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Molecular Defense Mechanisms of Sorghum Against Major Diseases

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Abstract Sorghum is a very important food and energy crop in the world, but it is often affected by many diseases, such as anthracnose, grain mold, bacterial stripe disease, and pests like aphids. These problems will cause the yield of sorghum to decline and also affect its quality. In recent years, molecular biology and multi-omics techniques have developed rapidly, which has also helped us more clearly understand the disease resistance mechanism of sorghum. Current research indicates that sorghum defuses pathogens in multiple layers. It can first identify the signals related to pathogens and then transmit these signals, such as through MAPK or some hormone routes. Then, many disease-resistant genes will be activated in sorghum, including some NLR receptors, PR proteins, antimicrobial peptides, and 3-deoxyanthocyanins, etc. Meanwhile, the metabolic process of sorghum will also be rearranged, thereby enhancing its broad-spectrum resistance to fungi, bacteria and insects. The integration of multi-omics data (such as genomics, transcriptomics, and metabolomics) offers us a more comprehensive picture, which includes many complex regulatory networks, such as disease-resistant genes, signaling pathways, and various metabolites. Genome editing technologies, such as CRISPR/Cas9, as well as molecular marker-assisted selection, also make disease-resistant breeding more precise and efficient. The utilization of the microbiome to help sorghum defend against diseases or the application of some biological control methods is also regarded as very promising. Future research needs to integrate multi-omics and systems biology to conduct a more in-depth study on how sorghum defuses against the simultaneous infection of multiple pathogens. At the same time, it is also necessary to better integrate molecular breeding with traditional breeding to enhance the efficiency of selecting disease-resistant varieties and achieve more stable and sustainable disease management.

Keywords Sorghum; Molecular defense mechanism; Disease-resistant breeding; Multi-omics; Pathogen interaction

1 Introduction

Sorghum bicolor is the fifth largest grain in the world and is mainly grown in arid and semi-arid regions. It can be used not only as food, but also as feed, energy crops and industrial raw materials. It is of great significance to food security and economic development. Sorghum has a strong adaptability to the environment and good nutritional value, so in many developing countries, many people take it as their staple food. Meanwhile, it is also receiving increasing attention in bioenergy and sustainable agriculture (Kazungu et al., 2023; Khaskheli et al., 2025).

Although sorghum can adapt to many adverse environments, its growth is still affected by various diseases, especially those caused by fungi, bacteria and insects. Common fungal diseases include anthracnose (*Colletotrichum sublineola*), valley mold, stem rot, powdery mildew, rust, etc. All of them can significantly reduce the yield and quality of sorghum (Govintharaj et al., 2025). In addition, bacterial leaf spot disease (*Burkholderia andropogonis*) and pests (such as sugarcane aphids) can also cause serious damage (Huang et al., 2022; Rizvi et al., 2024; Ikuze et al., 2025). These diseases will not only reduce the yield, but also may accumulate some harmful toxins in crops, ultimately affecting food safety and human health (Ackerman et al., 2021).

The disease resistance of sorghum mainly stems from a relatively complex molecular defense network within its body. It can first identify pathogen-related signals (PAMP), initiate the PTI response, and then generate a stronger specific response through resistance genes. Then, multiple signaling pathways within the plant will be activated, such as those related to salicylic acid, jasmonic acid and ethylene. Meanwhile, sorghum also produces antimicrobial peptides, some secondary metabolites (such as 3-deoxyanthocyanins, flavonoids and phenolic compounds), etc. to enhance defense capabilities (Pant and Huang, 2022; Fang et al., 2023). However, we still do not have a sufficient understanding of the molecular mechanisms by which sorghum responds to attacks by different pathogens, especially the regulatory methods in different genotypes and different tissues (such as grains), many of which remain unclear (Nida et al., 2021).

Further clarifying the molecular defense mechanism of sorghum can not only help us better understand its genetic basis for disease resistance, but also provide new theories and more specific targets for breeding disease-resistant varieties and conducting more sustainable disease management.

2 Overview of the Immune System of Sorghum

2.1 Basic immunity (PTI)

The basic immunity (PTI) of sorghum is its first line of defense against pathogen invasion. This process mainly relies on pattern recognition receptors (PRRs) on the cell membrane. These recipients can recognize the molecular characteristics (PAMPs) of pathogens, such as flagellin or chitin, and then activate subsequent defense signals (Cui et al., 2021) (Figure 1). Once PTI is activated, a series of reactions will occur rapidly in plants, such as increased reactive oxygen species (ROS), stronger cell walls, production of some antibacterial substances, and initiation of the expression of many defense genes (Ding et al., 2022). In sorghum, after the addition of PAMP, the expressions of many PRR and defension-related genes will increase, thereby enhancing resistance to multiple pathogens (Jiang et al., 2023). In addition, the post-translational modification processes of some proteins (such as acetylation) can also affect PTI, altering the activity and stability of defense proteins.

