Molecular Identification and Integrated Management of Fungal Pathogens Affecting Maize: Recent advances and Future Perspectives

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ABSTRACT

Maize (Zea mays L.) is one of the most important cereal crops globally, serving as a major source of food, animal feed, and industrial raw materials. However, maize productivity is significantly threatened by fungal pathogens that cause diseases such as ear rot, stalk rot, leaf blight, gray leaf spot, and smut. Major pathogens responsible for these diseases include Fusarium species, Exserohilum turcicum, Bipolaris maydis, Cercospora zeina, and Ustilago maydis. These pathogens not only reduce crop yield and grain quality but also produce harmful mycotoxins that pose serious health risks to humans and livestock. Accurate identification and effective management of these fungal pathogens are therefore essential for ensuring sustainable maize production and global food security. Recent advances in molecular biology have significantly improved the detection and identification of maize fungal pathogens. Techniques such as polymerase chain reaction (PCR), quantitative PCR (qPCR), next-generation sequencing (NGS), multilocus sequence typing (MLST), loop-mediated isothermal amplification (LAMP), and CRISPR-based diagnostics enable rapid, precise, and sensitive pathogen detection. These molecular approaches help distinguish closely related fungal species and facilitate early disease diagnosis and epidemiological monitoring. Alongside improved diagnostics, integrated disease management strategies have been developed to control fungal diseases in maize. These strategies combine cultural practices, resistant maize varieties developed through marker-assisted breeding, biological control using beneficial microorganisms, and targeted fungicide application. Emerging technologies such as RNA-based gene silencing, genomic selection, microbiome engineering, and high-throughput phenotyping also offer promising tools for sustainable disease control. Integrating molecular diagnostics with these management strategies will be crucial for mitigating fungal diseases and improving maize productivity in the future.

Keywords: *Molecular diagnostics, fungal pathogens, integrated disease management, Maize diseases*

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INTRODUCTION

Maize (*Zea mays* L.) is one of the most widely cultivated cereal crops globally and serves as a fundamental component of food security, animal feed, and industrial raw materials. The crop is grown across diverse agroecological zones ranging from temperate to tropical regions, contributing significantly to the global agricultural economy. According to recent agricultural reports, maize accounts for a substantial proportion of cereal production worldwide due to its high productivity and adaptability to various environmental conditions. Beyond its role in direct human consumption, maize is extensively used in livestock feed, biofuel production, starch manufacturing, and other industrial applications. Despite its global significance, maize productivity is severely constrained by several biotic stresses, particularly fungal diseases that affect plant growth, grain quality, and overall yield (Bugingo et al., 2025; Harish et al., 2023). These diseases can cause substantial economic losses and threaten food safety through contamination with toxic fungal metabolites. Among the most destructive fungal diseases affecting maize are Fusarium ear rot, Fusarium stalk rot, northern corn leaf blight, southern corn leaf blight, gray leaf spot, and maize smut. Species belonging to the genus *Fusarium* are especially important because they infect multiple plant tissues and produce harmful mycotoxins such as fumonisins, zearalenone, and trichothecenes, which pose serious health risks to humans and livestock (Opoku et al., 2024; Yang et al., 2022). Other major pathogens include *Exserohilum turcicum*, which causes northern corn leaf blight; *Bipolaris maydis*, responsible for southern leaf blight; and *Cercospora zeina*, the causal agent of gray leaf spot disease. These pathogens significantly reduce photosynthetic efficiency by damaging leaf tissues, leading to poor grain filling and yield losses. In addition, *Ustilago maydis*, the causal agent of maize smut, infects various plant organs and disrupts normal plant development. The prevalence and severity of these diseases are influenced by several factors including environmental conditions, cropping systems, host susceptibility, and pathogen genetic diversity (Jambhulkar et al., 2024).

The impact of fungal pathogens on maize production has become increasingly severe in recent years due to climate variability and global agricultural intensification. Changes in temperature, humidity, and rainfall patterns create favorable conditions for the proliferation and spread of fungal pathogens. Moreover, increased international trade and movement of agricultural commodities facilitate the introduction of new pathogen strains into previously unaffected regions. These factors contribute to the emergence of new pathogenic species and the evolution of more virulent fungal populations capable of overcoming existing resistance mechanisms (Deressa et al., 2025). Consequently, early detection and accurate identification of fungal pathogens are critical for effective disease monitoring and management. Historically, the identification of fungal pathogens in maize relied primarily on conventional morphological methods. These methods involve observing colony morphology, spore structures, pigmentation, and other phenotypic characteristics under laboratory conditions. While morphological identification remains useful for preliminary diagnosis, it often lacks accuracy due to the high degree of morphological similarity among closely related fungal species. Additionally, environmental conditions such as temperature, nutrient availability, and culture media can influence fungal morphology, leading to misidentification or inconsistent results (Harish & Venkateshbabu, 2024). Such limitations highlight the need for more reliable and precise identification methods.

