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# QTL Mapping of Resistance to Ear Rot in Maize Based on SNP Markers and Improvement of High-Yield and Disease-Resistance Traits

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**Abstract** Ear rot is an important disease affecting maize production, resulting in serious yield loss and quality decline. Using a set of maize line populations, QTL mapping was performed to identify genomic regions associated with ear rot resistance. This study found several significant QTLS associated with ear rot resistance, some of which overlapped with regions controlling yield traits, suggesting that both resistance and yield could be improved. The SNP markers identified were used in marker-assisted selection (MAS) strategies to accelerate the development of high-yielding and disease-resistant maize varieties. The aim of this study was to use single nucleotide polymorphism (SNP) markers to locate quantitative trait loci (QTL) for maize ear rot resistance, and to improve high yield and disease resistance. These findings provide important genetic insights into ear rot resistance in maize and provide a framework for future breeding efforts aimed at improving maize productivity and disease resistance.

**Keywords** QTL mapping; SNP markers; Resistance to ear rot; Maize breeding; High yield traits

## 1 Introduction

Ear rot diseases, particularly Fusarium ear rot (FER) and Gibberella ear rot (GER), are among the most devastating afflictions affecting maize (*Zea mays* L.) globally (Mukanga et al., 2010; Mesterházy et al., 2012; Gxasheka et al., 2015). These diseases not only significantly reduce maize yield but also compromise grain quality through contamination with harmful mycotoxins such as fumonisins and deoxynivalenol, which pose serious health risks to humans and animals (Lanubile et al., 2017; Yao et al., 2020; Akohoue and Miedaner, 2022). The economic impact of these diseases is profound, with losses estimated to be around 30% of the total yield in affected regions (Gaikpa and Miedaner, 2019). Traditional methods of disease control, including chemical treatments and agronomic practices, have proven to be insufficient and costly, highlighting the need for sustainable solutions through genetic resistance (Lanubile et al., 2017).

Quantitative trait loci (QTL) mapping has emerged as a powerful tool in identifying genetic regions associated with resistance to ear rot diseases in maize. This approach involves the use of dense genome-wide single nucleotide polymorphisms (SNPs) to locate QTLs that confer resistance to FER and GER (Wen et al., 2020; Zhou et al., 2021). Recent studies have successfully identified multiple QTLs and candidate genes that are linked to resistance traits, enabling the development of maize varieties with enhanced resistance to these diseases (Ali et al., 2005; Yao et al., 2020). For instance, meta-analysis and co-expression studies have revealed stable QTLs and candidate genes that can be integrated into breeding programs to improve selection efficiency and reduce mycotoxin contamination (Akohoue and Miedaner, 2022). Additionally, genome-wide association studies (GWAS) and transcriptome analyses have identified significant SNPs and differentially expressed genes involved in early immune responses to ear rot pathogens, further elucidating the genetic architecture of resistance (Yao et al., 2020; Yuan et al., 2022).

This study systematically investigated QTL mapping for ear rot resistance in maize using SNP markers, using advanced genetic mapping techniques including meta-analysis, GWAS, and transcriptomic analysis to provide a comprehensive understanding of the genetic basis for ear rot resistance and to facilitate the application of these findings in practical breeding programs. The aim of this study was to identify and validate QTLS associated with

FER and GER tolerance in maize and to explore the potential to improve maize yield and disease resistance traits by integrating refined QTLS into genomics-assisted breeding strategies to develop superior maize varieties with enhanced ear rot resistance and reduced mycotoxin accumulation. This study hopes to contribute to the development of sustainable and effective strategies for the management of ear rot in maize, ultimately improving crop yield and quality while ensuring food safety.

## 2 Ear Rot Disease in Maize: Overview and Challenges

### 2.1 Pathogens causing ear rot in maize

Ear rot in maize is primarily caused by fungal pathogens, with Fusarium species being the most prevalent and destructive. *Fusarium verticillioides* and *Fusarium graminearum* are the main culprits, leading to Fusarium ear rot (FER) and Gibberella ear rot (GER), respectively. These pathogens not only reduce grain yield and quality but also contaminate the maize with harmful mycotoxins such as fumonisins and deoxynivalenol (DON), posing significant health risks to humans and animals (Lanubile et al., 2017; Yao et al., 2020; Zhou et al., 2021; Akohoue and Miedaner, 2022).