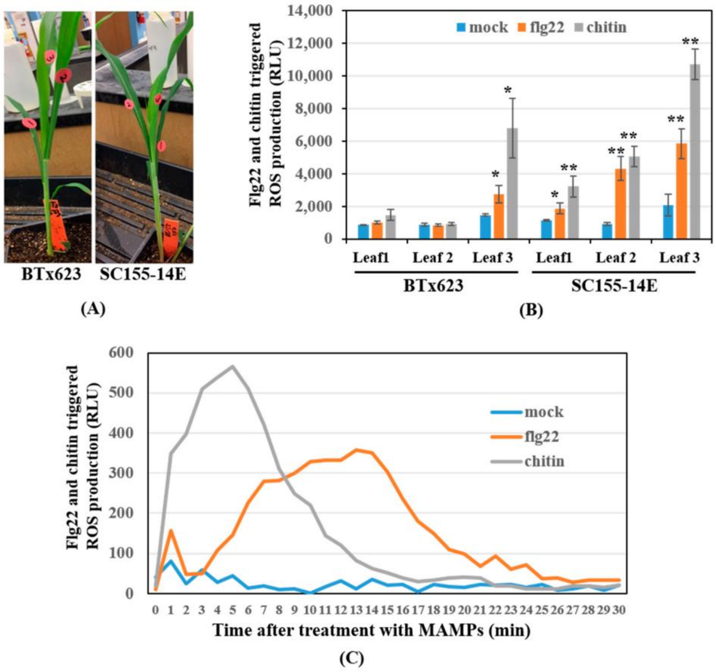

Figure 1 Effect of leaf position on the ROS response to MAMP elicitation in sorghum genotypes BTx623 and SC155-14E. (A) Fifteen-day old BTx623 and SC155-14E plants. The leaves from bottom to top were marked as leaf #1 (older leaf), leaf #2 (2nd youngest leaf) and leaf #3 (youngest leaf). (B) ROS response to flg22 or chitin elicitation of all three leaves of fifteen-day old BTx623 and SC155-14E plants. RLU, relative light units; Error bars indicate ± SEM; n = 8; * <0.05 (t test) and ** <0.01. (C) Time course of flg22-triggered and chitin-triggered ROS production in leaf # 2 of SC155-14E (Adopted from Cui et al., 2021)

2.2 Effector triggering immunity (ETI)

When pathogens secrete effectors and attempt to inhibit PTI, plants initiate a second line of immunity, namely effector triggered immunity (ETI). ETI is mainly mediated by intracellular resistance proteins, many of which are NLR receptors. They can directly or indirectly identify these effectors and then trigger stronger and more targeted defense responses (Nguyen et al., 2021; Khan et al., 2025). ETI is often accompanied by rapid programmed cell death (HR) to prevent the further spread of pathogens and promote systemic resistance formation (Guo and Cheng, 2022; Yu et al., 2024). ETI not only enhances the expression of PTI-related genes, but also makes ROS burst stronger, and the signal transduction response faster and more persistent.

2.3 Interaction and synergy between PTI and ETI

Recent studies have found that PTI and ETI are actually not two completely separate routes, but an integrated system with high synergy (Yu et al., 2024). ETI can restore or enhance PTI by strengthening some key components in PTI (such as PRR, signal proteins, ROS-generating enzymes, etc.), forming an "amplification" effect (Nguyen et al., 2021; Yuan et al., 2021). PTI and ETI share many links in signal transduction, gene expression and defense substance production, but ETI comes faster and is stronger. This interaction enables plants to be more flexible and have more redundant protection when facing different pathogens or environmental pressures. However, although there have been many studies on the PTI-ETI interaction in model plants, in crops such as sorghum, the related molecular mechanisms still require further in-depth research (Cui et al., 2021; Fang et al., 2023).

3 The Molecular Signaling Pathways of Sorghum Defense

3.1 Hormone-mediated defense

Hormones in plants play a very important regulatory role in the disease resistance process of sorghum. Hormones such as salicylic acid (SA), jasmonic acid (JA), and abscisic acid (ABA) usually rise when sorghum is attacked by fungi, bacteria or insects. Moreover, in some varieties with stronger resistance, the increase of these hormones is more obvious. Similar situations can be observed in materials resistant to aphids or valley mold disease (Huang et al., 2022; Shrestha et al., 2024) (Figure 2). Exogenous addition of some SA, JA or ABA can also reduce disease damage in originally susceptible sorghum and lower the mortality rate. This indicates that these hormones can indeed positively regulate defense (Pant and Huang, 2022). In addition, SA and JA can not only cooperate with each other but also may restrain each other. They jointly regulate the expression of subsequent defense genes and the accumulation of resistance substances.