In recent decades, molecular diagnostic techniques have revolutionized the detection and characterization of plant pathogens, including fungi affecting maize. Molecular identification methods rely on analyzing specific genetic markers that provide high-resolution information about pathogen taxonomy and phylogenetic relationships. Among these markers, the internal transcribed spacer (ITS) region of ribosomal DNA is widely used for general fungal identification due to its high variability among species. However, for closely related species such as those within the *Fusarium* genus, additional genes such as translation elongation factor 1-alpha (TEF-1α), RNA polymerase II subunit (RPB2), and beta-tubulin are commonly used to improve taxonomic resolution (Stoeva et al., 2025; Gherbawy et al., 2025). These molecular markers enable researchers to distinguish between cryptic species that are otherwise difficult to differentiate morphologically. Polymerase chain reaction (PCR)-based techniques remain among the most widely used molecular diagnostic tools in plant pathology. Conventional PCR allows rapid amplification of target DNA sequences for species identification, while quantitative PCR (qPCR) enables real-time detection and quantification of pathogen DNA in infected plant tissues. These techniques have been successfully applied to detect major maize pathogens such as *Fusarium verticillioides*, *Fusarium graminearum*, and *Fusarium temperatum* in both field samples and stored grains (Deressa et al., 2025). Furthermore, multiplex PCR assays allow simultaneous detection of multiple pathogens in a single reaction, thereby improving diagnostic efficiency in disease surveillance programs.

Recent advances in high-throughput sequencing technologies have further enhanced the accuracy and speed of pathogen identification. Next-generation sequencing (NGS) platforms enable comprehensive analysis of fungal genomes and microbial communities associated with maize plants and soils. These technologies facilitate the identification of previously unknown pathogens, the characterization of pathogen population structures, and the detection of virulence-associated genes. Multi-omics approaches, including genomics, transcriptomics, and metabolomics, are increasingly being used to investigate the complex interactions between maize plants and fungal pathogens (Ansari et al., 2026; Bugingo et al., 2025). Such insights are essential for understanding disease epidemiology and developing innovative management strategies. In addition to improving pathogen identification, molecular technologies have also contributed significantly to disease management strategies in maize production systems.

Marker-assisted selection (MAS) and genomic-assisted breeding have enabled the development of maize varieties with improved resistance to fungal pathogens. By identifying molecular markers linked to disease resistance genes, breeders can rapidly select resistant genotypes without relying solely on time-consuming field evaluations (Lenort et al., 2025). Similarly, advances in genome editing technologies and RNA-based disease control approaches have opened new possibilities for targeted pathogen suppression and improved crop resilience. Integrated disease management strategies that combine molecular diagnostics with cultural practices, biological control agents, and resistant cultivars are increasingly recognized as the most sustainable approach for controlling maize fungal diseases. Such strategies allow for early detection of pathogens, accurate risk assessment, and timely implementation of control measures. Despite these advances, several challenges remain, including the emergence of new pathogen strains, limited accessibility of molecular technologies in developing regions, and the need for improved surveillance systems. Therefore, this review aims to synthesize recent research advances in the molecular identification of fungal pathogens affecting maize and evaluate current integrated management strategies. Particular emphasis is placed on emerging molecular diagnostic tools, genomic technologies, and sustainable disease control approaches developed between 2022 and 2026. Understanding these developments is essential for improving maize disease management and ensuring sustainable crop production in the face of evolving pathogen threats.

Major Fungal Pathogens Affecting Maize

Maize production worldwide is threatened by a wide range of fungal pathogens that infect plants at different developmental stages, including seedling, vegetative, and reproductive phases. These pathogens can cause significant yield losses, reduce grain quality, and compromise food safety through contamination with toxic secondary metabolites. Among the most economically important fungal pathogens affecting maize are species belonging to the genus *Fusarium*, which are responsible for diseases such as ear rot, stalk rot, and seedling blight. *Fusarium verticillioides*, *Fusarium graminearum*, and *Fusarium proliferatum* are widely recognized as major causal agents of ear rot diseases in maize-growing regions worldwide. These pathogens infect maize kernels and produce mycotoxins including fumonisins, zearalenone, and trichothecenes, which pose serious health risks to humans and livestock (Shang et al., 2022; Harish et al., 2023). In addition to yield losses, contamination with mycotoxins significantly reduces the market value of maize grain and can lead to rejection in international trade. The epidemiology of *Fusarium* species is complex due to their ability to survive in crop residues and soil for extended periods. These pathogens can infect maize plants through wounds or natural openings, particularly under environmental conditions characterized by high humidity and moderate temperatures. Molecular phylogenetic studies have revealed that the *Fusarium* genus comprises numerous cryptic species that cannot be reliably distinguished using morphological traits alone. Consequently, molecular markers such as the internal transcribed spacer (ITS), translation elongation factor 1-alpha (TEF-1α), and beta-tubulin genes are frequently used to resolve species complexes and understand pathogen diversity (Gherbawy et al., 2025). Recent genomic studies have also identified genes associated with virulence and toxin production in *Fusarium* species, providing valuable insights into their pathogenic mechanisms and evolutionary relationships (Figure 1).

In addition to *Fusarium* pathogens, several foliar fungi are responsible for severe diseases in maize production systems. One of the most significant foliar diseases is northern corn leaf blight, caused by *Exserohilum turcicum*. This pathogen infects maize leaves and produces elongated necrotic lesions that reduce the photosynthetic capacity of plants, leading to premature senescence and decreased grain yield. Northern corn leaf blight is particularly prevalent in regions with cool and humid climates, where disease epidemics can develop rapidly. Recent research has shown that *E. turcicum* populations exhibit substantial genetic diversity and adaptive potential, which can influence the effectiveness of resistant maize varieties (Nsibo et al., 2024; Chao et al., 2025). Understanding the population structure and evolutionary dynamics of this pathogen is therefore essential for developing durable resistance strategies. Another important foliar pathogen is *Bipolaris maydis*, the causal agent of southern corn leaf blight. This disease gained historical significance during the 1970 maize epidemic in the United States, which resulted in devastating crop losses due to the widespread cultivation of susceptible maize hybrids. Although modern breeding programs have improved resistance, southern corn leaf blight remains a concern in tropical and subtropical maize-growing regions. Infection by *B. maydis* typically results in small, elongated lesions that expand under favorable environmental conditions, eventually leading to extensive leaf damage. Molecular studies have identified multiple pathogenic races of *B. maydis*, each characterized by different virulence patterns and host specificity (Khaengraeng & Mhuantong, 2025). The existence of these pathogenic races highlights the importance of continuous pathogen monitoring and the development of resistant cultivars. Gray leaf spot is another major fungal disease affecting maize, caused primarily by *Cercospora zeina* and *Cercospora zeae-maydis*. Among these, *C. zeina* is particularly widespread in Africa and other maize-producing regions. The disease is characterized by rectangular gray lesions on maize leaves, which can coalesce and cause extensive leaf blighting under favorable environmental conditions. Severe infections