### 2.2 Economic impact and yield loss due to ear rot

The economic impact of ear rot diseases in maize is substantial. Yield losses can reach up to 30% annually due to these fungal infections. The contamination of maize with mycotoxins further exacerbates the economic burden by reducing the marketability and safety of the grain. Infected maize is often unsuitable for consumption, leading to significant financial losses for farmers and the agricultural industry (Lanubile et al., 2017; Akohoue and Miedaner, 2022; Sobiech et al., 2022). The presence of mycotoxins also necessitates additional costs for testing and mitigation, further straining economic resources (Yao et al., 2020).

### 2.3 Current management strategies and their limitations

Current management strategies for ear rot in maize include chemical treatments, agronomic practices, and breeding for resistant varieties. However, these methods have several limitations. While fungicides can reduce the incidence of ear rot, they are often not entirely effective and can increase production costs. Additionally, the overuse of chemicals can lead to environmental concerns and the development of resistant fungal strains (Lanubile et al., 2017). Practices such as crop rotation, proper irrigation, and timely harvesting can help manage ear rot, but they are not foolproof. Environmental factors and the persistent nature of Fusarium spores can still lead to outbreaks despite these measures (Lanubile et al., 2017; Sobiech et al., 2022). Genetic resistance is considered the most sustainable approach. Significant progress has been made in identifying quantitative trait loci (QTL) and candidate genes associated with resistance to FER and GER. However, the polygenic nature of resistance and the influence of environmental factors make breeding for resistance a complex and ongoing challenge (Ali et al., 2005; Ding et al., 2008; Wu et al., 2020).

## 3 QTL Mapping: Concept and Importance in Plant Breeding

Quantitative trait loci (QTL) mapping is a powerful tool in plant breeding, particularly for identifying genetic regions associated with complex traits such as disease resistance and yield (Takuno et al., 2012; Dhingani et al., 2015). This section delves into the definition, principles, and applications of QTL mapping, with a focus on its role in improving maize resistance to ear rot diseases (Jiménez-Galindo et al., 2017).

### 3.1 Definition and principles of QTL mapping

QTL mapping is a statistical method used to identify regions of the genome that are associated with specific quantitative traits. These traits are typically controlled by multiple genes and influenced by environmental factors. The process involves crossing two parent lines that differ in the trait of interest, followed by genotyping and phenotyping their offspring. By analyzing the correlation between genetic markers and phenotypic variation, researchers can pinpoint the genomic regions, or QTLs, that contribute to the trait.

### 3.2 Role of QTL mapping in identifying resistance traits

QTL mapping plays a crucial role in identifying genetic loci associated with resistance to diseases such as Fusarium and Gibberella ear rots in maize. These diseases significantly reduce yield and grain quality by contaminating crops with mycotoxins. Identifying stable QTLs for resistance traits enables breeders to incorporate these loci into breeding programs, thereby improving the selection efficiency for disease-resistant varieties. For instance, studies have identified multiple QTLs associated with resistance to Fusarium ear rot (FER) and Gibberella ear rot (GER), which can be used to develop maize varieties with enhanced resistance (Figure 1) (Ding et al., 2008; Wu et al., 2020; Zhou et al., 2021; Akohoue and Miedaner, 2022; Yuan et al., 2022).

