genetic architecture of maize kernel size traits by combined linkage and association mapping, Plant Biotechnology Journal, 18: 207-221.
https://doi.org/10.1111/pbi.13188

Longmei N., Gill G., Zaidi P., Kumar R., Nair S., Hindu V., Vinayan M., and Vikal Y., 2021, Genome wide association mapping for heat tolerance in sub-tropical maize, BMC Genomics, 22: 154.
https://doi.org/10.1186/s12864-021-07463-y

Mammadov J., Chen W., Ren R., Pai R., Marchione W., Yalçin F., Witsenboer H., Greene T., Thompson S., and Kumpatla S., 2010, Development of highly polymorphic SNP markers from the complexity reduced portion of maize (*Zea mays* L.) genome for use in marker-assisted breeding, Theoretical and Applied Genetics, 121: 577-588.
https://doi.org/10.1007/s00122-010-1331-8

Moussa A., Mandozai A., Jin Y., Qu J., Zhang Q., Zhao H., Anwari G., Khalifa M., Lamboro A., Noman M., Bakasso Y., Zhang M., Guan S., and Wang P., 2021, Genome-wide association screening and verification of potential genes associated with root architectural traits in maize (*Zea mays* L.) at multiple seedling stages, BMC Genomics, 22: 558.
https://doi.org/10.1186/s12864-021-07874-x

Müller B., Filho J., Lima B., Garcia C., Missiaggia A., Aguiar A., Takahashi E., Kirst M., Gezan S., Silva-Junior O., Neves L., and Grattapaglia D., 2018, Independent and Joint-GWAS for growth traits in *Eucalyptus* by assembling genome-wide data for 3373 individuals across four breeding populations, The New Phytologist, 221(2): 818-833.
https://doi.org/10.1111/nph.15449

Parisseaux B., and Bernardo R., 2004, In silico mapping of quantitative trait loci in maize, Theoretical and Applied Genetics, 109: 508-514.
https://doi.org/10.1007/s00122-004-1666-0

Rafalski A., 2002, Applications of single nucleotide polymorphisms in crop genetics, Current Opinion in Plant Biology, 5(2): 94-100.
https://doi.org/10.1016/S1369-5266(02)00240-6

Ribaut J., and Ragot M., 2006, Marker-assisted selection to improve drought adaptation in maize: the backcross approach, perspectives, limitations, and alternatives, Journal of Experimental Botany, 58(2): 351-360.
https://doi.org/10.1093/JXB/ERL214

Romay M., Millard M., Glaubitz J., Peiffer J., Swarts K., Casstevens T., Elshire R., Acharya C., Mitchell S., Flint-Garcia S., McMullen M., Holland J., Buckler E., and Gardner C., 2013, Comprehensive genotyping of the USA national maize inbred seed bank, Genome Biology, 14: R55-R55.
https://doi.org/10.1186/gb-2013-14-6-r55

Sethi M., Saini D., Devi V., Kaur C., Singh M., Singh J., Pruthi G., Kaur A., Singh A., and Chaudhary D., 2023, Unravelling the genetic framework associated with grain quality and yield-related traits in maize (*Zea mays* L.), Frontiers in Genetics, 14: 1248697.
https://doi.org/10.3389/fgene.2023.1248697

Shikha K., Shahi J., Vinayan M., Zaidi P., Singh A., and Sinha B., 2021, Genome-wide association mapping in maize: status and prospects, 3 Biotech, 11: 244.
https://doi.org/10.1007/s13205-021-02799-4

Sibov S., Souza C., Garcia A., Silva A., Garcia A., Mangolin C., Benchimol L., and Souza A., 2004, Molecular mapping in tropical maize (*Zea mays* L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant height, ear height and grain moisture, Hereditas, 139(2): 107-115.
https://doi.org/10.1111/J.1601-5223.2003.01667.X

Su C., Wang W., Gong S., Zuo J., Li S., and Xu S., 2017, High density linkage map construction and mapping of yield trait QTLs in maize (*Zea mays*) using the genotyping-by-sequencing (GBS) technology, Frontiers in Plant Science, 8: 706.
https://doi.org/10.3389/fpls.2017.00706