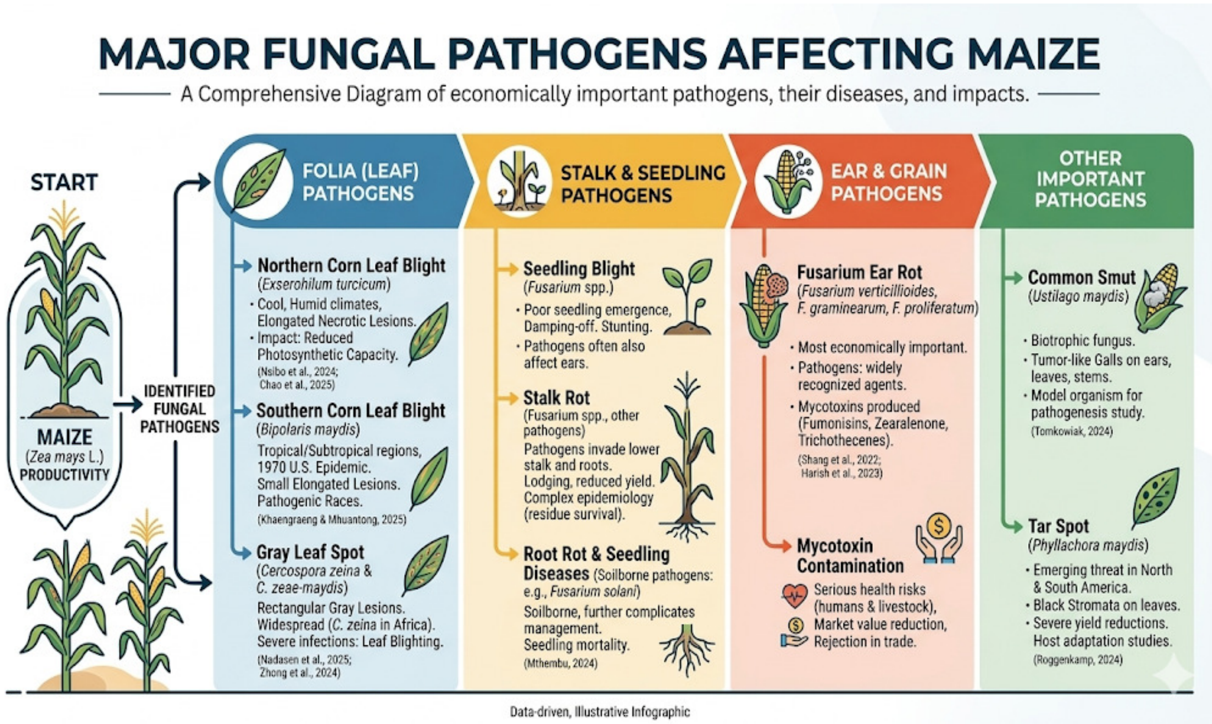

Figure 1: Major Fungal pathogen of Maize

significantly reduce photosynthetic activity and lead to yield losses that may exceed 30–50% in susceptible varieties. Recent molecular and transcriptomic studies have provided new insights into the infection strategies employed by *C. zeina*. For example, genome-wide analyses have revealed the presence of effector proteins that enable the pathogen to suppress host immune responses and establish successful infections (Nadasen et al., 2025; Zhong et al., 2024). These findings contribute to a better understanding of host–pathogen interactions and support the development of molecular breeding strategies for disease resistance.

Another important fungal pathogen affecting maize is *Ustilago maydis*, the causal agent of common smut disease. Unlike many other maize pathogens, *U. maydis* is a biotrophic fungus that infects living plant tissues and induces the formation of tumor-like galls on leaves, stems, and ears. Although the disease is often considered less destructive than other maize diseases, severe infections can still lead to significant yield losses. Interestingly, *U. maydis* has also become a model organism for studying fungal pathogenesis due to its relatively simple genome and well-characterized infection cycle. Genomic and transcriptomic analyses have revealed numerous effector proteins that play critical roles in manipulating host cellular processes during infection (Tomkowiak, 2024). Research on *U. maydis* has therefore contributed significantly to understanding the molecular mechanisms underlying plant–fungus interactions. In recent years, additional fungal pathogens have emerged as potential threats to maize production. For example, *Phyllachora maydis*, the causal agent of tar spot disease, has gained increasing attention due to its rapid spread in North and South America. Tar spot is characterized by black stromata on maize leaves and can lead to severe yield reductions under favorable environmental conditions. Genetic investigations have begun to explore the molecular basis of virulence and host adaptation in this pathogen, highlighting the importance of surveillance and early detection strategies (Roggenkamp, 2024). Similarly, soilborne fungal pathogens such as *Fusarium solani* and other root-infecting species have been reported to cause root rot and seedling diseases in maize fields, further complicating disease management efforts (Mthembu, 2024).