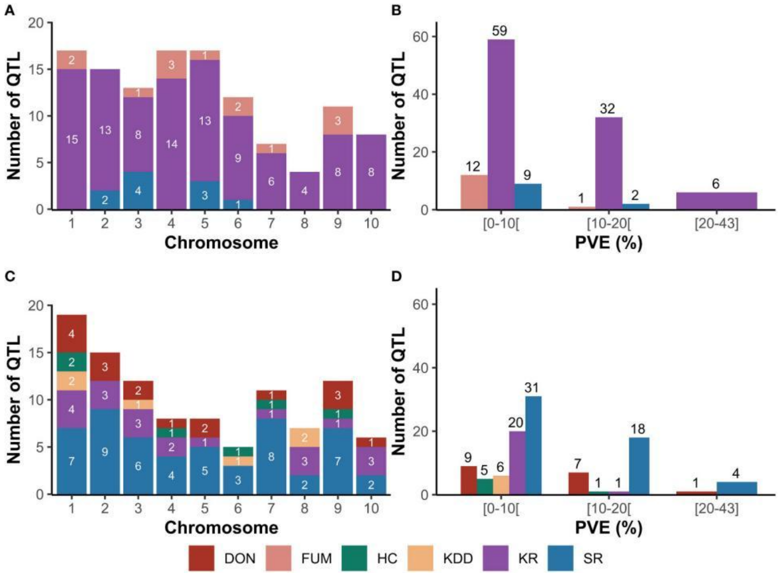

Figure 1 Original QTL reported from SNP-based mapping studies for Fusarium ear rot (FER) and Gibberella ear rot (GER) (Adopted from Akohoue and Miedaner, 2022)

Image caption (A), distribution of QTL for FER across chromosomes; (B), phenotypic variance explained (PVE) by QTL for FER; (C), distribution of QTL for GER across chromosomes; (D), phenotypic variance explained by QTL for GER. DON, deoxynivalenol accumulation; FUM , fumonisin accumulation; HC, husk coverage; KDD, kernel dry-down rate; KR, kernel resistance; SR, silk resistance (Adopted from Akohoue and Miedaner, 2022)

### 3.3 Application of SNP markers in QTL mapping for disease resistance

Single nucleotide polymorphisms (SNPs) are the most abundant type of genetic variation in the genome and serve as valuable markers in QTL mapping. SNP markers provide high-resolution mapping, which is essential for identifying precise genomic regions associated with disease resistance. For example, SNP-based QTL mapping has been used to identify loci associated with resistance to Fusarium and Gibberella ear rots in maize. These markers facilitate the integration of QTLs into genomics-assisted breeding programs, enabling the development of maize varieties with improved resistance to these diseases (Ding et al., 2008; Chen et al., 2016; Lanubile et al., 2017; Giomi et al., 2021; Akohoue and Miedaner, 2022; Yuan et al., 2022; Zhou and Jiang, 2024).

## 4 SNP Markers in Maize Genomics

### 4.1 Overview of single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are the most common type of genetic variation among individuals of a species (Rafalski, 2002; Zhu et al., 2003). In maize, SNPs are valuable markers for genetic studies due to their abundance and stable inheritance patterns. They represent a single base-pair change in the DNA sequence and can be used to track the inheritance of genes associated with important traits, such as disease resistance and yield improvement.

### 4.2 Advantages of SNP markers in maize genetic studies

SNP markers offer several advantages in maize genetic studies. SNPs are densely distributed across the maize genome, providing high-resolution mapping of genetic traits (Lanubile et al., 2017; Akohoue and Miedaner, 2022). And SNPs are stable and reproducible, making them reliable markers for genetic mapping and breeding programs (Zhou et al., 2021; Yuan et al., 2022). Advances in genotyping technologies have made SNP detection cost-effective, facilitating large-scale genetic studies (Gaikpa and Miedaner, 2019). SNP markers are instrumental in identifying QTL associated with traits such as resistance to Fusarium and Gibberella ear rots, which are critical for improving maize resilience and yield (Giomi et al., 2021; Akohoue and Miedaner, 2022).

### 4.3 Development and identification of SNP markers linked to resistance traits

The development and identification of SNP markers linked to resistance traits in maize involve several steps. QTL mapping studies have identified numerous SNPs associated with resistance to ear rots. For instance, a study identified 14 resistant QTLs for Gibberella ear rot (GER) using a combination of QTL mapping and GradedPool-Seq (GPS) (Yuan et al., 2022). GWAS have been used to detect alleles associated with increased resistance to Fusarium ear rot (FER). One study identified 45 SNPs and 15 haplotypes significantly associated with FER resistance (Chen et al., 2016). Meta-analysis of multiple studies has refined the identification of stable QTL and candidate genes. For example, a meta-analysis re-analyzed 224 QTL and identified 40 meta-QTL (MQTL) associated with resistance to Fusarium and Gibberella ear rots. Identified SNP markers and candidate genes are validated through cross-validation with transcriptomic data and other genetic studies. This ensures the reliability of the markers for use in breeding programs (Zhou et al., 2021; Akohoue and Miedaner, 2022). These SNP markers and associated QTL provide valuable resources for breeding programs aimed at improving maize resistance to ear rots and other diseases, ultimately enhancing yield and grain quality.