Susmitha P., Kumar P., Yadav P., Sahoo S., Kaur G., Pandey M., Singh V., Tseng T., and Gangurde S., 2023, Genome-wide association study as a powerful tool for dissecting competitive traits in legumes, Frontiers in Plant Science, 14: 1123631.
https://doi.org/10.3389/fpls.2023.1123631

Tomkowiak A., Bocianowski J., Spychała J., Grynia J., Sobiech A., and Kowalczewski P., 2021, DArTseq-based high-throughput SilicoDArT and SNP markers applied for association mapping of genes related to maize morphology, International Journal of Molecular Sciences, 22(11): 5840.
https://doi.org/10.3390/ijms22115840

Wallace J., Zhang X., Beyene Y., Semagn K., Olsen M., Prasanna B., and Buckler E., 2016, Genome-wide association for plant height and flowering time across 15 tropical maize populations under managed drought stress and well-watered conditions in sub-Saharan Africa, Crop Science, 56: 2365-2378.
https://doi.org/10.2135/CROPSCI2015.10.0632

Xiao Y., Liu H., Wu L., Warburton M., and Yan J., 2017, Genome-wide association studies in maize: praise and stargaze, Molecular Plant, 10(3): 359-374.
https://doi.org/10.1016/j.molp.2016.12.008

Yan J., Yang X., Shah T., Sanchez-Villeda H., Li J., Warburton M., Zhou Y., Crouch J., and Xu Y., 2010, High-throughput SNP genotyping with the GoldenGate assay in maize, Molecular Breeding, 25: 441-451.
https://doi.org/10.1007/s11032-009-9343-2

Yang N., Lu Y., Yang X., Huang J., Zhou Y., Ali F., Wen W., Liu J., Li J., and Yan J., 2014, Genome wide association studies using a mew nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel, PLoS Genetics, 10(9): e1004573.
https://doi.org/10.1371/journal.pgen.1004573

Yin X., Bi Y., Jiang F., Guo R., Zhang Y., Fan J., Kang M., and Fan X., 2022, Fine mapping of candidate quantitative trait loci for plant and ear height in a maize nested-association mapping population, Frontiers in Plant Science, 13: 963985.
https://doi.org/10.3389/fpls.2022.963985

Yuan Y., Cairns J., Babu R., Gowda M., Makumbi D., Magorokosho C., Zhang A., Liu Y., Wang N., Hao Z., Vicente F., Olsen M., Prasanna B., Lu Y., and Zhang X., 2019, Genome-wide association mapping and genomic prediction analyses reveal the genetic architecture of grain yield and flowering time under drought and heat stress conditions in maize, Frontiers in Plant Science, 9: 1919.
https://doi.org/10.3389/fpls.2018.01919

Zhang X., Guan Z., Li Z., Liu P., Ma L., Zhang Y., Pan L., He S., Zhang Y., Li P., Ge F., Zou C., He Y., Gao S., Pan G., and Shen Y., 2020, A combination of linkage mapping and GWAS brings new elements on the genetic basis of yield-related traits in maize across multiple environments, Theoretical and Applied Genetics, 133: 2881-2895.
https://doi.org/10.1007/s00122-020-03639-4

Zhao Y., and Su C., 2019, Mapping quantitative trait loci for yield-related traits and predicting candidate genes for grain weight in maize, Scientific Reports, 9: 16112.
https://doi.org/10.1038/s41598-019-52222-5

Zhou J., and Xu L.M., 2024, Conventional breeding vs. genetic engineering in maize: a comparative study, Maize Genomics and Genetics, 15(2): 49-59.

Zhou Z., Zhang C., Zhou Y., Hao Z., Wang Z., Zeng X., Di H., Li M., Zhang D., Yong H., Zhang S., Weng J., and Li X., 2016, Genetic dissection of maize plant architecture with an ultra-high density bin map based on recombinant inbred lines, BMC Genomics, 17: 178.
https://doi.org/10.1186/s12864-016-2555-z