Overall, the diversity and adaptability of fungal pathogens affecting maize present significant challenges for sustainable crop production. These pathogens vary widely in their infection strategies, host specificity, and environmental requirements, making disease management particularly complex. Advances in molecular identification and genomic technologies have greatly improved our ability to detect and characterize these pathogens, allowing researchers to better understand their epidemiology and evolutionary dynamics. Continued research on the biology, genetics, and ecology of maize fungal pathogens will be essential for developing effective integrated disease management strategies and ensuring global maize productivity in the face of emerging disease threats (Figure 1).

Molecular Approaches for Identification of Maize Fungal Pathogens

Advances in molecular biology and genomics have revolutionized the identification and characterization of fungal pathogens affecting maize. Traditional identification methods based on morphological traits and pathogenicity tests often lack precision because many fungal species exhibit overlapping morphological features and phenotypic plasticity. Molecular diagnostic approaches have therefore become essential tools for accurate pathogen detection, species differentiation, and epidemiological studies. These techniques rely on the analysis of specific DNA or RNA sequences that serve as genetic markers for pathogen identification. Among the most commonly used genomic regions are the internal transcribed spacer (ITS) region of ribosomal DNA, the translation elongation factor 1-alpha (TEF-1α) gene, β-tubulin genes, and RNA polymerase II subunits (RPB1 and RPB2). These markers provide high taxonomic resolution and are widely used in phylogenetic studies of maize fungal pathogens, particularly species within the *Fusarium* genus (Shang et al., 2022; Gherbawy et al., 2025). The adoption of molecular markers has significantly improved the accuracy of fungal pathogen identification and has enabled researchers to differentiate closely related or cryptic species that cannot be distinguished through conventional morphological methods. Polymerase chain reaction (PCR) remains one of the most widely used molecular techniques for pathogen detection due to its high sensitivity, specificity, and rapid processing time. Conventional PCR assays allow amplification of targeted DNA regions using species-specific primers, enabling precise identification of fungal pathogens present in infected plant tissues. PCR-based diagnostic methods have been widely applied to detect maize pathogens such as *Fusarium verticillioides*, *Fusarium graminearum*, *Exserohilum turcicum*, and *Bipolaris maydis*. For instance, molecular assays targeting the ITS and TEF-1α genes have proven effective in distinguishing multiple *Fusarium* species responsible for maize ear rot and stalk rot diseases (Deressa et al., 2025). These PCR-based approaches are particularly valuable in plant disease diagnostics laboratories, where rapid identification of pathogens is required to support disease management decisions. Furthermore, multiplex PCR techniques enable simultaneous detection of multiple pathogens within a single reaction, thereby improving efficiency in large-scale disease monitoring programs.

Quantitative polymerase chain reaction (qPCR), also known as real-time PCR, represents a significant advancement in molecular diagnostics because it allows both detection and quantification of pathogen DNA in plant tissues. Unlike conventional PCR, which only confirms the presence or absence of a pathogen, qPCR provides quantitative data on pathogen load during infection. This capability is particularly important for studying disease progression and evaluating the effectiveness of control strategies. Real-time PCR assays have been developed for several maize pathogens, enabling early detection before visible symptoms appear in the field. Early detection is critical for implementing timely disease management interventions and preventing disease outbreaks. For example, a SYBR Green-based qPCR assay was developed for the rapid detection of *Trichoderma afroharzianum*, a fungus associated with maize ear rot, demonstrating high sensitivity and specificity in infected maize samples (Sanna et al., 2026). Similarly, qPCR-based diagnostic tools have been widely used in seed health testing and quarantine programs to prevent the spread of fungal pathogens through contaminated planting materials. In addition to PCR-based methods, isothermal nucleic acid amplification technologies have emerged as promising alternatives for rapid field diagnostics. Loop-mediated isothermal amplification (LAMP) is one such technique that allows DNA amplification under constant temperature conditions without the need for sophisticated laboratory equipment. LAMP assays have been successfully applied for the detection of various plant pathogens, including *Fusarium* species affecting maize. Compared with conventional PCR, LAMP offers several advantages such as rapid reaction time, high amplification efficiency, and suitability for on-site diagnostic applications (Niessen, 2023). The development of portable LAMP-based diagnostic kits has enabled farmers and plant protection specialists to detect pathogens directly in the field, thereby improving disease surveillance and management practices.

Recent advances in high-throughput sequencing technologies have further expanded the capabilities of molecular pathogen detection. Next-generation sequencing (NGS) platforms allow comprehensive analysis of fungal genomes and microbial communities associated with maize plants and soils. Metagenomic sequencing approaches enable researchers to simultaneously identify multiple microorganisms present within plant tissues, including both pathogenic and beneficial microbes. This technology has revealed a previously hidden diversity of fungal species in maize agroecosystems and has improved understanding of pathogen interactions within plant microbiomes (Sobiech et al., 2022; Zhang et al., 2023). Metabarcoding approaches based on ITS sequencing are particularly useful for studying fungal community structure and detecting emerging pathogens that may not be identifiable through targeted PCR methods. Another important molecular approach for pathogen identification is multilocus sequence typing (MLST), which involves analyzing multiple genetic loci to characterize fungal isolates. MLST provides detailed insights into the genetic diversity, population structure, and evolutionary relationships of fungal pathogens. This technique has been widely used to study population dynamics of *Fusarium* species associated with maize diseases. By analyzing multiple gene sequences, researchers can

Table 1: Molecular techniques used for identification of maize fungal pathogens (2022–2026).