## 5 QTL Mapping of Resistance to Ear Rot in Maize

### 5.1 Identification of QTLs associated with ear rot resistance

Quantitative trait loci (QTL) mapping has been extensively used to identify genomic regions associated with resistance to ear rot in maize (Chen et al., 2017). Several studies have identified multiple QTLs that contribute to resistance against Fusarium ear rot (FER) and Gibberella ear rot (GER). For instance, a meta-analysis re-analyzed 224 QTLs from 15 studies and identified 40 meta-QTLs (MQTLs) associated with resistance traits such as fumonisin and deoxynivalenol accumulation, silk and kernel resistances, kernel dry-down rate, and husk coverage (Akohoue and Miedaner, 2022). Another study using a multiparent advanced-generation intercross (MAGIC) population identified 13 minor QTLs across various chromosomes, highlighting the quantitative nature of ear rot resistance (Figure 2) (Butrón et al., 2019). Additionally, a study using a recombinant inbred line (RIL) population identified 11 QTLs for GER resistance, with six additive and six epistatic QTLs contributing to the genetic architecture of resistance (Zhou et al., 2021).

### 5.2 Integration of SNP markers with QTL mapping for better resolution

The integration of single nucleotide polymorphism (SNP) markers with QTL mapping has significantly improved the resolution and accuracy of identifying resistance loci. For example, a study combining QTL mapping with GradedPool-Seq (GPS) identified 14 resistant QTLs and five significant SNPs associated with GER resistance, with a peak SNP on chromosome 4 overlapping with a QTL, suggesting a potential target region for resistance (Yuan et al., 2022). Another study employed a high-density SNP array to genotype a RIL population, leading to the identification of 11 QTLs for GER resistance, including five stable QTLs (Zhou et al., 2021). Furthermore, a genome-wide association study (GWAS) in tropical maize germplasm identified 45 SNPs and 15 haplotypes associated with FER resistance, with eight loci colocated with QTLs identified through linkage mapping (Chen et al., 2016).

### 5.3 Key regions of the maize genome involved in ear rot resistance

Several key regions of the maize genome have been consistently identified as being involved in ear rot resistance. For instance, the meta-analysis identified 14 refined MQTLs on chromosomes 1, 2, 3, 4, 7, and 9, with some regions harboring promising candidate genes such as terpene synthase21 (*tps21*) and flavonoid O-methyltransferase2 (*fomt2*) (Akohoue and Miedaner, 2022). Another study highlighted the importance of regions on chromosomes 3 and 7, specifically 210~220 Mb on chromosome 3 and 166~173 Mb on chromosome 7, which contain QTLs for FER resistance and fumonisin content (Butrón et al., 2019). Additionally, a study mapping QTLs for disease resistance and associated traits identified significant QTLs in bins 1.06, 2.03, 3.06, 5.04, 5.07, and 6.05, with the most important QTLs overlapping in bin 2.03 (Giomi et al., 2021). These key genomic regions provide valuable targets for breeding programs aimed at improving ear rot resistance in maize.

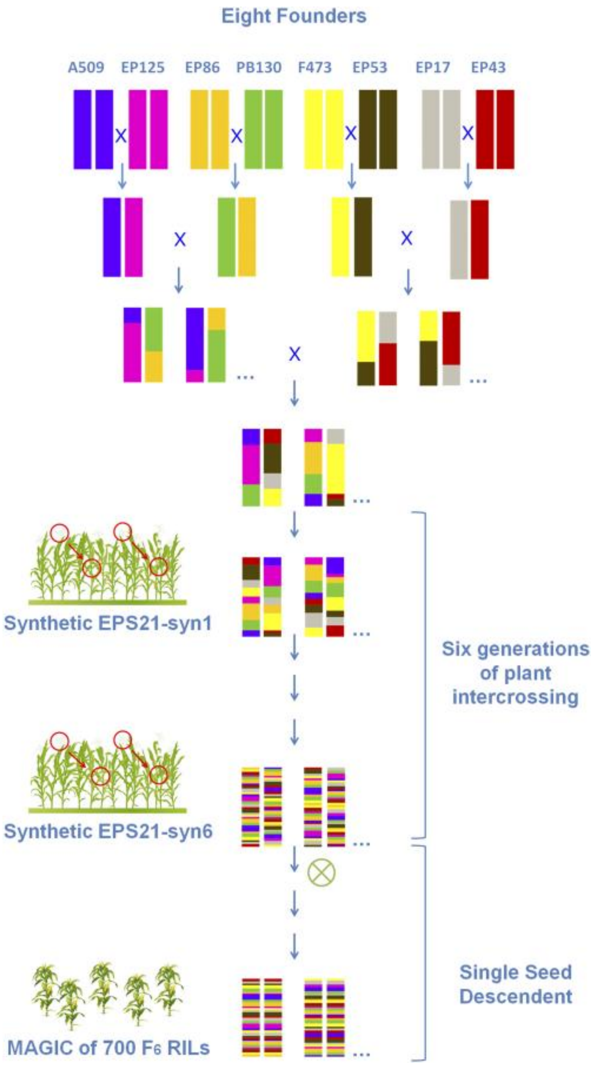

Figure 2 Scheme of the procedure used to develop the recombinant inbred lines (RIL) that constitute the multiparent advanced-generation intercross (MAGIC) population derived from intercrossing eight inbred founders (Adopted from Butrón et al., 2019)

## 6 Genomic Tools and Techniques for Trait Improvement

### 6.1 Genomic selection and marker-assisted selection (MAS)

Genomic selection (GS) and marker-assisted selection (MAS) are pivotal in modern maize breeding programs aimed at improving resistance to ear rot diseases such as Fusarium ear rot (FER) and Gibberella ear rot (GER). GS leverages genome-wide markers to predict the genetic value of breeding candidates, thus accelerating the selection process. MAS, on the other hand, focuses on specific markers linked to desirable traits. For instance, the integration of QTL mapping and GWAS has identified several SNPs and QTLs associated with FER and GER resistance, which can be utilized in MAS to enhance disease resistance in maize (Chen et al., 2016; Guo et al., 2020; Wu et al., 2020; Akohoue and Miedaner, 2022).

### 6.2 Application of genome-wide association studies (GWAS) in identifying resistance loci

GWAS has been instrumental in identifying genetic loci associated with resistance to ear rot diseases in maize. By analyzing a large number of SNP markers across diverse maize populations, researchers have pinpointed numerous loci linked to FER and GER resistance. For example, a study identified 45 SNPs and 15 haplotypes significantly associated with FER resistance, which were located within or adjacent to 38 candidate genes (Chen et al., 2016). Another study revealed 69 SNPs associated with GER resistance, providing valuable insights into the genetic basis of this trait (Yuan et al., 2023). These findings underscore the complexity of ear rot resistance, which is governed by multiple genes with minor effects (Yao et al., 2020; Zhang et al., 2023).

### 6.3 Using SNPs and QTL data to accelerate breeding programs

The integration of SNP and QTL data is crucial for accelerating maize breeding programs aimed at improving resistance to ear rot diseases. By combining GWAS and QTL mapping, researchers can validate significant loci and identify candidate genes for resistance (Leprévost et al., 2023). For instance, the integration of GWAS and QTL mapping in a study identified eight colocated loci on chromosomes 2, 3, 4, 5, 9, and 10, which are associated with FER resistance (Chen et al., 2016). Similarly, another study using a combination of QTL mapping and GradedPool-Seq identified significant SNPs and candidate genes for GER resistance (Yuan et al., 2022). These integrated approaches enable the development of molecular markers that can be used in MAS and GS to enhance the efficiency of breeding programs (Wu et al., 2020; Akohoue and Miedaner, 2022).

## 7 Improving High Yield and Disease Resistance in Maize

### 7.1 The relationship between disease resistance and yield potential

The relationship between disease resistance and yield potential in maize is complex and multifaceted. Fusarium ear rot (FER) and Gibberella ear rot (GER) are two significant diseases that not only reduce yield but also affect grain quality through mycotoxin contamination (Ding et al., 2008; Zhou et al., 2021). The genetic improvement of maize for resistance to these diseases involves identifying stable quantitative trait loci (QTL) that can be used in breeding programs to enhance both yield and disease resistance (Gaikpa and Miedaner, 2019; Akohoue and Miedaner, 2022). Studies have shown that resistance to these diseases is often controlled by multiple minor-effect QTLs, which collectively contribute to the overall resistance (Chen et al., 2016; Zhou et al., 2021). This polygenic nature of resistance implies that improving disease resistance can be achieved without necessarily compromising yield potential, provided that the breeding strategies are well-designed to balance both traits (Lanubile et al., 2017; Miedaner et al., 2020).