Study	Pathogen Investigated	Molecular Technique	Key Findings
Shang et al., 2022	Fusarium spp.	PCR, ITS sequencing	Improved detection of ear rot pathogens in maize
Harish et al., 2023	Fusarium spp.	MLST, phylogenetic analysis	Revealed genetic diversity among isolates
Nsibo et al., 2024	Exserohilum turcicum, Bipolaris maydis	Population genomics	Identified regional pathogen diversity
Sanna et al., 2026	Trichoderma afroharzianum	Real-time PCR	Developed rapid pathogen detection assay
Sobiech et al., 2022	Fusarium spp.	NGS, marker analysis	Identified resistance-associated molecular markers
Gherbawy et al., 2025	Fusarium spp.	TEF-1α sequencing	Clarified species boundaries and phylogeny
Deressa et al., 2025	Fusarium verticillioides	Multiplex PCR	Simultaneous detection of multiple pathogens
Zhang et al., 2023	Fusarium, Cercospora, Bipolaris	Metabarcoding, NGS	Characterized fungal community in maize phyllosphere
Bugingo et al., 2025	Fusarium, Exserohilum	Whole-genome sequencing	Identified virulence genes and mycotoxin clusters
Niessen, 2023	Fusarium solani	LAMP	Developed field-applicable rapid detection assay
Tomkowiak, 2024	Ustilago maydis	RNA-seq, genome analysis	Elucidated host-pathogen interaction genes
Ansari et al., 2026	Fusarium spp., Bipolaris spp.	CRISPR-based detection	High-specificity pathogen detection
Chao et al., 2025	Exserohilum turcicum	Whole-genome sequencing	Population diversity and host adaptation revealed
Nadasen et al., 2025	Cercospora zeina	Transcriptomics	Identified effectors suppressing host immunity
Zhong et al., 2024	Cercospora zeina	GWAS, genomic markers	Discovered genes conferring quantitative resistance
Roggenkamp, 2024	Phyllachora maydis	ITS, TEF-1α sequencing	Confirmed species identity and pathogenicity
Yang et al., 2022	Fusarium graminearum	MLST	Revealed population structure in maize-growing regions
Lenort et al., 2025	Fusarium spp.	qPCR	Quantified pathogen load for early detection
Mthembu, 2024	Fusarium solani, soilborne fungi	ITS sequencing	Detected root rot pathogens in maize fields
Sobiech et al., 2023	Fusarium verticillioides	NGS and SNP markers	Linked resistance loci to ear rot susceptibility

identify genetic lineages, track pathogen spread across geographic regions, and detect the emergence of new virulent strains (Gherbawy et al., 2025). Such information is essential for designing effective disease management strategies and breeding programs aimed at improving host resistance. Whole-genome sequencing (WGS) has further enhanced our understanding of maize fungal pathogens by providing complete genomic information about pathogen species. Genome sequencing enables identification of genes associated with virulence, pathogenicity, and mycotoxin production. In the case of *Fusarium verticillioides*, genomic studies have identified gene clusters responsible for fumonisin biosynthesis, providing insights into the molecular basis of mycotoxin production and its regulation during infection (Bugingo et al., 2025). Transcriptomic analyses using RNA sequencing (RNA-seq) have also been employed to investigate gene expression patterns during host–pathogen interactions, revealing key molecular mechanisms involved in fungal infection and host defense responses. More recently, CRISPR-based diagnostic technologies have emerged as innovative tools for rapid pathogen detection. These systems utilize CRISPR-associated enzymes that recognize specific DNA sequences and produce detectable signals when target pathogens are present. CRISPR diagnostics offer extremely high sensitivity and specificity and can potentially be adapted for field-based detection of plant pathogens. Although still in early stages of development for plant disease diagnostics, CRISPR-based detection methods hold significant promise for future maize disease surveillance programs (Table 1).

Integrated Management Strategies for Maize Fungal Diseases

The management of fungal diseases in maize requires a holistic and integrated approach that combines cultural, genetic, biological, and chemical control methods.

Table 2: Integrated management strategies for maize fungal diseases.

Study	Disease/Pathogen	Management Strategy	Major Outcome
Arif et al., 2025	Fusarium ear rot	Integrated pest management (IPM)	Reduced disease incidence in field trials
Nsibo et al., 2024	Foliar fungal pathogens	Host resistance, surveillance	Improved disease monitoring
Sobiech et al., 2022	Fusarium diseases	Marker-assisted breeding	Enhanced resistance in maize lines
Tomkowiak, 2024	Maize smut	Genomic resistance markers	Identified candidate resistance genes
Ansari et al., 2026	Multiple pathogens	RNA-based control technologies	Eco-friendly disease suppression
Moya-Elizondo et al., 2023	Fusarium spp., Bipolaris spp.	Biological control (Trichoderma/Bacillus spp.)	Suppressed pathogen growth and improved plant health
Zhong et al., 2024	Gray leaf spot	Genomic selection and GWAS	Developed quantitative resistant maize lines
Paul et al., 2023	Foliar pathogens	Targeted fungicide application	Controlled epidemics while minimizing resistance risk
Berg et al., 2024	Fusarium, Cercospora	Microbiome engineering	Improved plant resilience and disease suppression
Deressa et al., 2025	Fusarium verticillioides	Crop rotation, residue management	Reduced soil inoculum and disease incidence
Gaffar & Koch, 2023	Fusarium spp.	RNAi-based control (HIGS/SIGS)	Significant reduction of pathogen infection
Chao et al., 2025	Exserohilum turcicum	Resistant cultivar deployment	Limited disease outbreaks in field trials
Bugingo et al., 2025	Fusarium, Bipolaris	Molecular diagnostics + IPM	Early detection improved management efficiency
Roggenkamp, 2024	Tar spot (Phyllachora maydis)	Cultural + resistant varieties	Reduced epidemic spread under high disease pressure
Shang et al., 2022	Fusarium ear rot	PCR-based seed health testing	Prevented introduction of infected seeds
Nsibo et al., 2023	Bipolaris maydis	Foliar fungicide rotation	Mitigated fungicide resistance development
Niessen, 2023	Fusarium solani	Field-deployable LAMP diagnostics + cultural control	Rapid detection and management in smallholder farms
Sanna et al., 2026	Trichoderma afroharzianum	Biological and chemical integration	Optimized pathogen suppression in maize ears
Mthembu, 2024	Root-infecting fungi	Resistant rootstock + soil amendments	Enhanced seedling survival and yield
Zhong et al., 2023	Gray leaf spot	High-throughput phenotyping + genomic selection	Accelerated breeding of resistant varieties