### 7.2 Strategies for breeding maize varieties with high yield and disease resistance

Several strategies have been employed to breed maize varieties that combine high yield and disease resistance. One effective approach is the use of genomics-assisted breeding, which integrates QTL mapping, genome-wide association studies (GWAS), and genomic selection to identify and select for resistance genes (Gaikpa and Miedaner, 2019; Miedaner et al., 2020; Yuan et al., 2022). For instance, meta-analysis and co-expression analysis have been used to identify stable QTL and candidate genes that confer resistance to both FER and GER, which can then be incorporated into elite cultivars through backcross breeding strategies (Akohoue and Miedaner, 2022). Additionally, the use of multi-parent QTL mapping has revealed stable QTL that can be utilized to enhance GER resistance in different maize germplasms (Galiano-Carneiro et al., 2020). Marker-assisted selection (MAS) is another strategy that facilitates the selection of resistance traits by using closely linked markers to major resistance QTL, thereby improving the efficiency of breeding programs (Ding et al., 2008; Giomi et al., 2021).

### 7.3 Challenges in combining yield and resistance traits in breeding

Combining yield and resistance traits in maize breeding presents several challenges. One major challenge is the genetic complexity of disease resistance, which is often controlled by multiple QTL with small effects, making it difficult to achieve significant improvements through traditional breeding methods alone (Chen et al., 2016). Additionally, the interactions between different QTL and the environment can complicate the selection process, as resistance traits may not consistently express across different environments (Ding et al., 2008; Zhou et al., 2021). Another challenge is the potential trade-off between yield and resistance, where selecting for one trait may inadvertently affect the other. For example, some QTL associated with disease resistance may have pleiotropic effects that influence yield-related traits (Giomi et al., 2021). To overcome these challenges, a combination of advanced genomic tools, such as genomic selection and integrated breeding strategies, is necessary to accurately predict and select for genotypes that exhibit both high yield and strong disease resistance (Lanubile et al., 2017; Gaikpa and Miedaner, 2019; Miedaner et al., 2020).

## 8 Case Study: Successful QTL Mapping and Resistance Breeding in Maize

### 8.1 Background and significance of the breeding program

Fusarium ear rot (FER) and Gibberella ear rot (GER) are significant diseases affecting maize, leading to reduced yield and grain quality due to mycotoxin contamination. These diseases pose a global threat to maize production, necessitating the development of resistant maize varieties. Genetic improvement through the identification of stable quantitative trait loci (QTL) is crucial for enhancing resistance to these diseases and improving selection efficiency in breeding programs (Chen et al., 2016; Akohoue and Miedaner, 2022; Yuan et al., 2022). The breeding program aims to integrate QTL mapping and single nucleotide polymorphism (SNP) markers to develop maize varieties with improved resistance to FER and GER, thereby ensuring higher yield and better grain quality.

### 8.2 Methodology: QTL mapping and SNP marker integration

The methodology involved the use of various populations and advanced genetic techniques to map QTL associated with resistance to FER and GER. For instance, a meta-analysis of 224 QTL identified in 15 studies was conducted using dense genome-wide SNP markers to identify meta-QTL (MQTL) and candidate genes (Akohoue and Miedaner, 2022). Another study utilized a set of 246 diverse inbred lines from the IBM Syn10 DH population to detect QTL associated with GER resistance, combining QTL mapping with GradedPool-Seq (GPS) to identify significant SNPs (Figure 3) (Yuan et al., 2022). Additionally, genome-wide association studies (GWAS) and linkage mapping were employed to detect alleles and validate QTL associated with FER resistance in tropical maize germplasm (Chen et al., 2016). These approaches enabled the identification of genomic regions and candidate genes linked to disease resistance, facilitating the integration of these markers into breeding programs.