Because fungal pathogens often survive in soil, crop residues, or infected seeds, relying on a single management strategy is rarely sufficient to control disease outbreaks. Integrated disease management (IDM) strategies aim to reduce pathogen inoculum, enhance host resistance, and minimize environmental conditions favorable for disease development (Table 2). In maize production systems, these strategies play a crucial role in ensuring sustainable crop productivity and minimizing yield losses caused by fungal pathogens such as *Fusarium spp.*, *Exserohilum turcicum*, *Bipolaris maydis*, and *Cercospora zeina* (Arif et al., 2025; Nsibo et al., 2024). The integration of modern molecular diagnostics with traditional agronomic practices has further strengthened disease management programs by enabling early detection and targeted interventions. Cultural practices remain one of the most fundamental components of integrated management strategies for maize fungal diseases. Practices such as crop rotation, residue management, optimal planting density, and proper irrigation scheduling significantly influence the epidemiology of fungal pathogens. Crop rotation with non-host crops, for example legumes or cereals that are less susceptible to maize pathogens, helps reduce pathogen inoculum in the soil and interrupts disease cycles. Residue management practices such as tillage or removal of infected plant debris can further decrease the survival of fungal pathogens that overwinter in crop residues. In addition, adjusting planting dates and plant spacing can improve air circulation within the crop canopy, thereby reducing humidity levels that favor fungal growth and spore germination (Deressa et al., 2025). Adequate nutrient management also contributes to disease suppression by promoting vigorous plant growth and strengthening plant defense mechanisms. For instance, balanced fertilization with nitrogen, phosphorus, and potassium has been shown to enhance maize resistance against several fungal pathogens.

Host plant resistance is widely regarded as one of the most effective and environmentally sustainable strategies for controlling maize fungal diseases. The development of resistant maize varieties has been significantly accelerated by advances in molecular breeding and genomic technologies. Marker-assisted selection (MAS) allows plant breeders to identify and select genetic markers associated with disease resistance traits, thereby improving the efficiency of breeding programs. Several resistance genes and quantitative trait loci (QTLs) associated with resistance to *Fusarium* ear rot, northern corn leaf blight, and gray leaf spot have been identified through genome-wide association studies (GWAS) and high-throughput sequencing technologies (Sobiech et al., 2022; Zhong et al., 2024). These molecular markers enable breeders to screen large populations of maize lines for disease resistance without relying solely on time-consuming field evaluations. Furthermore, genomic selection and gene editing technologies are increasingly being explored to enhance resistance against complex fungal pathogens that involve multiple virulence factors. Biological control has emerged as an environmentally friendly alternative to chemical fungicides for managing maize fungal diseases. Beneficial microorganisms such as *Trichoderma spp.*, *Bacillus spp.*, and *Pseudomonas spp.* have demonstrated considerable potential in suppressing fungal pathogens through multiple mechanisms. These mechanisms include competition for nutrients and space, production of antifungal metabolites, parasitism of pathogenic fungi, and induction of systemic resistance in host plants (Moya-Elizondo et al., 2023). Among these beneficial microbes, species of the genus *Trichoderma* are particularly well studied due to their ability to colonize plant roots and protect plants from soil-borne pathogens such as *Fusarium*. Similarly, *Bacillus* species produce various antimicrobial compounds that inhibit the growth of pathogenic fungi and enhance plant defense responses. Recent studies have also explored the use of microbial consortia and endophytic fungi as biological control agents, providing promising alternatives for sustainable disease management.

Chemical fungicides continue to play an important role in maize disease management, particularly during severe disease outbreaks or under highly conducive environmental conditions. Fungicides belonging to different chemical classes, such as triazoles, strobilurins, and succinate dehydrogenase inhibitors (SDHIs), are commonly used to control foliar fungal diseases including northern corn leaf blight and gray leaf spot. These fungicides inhibit critical metabolic pathways in fungal cells, thereby preventing pathogen growth and infection. However, the excessive or indiscriminate use of fungicides can lead to the development of fungicide resistance in pathogen populations, as well as negative environmental impacts. Therefore, modern integrated pest management (IPM) strategies emphasize the judicious and targeted use of fungicides in combination with other disease management approaches (Paul et al., 2023). Monitoring pathogen populations and applying fungicides only when disease thresholds are exceeded can significantly reduce the risk of resistance development and environmental contamination. Recent technological advancements have also contributed to the improvement of integrated disease management strategies in maize production systems. Precision agriculture tools, remote sensing technologies, and digital disease surveillance systems allow farmers to monitor crop health and detect disease symptoms at early stages. These technologies enable site-specific disease management practices, such as targeted fungicide applications or localized biological control treatments. Additionally, molecular diagnostic tools such as PCR and next-generation sequencing have improved the accuracy and speed of pathogen detection, enabling more effective disease monitoring and forecasting systems (Bugingo et al., 2025). Such innovations support the development of data-driven disease management strategies that optimize resource use and reduce environmental impacts. Another promising approach in integrated disease management is the use of RNA-based technologies for controlling fungal pathogens. RNA interference (RNAi) strategies involve targeting essential fungal genes responsible for virulence or survival. Spray-induced gene silencing (SIGS) and host-induced gene silencing (HIGS) are emerging techniques that can suppress pathogen gene expression without the need for traditional chemical fungicides. Although these technologies are still under development, preliminary studies have demonstrated their potential effectiveness against several plant pathogenic fungi (Ansari et al., 2026). As research in this field continues to advance, RNA-based approaches may become valuable components of sustainable disease management strategies. By combining cultural practices, resistant cultivars, biological control agents, and judicious fungicide use, farmers can significantly reduce disease incidence and minimize crop losses. The integration of molecular diagnostics and modern genomic technologies further enhances disease management by enabling early detection, accurate pathogen identification, and targeted control measures. Continued research and collaboration among plant pathologists, breeders, and agronomists will be essential to develop innovative and sustainable solutions for managing maize fungal diseases in the face of evolving pathogen populations and changing environmental conditions (Table 2).

Emerging Technologies and Future Perspectives

Rapid technological advancements in molecular biology, genomics, and biotechnology are transforming the detection and management of fungal pathogens affecting maize. Conventional diagnostic and disease management approaches, although effective to some extent, often face limitations such as delayed detection, pathogen evolution, and environmental concerns associated with chemical control methods. Emerging technologies are therefore being explored to improve early pathogen detection, enhance disease resistance in crops, and develop environmentally sustainable disease management strategies. These innovations are expected to play a critical role in addressing the growing challenges posed by fungal pathogens in maize production systems, particularly under changing climatic conditions and increasing global demand for food security (Bugingo et al., 2025; Nsibo et al., 2024). One of the most promising developments in plant disease diagnostics is the application of CRISPR-based detection technologies. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) systems, originally discovered as adaptive immune mechanisms in bacteria, have been adapted for highly sensitive molecular diagnostics. CRISPR-based platforms such as SHERLOCK and DETECTR utilize CRISPR-associated enzymes to recognize specific DNA or RNA sequences of pathogens and generate detectable signals. These systems allow rapid, accurate, and portable detection of plant pathogens, often within minutes. Recent studies have demonstrated the potential of CRISPR diagnostics in identifying fungal pathogens in plant tissues with high specificity and sensitivity (Ansari et al., 2026). For maize diseases, such technologies could enable on-site detection of pathogens such as *Fusarium verticillioides*, *Exserohilum turcicum*, and *Cercospora zeina*, thereby facilitating rapid disease surveillance and early intervention strategies. The development of portable diagnostic devices integrating CRISPR technology with smartphone-based detection systems could further enhance field-based pathogen monitoring.

Another emerging strategy for controlling fungal diseases in maize is the use of RNA-based technologies, particularly RNA interference (RNAi). RNAi is a natural biological mechanism that regulates gene expression through the degradation of specific messenger RNA (mRNA) molecules. In plant disease management, RNAi can be used to silence genes that are essential for pathogen survival, virulence, or toxin production. Two main approaches have been explored in this context: host-induced gene silencing (HIGS) and spray-induced gene silencing (SIGS). In HIGS, plants are genetically engineered to produce RNA molecules that target specific pathogen genes during infection. In contrast, SIGS involves the external application of double-stranded RNA (dsRNA) molecules directly onto plant surfaces, where they are taken up by fungal pathogens and trigger gene silencing (Gaffar & Koch, 2023). Recent experimental studies have shown that SIGS can effectively suppress the growth of several fungal pathogens, including species of *Fusarium* that cause ear rot diseases in maize. Compared with conventional fungicides, RNA-based approaches offer several advantages, including high specificity, minimal environmental impact, and reduced risk of resistance development. Advances in genomics and high-throughput sequencing technologies have also significantly contributed to improving disease resistance in maize breeding programs. Whole-genome sequencing and genome-wide association studies (GWAS) have enabled the identification of numerous resistance genes and quantitative trait loci (QTLs) associated with resistance to major fungal pathogens. For example, genomic studies have identified candidate genes associated with resistance to gray leaf spot and northern corn leaf blight, providing valuable resources for maize improvement programs (Zhong et al., 2024). The integration of genomic selection methods allows breeders to predict the performance of breeding lines based on genomic information, thereby accelerating the development of disease-resistant maize varieties. These approaches are particularly useful for complex traits such as quantitative disease resistance, which is controlled by multiple genes and influenced by environmental factors (Figure 2).