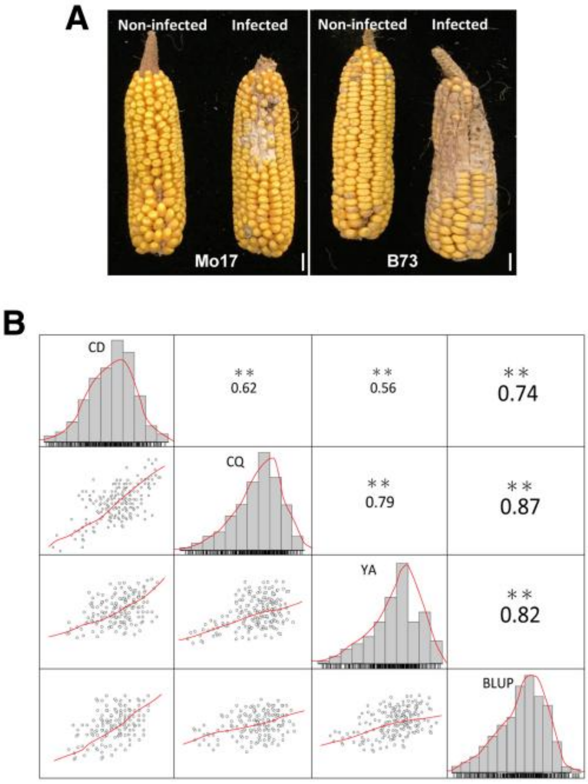

Figure 3 Phenotypic variation of Gibberella ear rot (GER) severity between the parental lines and the distribution of GER scale at three environments in IBM Syn10 DH populations (Adopted from Yuan et al., 2022)

Image caption: A, Phenotypic variation of GER severity in parental lines Mo 17 and B 73 after *Fusarium graminearum* inoculation in the field. Bar: 2 cm. B, The histograms display correlation and frequency distribution of the GER scale for IBM Syn10 DH populations at three independent environments and the best linear unbiased prediction; the scatterplots and the numbers display the pairwise scatter plot and pairwise correlation coefficient, as determined by the paired t test; the red curve shows the fitted model. ** indicates a significance level at $P < 0.01$ (Adopted from Yuan et al., 2022)

### 8.3 Outcomes: improved disease resistance and yield in maize varieties

The integration of QTL mapping and SNP markers has led to significant advancements in breeding maize varieties with enhanced resistance to FER and GER. For example, the meta-analysis identified 40 MQTL, with 29 associated with multiple FER- and GER-related traits, and 14 MQTL harboring 2 272 candidate genes (Akohoue and Miedaner, 2022). The combination of QTL mapping and GPS analysis identified seven candidate genes linked to GER resistance (Yuan et al., 2022). Furthermore, GWAS and linkage mapping revealed 45 SNPs and 15 haplotypes significantly associated with FER resistance, with eight colocated loci on chromosomes 2, 3, 4, 5, 9, and 10 (Chen et al., 2016). These findings have enabled the development of maize varieties with improved disease resistance and yield, contributing to more sustainable maize production.

### 8.4 Lessons learned and future application of these techniques in maize breeding

The successful application of QTL mapping and SNP marker integration in breeding programs has highlighted several key lessons. Firstly, the complexity of disease resistance traits necessitates the use of multiple genetic approaches to identify stable QTL and candidate genes (Akohoue and Miedaner, 2022). Secondly, the integration of advanced genomic tools, such as GWAS and GPS, enhances the precision and efficiency of identifying resistance loci (Yuan et al., 2022). Future applications of these techniques should focus on the continuous refinement of QTL and candidate gene identification, as well as the incorporation of these markers into genomics-assisted backcross breeding strategies to develop elite cultivars with enhanced resistance to multiple diseases (Chen et al., 2016; Akohoue and Miedaner, 2022). Additionally, exploring the genetic basis of resistance in diverse maize germplasm will further broaden the genetic pool for breeding programs, ensuring the development of robust and high-yielding maize varieties (Hou et al., 2024).

## 9 Challenges and Future Directions in QTL Mapping for Maize Resistance

### 9.1 Challenges in identifying stable QTLs across environments

Identifying stable quantitative trait loci (QTLs) for resistance to ear rot in maize across different environments remains a significant challenge. Environmental factors such as climate, soil type, and pathogen variability can influence the expression of resistance traits, making it difficult to pinpoint QTLs that consistently confer resistance. For instance, studies have shown that QTLs identified in one environment may not be effective in another due to these environmental interactions (Akohoue and Miedaner, 2022). Additionally, the genetic architecture of resistance traits often involves multiple minor-effect QTLs, which further complicates the identification of stable QTLs (Zhou et al., 2021; Yuan et al., 2022).