High-throughput phenotyping technologies are increasingly crucial for crop improvement and disease management. Traditional methods depend on manual observation and scoring of disease symptoms, which can be slow and subjective. Modern phenotyping platforms utilize advanced imaging, drones, and remote sensing systems to monitor plant health and identify early disease symptoms. These technologies allow for large-scale screening of maize germplasm for disease resistance under field conditions. For example, hyperspectral imaging and thermal sensors can detect physiological changes in plants before visible symptoms appear, helping researchers identify resistant genotypes more efficiently (Singh et al., 2023). When combined with genomic data, high-throughput phenotyping greatly improves the accuracy and efficiency of breeding programs focused on increasing disease resistance. Another promising research area involves microbiome-based approaches for disease management. The plant microbiome, which includes diverse microbial communities associated with plant tissues and the rhizosphere, plays a vital role in plant health and disease resistance. Advances in metagenomic sequencing have shown that beneficial microbes can suppress fungal pathogens through mechanisms such as competition, antibiosis, and induction of host immune responses. Manipulating the maize microbiome with microbial inoculants or microbiome engineering offers new opportunities for sustainable disease control (Berg et al., 2024). Identifying and using beneficial microbial communities can help protect maize from fungal infections and reduce reliance on chemical pesticides.

Climate change poses another major challenge for maize disease management since changing environmental conditions can disrupt pathogen distribution, virulence, and host susceptibility. Rising temperatures, increased

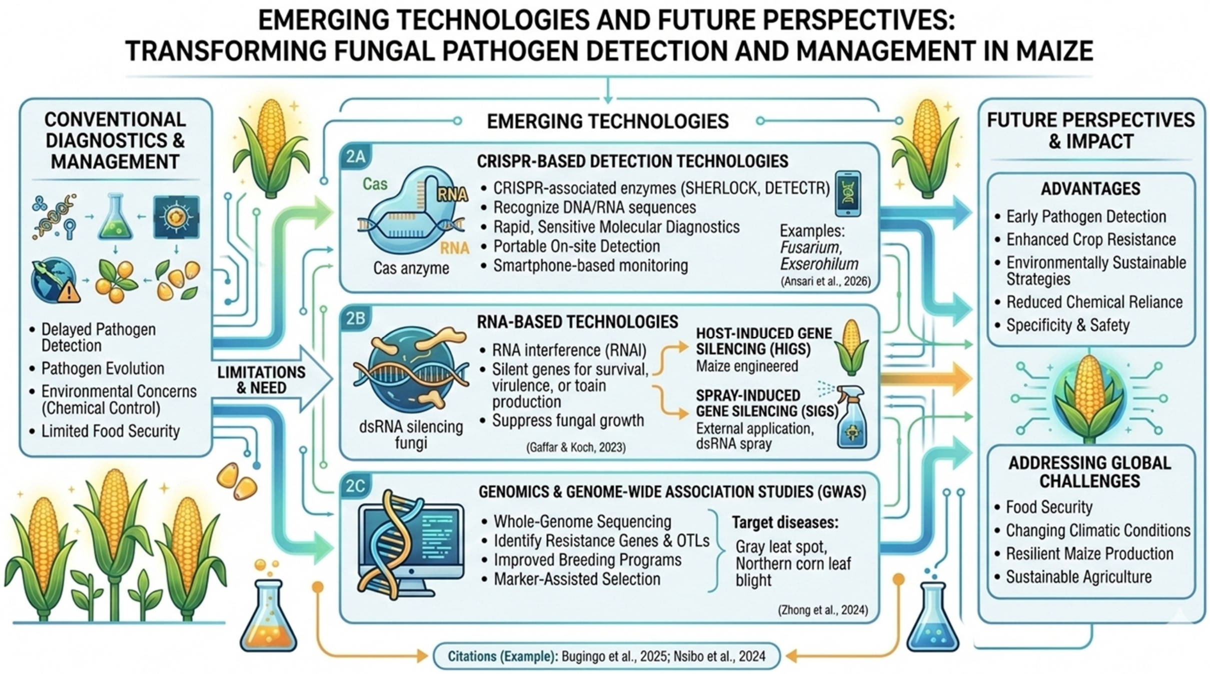

Figure 2: Emerging technologies and future perspectives for fungal pathogen detection and management in maize

humidity, and extreme weather events may foster the development and spread of new fungal pathogens. Therefore, future research should focus on creating climate-resilient maize varieties that can endure both abiotic stresses and pathogen attacks. Combining genomic selection, molecular diagnostics, and predictive disease modeling will be crucial for better disease forecasting and the development of adaptive management strategies (Bugingo et al., 2025). Despite these promising technological advances, significant challenges remain in applying research findings practically in agriculture. High costs, limited technical skills, and lack of infrastructure may hinder the adoption of advanced molecular technologies in developing regions where maize is a key staple crop. Additionally, regulatory frameworks for biotechnology-based disease management methods like RNAi and CRISPR diagnostics must be clearly established to ensure their safe and responsible use. Addressing these issues will require coordinated efforts among researchers, policymakers, agricultural extension services, and farmers (Figure 2).

CONCLUSION

Fungal pathogens remain a major constraint to global maize production, causing significant yield losses and mycotoxin contamination. Recent advances in molecular diagnostics, including PCR, qPCR, NGS, MLST, LAMP, and CRISPR-based platforms, have greatly improved the accuracy and speed of pathogen detection, enabling early intervention and informed disease management. Integrated management strategies combining cultural practices, host resistance, biological control, and judicious fungicide use have demonstrated substantial effectiveness in suppressing maize fungal diseases. Emerging technologies such as RNA-based control, genomic selection, high-throughput phenotyping, and microbiome engineering offer promising opportunities for sustainable and environmentally friendly disease management. Continued integration of molecular tools, innovative technologies, and traditional approaches will be essential for enhancing maize resilience and securing global food production.

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