### 9.2 Integrating multi-environment trials to refine QTL mapping

To address the challenge of environmental variability, integrating data from multi-environment trials is crucial. This approach allows researchers to identify QTLs that are consistently expressed across different conditions, thereby refining the mapping of resistance traits. For example, multi-parent QTL mapping and joint multiple environments analysis have been employed to identify QTLs with additive effects that are stable across various environments (Yuan et al., 2022). Such methods enhance the reliability of QTL mapping by accounting for genotype-by-environment interactions, leading to more robust identification of resistance loci (Ding et al., 2008; Galiano-Carneiro et al., 2020).

### 9.3 Opportunities for improving the precision and accuracy of QTL-based breeding

Advancements in genomic technologies and statistical methods offer new opportunities to improve the precision and accuracy of QTL-based breeding. Techniques such as meta-analysis and co-expression analysis can refine QTL mapping by integrating data from multiple studies, thereby identifying meta-QTLs that are more reliable for breeding programs (Akohoue and Miedaner, 2022). Additionally, combining QTL mapping with genome-wide association studies (GWAS) and RNA sequencing can uncover candidate genes within QTL regions, providing a more detailed understanding of the genetic basis of resistance (Chen et al., 2016; Xia et al., 2022). These integrated approaches can facilitate the development of molecular markers for marker-assisted selection, ultimately enhancing the efficiency of breeding programs aimed at improving resistance to ear rot in maize (Butrón et al., 2019; Wen et al., 2020).

## 10 Concluding Remarks

Quantitative trait loci (QTL) mapping has been instrumental in identifying genetic regions associated with resistance to ear rot diseases in maize, such as Fusarium ear rot (FER) and Gibberella ear rot (GER). Several studies have successfully mapped QTLs that confer resistance to these diseases. For instance, a meta-analysis identified 40 meta-QTLs (MQTLs) associated with multiple traits related to FER and GER resistance, with 29 MQTLs linked to 2~5 traits each. Another study mapped 11 QTLs for GER resistance, with a novel QTL, qGER4.09, showing potential for multi-pathogen resistance. Additionally, linkage mapping and genome-wide association studies (GWAS) have identified numerous QTLs and SNPs associated with yield-related traits and disease resistance, further elucidating the genetic basis of these complex traits.

Single nucleotide polymorphism (SNP) markers have played a crucial role in enhancing maize resistance to ear rot diseases and improving yield. SNP markers facilitate high-resolution mapping and the identification of candidate genes associated with disease resistance. For example, the use of dense genome-wide SNPs enabled the identification of stable MQTLs and candidate genes for FER and GER resistance. Similarly, SNP arrays have been used to genotype recombinant inbred line (RIL) populations, leading to the discovery of significant QTLs for GER resistance. The integration of SNP markers with QTL mapping and GWAS has also revealed genomic loci associated with yield-related traits, providing valuable information for marker-assisted selection in breeding programs.

Future research should focus on the following priorities to further improve maize resistance to ear rot diseases and enhance yield. Continued efforts are needed to validate and fine-map identified QTLs to narrow down the candidate regions and identify the underlying resistance genes. This will facilitate the development of more precise markers for breeding programs. Combining QTL mapping with transcriptomics, proteomics, and metabolomics can provide a comprehensive understanding of the molecular mechanisms underlying disease resistance and yield traits. This integrative approach will help identify key regulatory networks and pathways involved in these complex traits. Implementing genomic selection strategies that incorporate identified QTLs and SNP markers can accelerate the breeding of maize varieties with enhanced resistance and yield. This approach will enable the selection of individuals with favorable alleles for multiple traits, improving overall breeding efficiency.

Expanding the genetic diversity of breeding populations by incorporating diverse germplasm can uncover novel resistance alleles and enhance the genetic base of cultivated maize. This will provide new opportunities for improving disease resistance and yield stability. Given the impact of climate change on disease prevalence and crop performance, future research should also focus on developing maize varieties that are resilient to changing environmental conditions. This includes identifying QTLs and genes associated with stress tolerance and integrating them into breeding programs. By addressing these research priorities, the application of QTL mapping and genomic tools will continue to advance the development of high-yielding, disease-resistant maize varieties, contributing to global food security and agricultural sustainability.

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## 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.

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