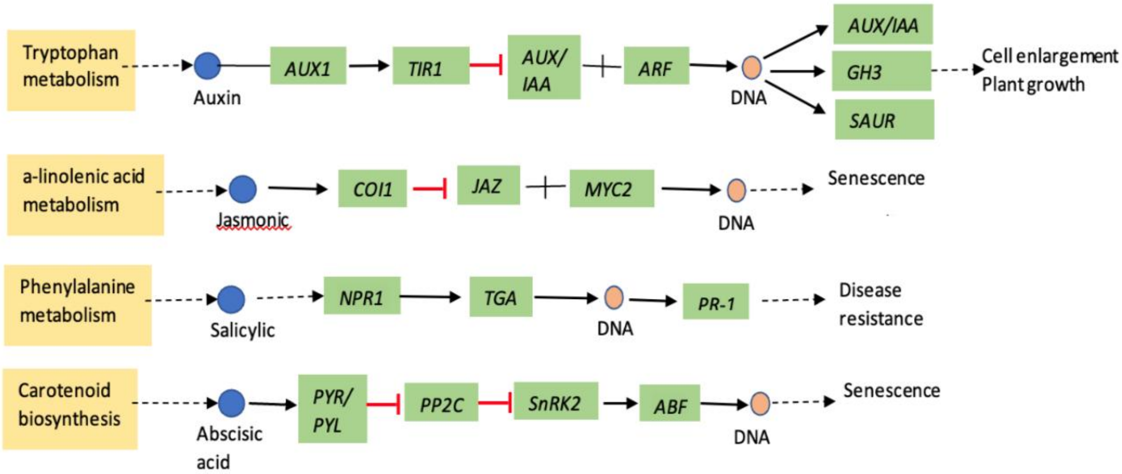

Figure 2 Schematic diagram of major plant hormone signal transduction pathway for sorghum (adapted from KEGG, yellow highlights are pathway name, dotted arrow represents multiple enzymatic steps, green highlights are genes in respective pathways). AUX-auxin influx carrier; TIR1-transport inhibitor response1; AUX/IAA-auxin/indole-3-acetic acid; ARF-auxin response factor; GH3-auxin responsive Gretchen hagen3; SAUR-small auxin upregulated RNA; COI1-coronatine-insensitive protein 1; JAZ-jasmonate ZIM-domain; MYC2-transcription factor MYC2; NPR1-regulatory protein NPR1; TGA-transcription factor TGA; PR-1-pathogenesis related-1; PYR/PYL-abscisic acid receptor PYR/PYL family; PP2C-protein phosophatase 2C; snRK2-serine/threonine-protein kinase; ABF-ABA responsive element biding factor (Adopted from Huang et al., 2022)

3.2 Reactive oxygen species (ROS) outbreak

Reactive oxygen species (such as H_2O_2) are very typical signals of sorghum in early defense. They can not only directly inhibit the growth of pathogens, but also act as signals to continue promoting the subsequent defense routes (Puri et al., 2023). In disease-resistant varieties, when pathogens infect or aphids feed on them, genes related to ROS generation will be rapidly upregulated. Meanwhile, some antioxidant enzymes (such as peroxidase, glutathione S-transferase, etc.) will also increase simultaneously to balance the number of ROS and prevent plant self-injury. ROS signaling can also promote the synthesis of SA and further enhance the expression of some defense proteins (such as PR protein).

3.3 Calcium signaling and MAPK cascading

Calcium ions (Ca^{2+}) are very crucial signaling molecules in plant defense. After pathogen or insect attacks, genes such as calmodulin (CAM) and calmodulin-like protein (CMLs) are rapidly upregulated in sorghum. These genes can sense calcium signals and continue to initiate subsequent cascade reactions (Khasin et al., 2021). Meanwhile, the MAPK cascade is also very important in sorghum defense, as it can amplify signals and promote various defense responses. The expression of genes such as MAPK17/18 and MEKK3 in resistant materials is significantly increased, thereby promoting ROS generation, cell death response and the expression of defense genes. MAPK can also add phosphate to some transcription factors, enabling them to better regulate downstream defense genes.

3.4 Transcriptional regulatory factors

Many transcription factors (TFs) are also involved in the defense regulation of sorghum. Members of the WRKY, MYB, AP2/ERF families can be induced to express after pathogen or insect infection. They can regulate the synthesis of defense genes, some secondary metabolites (such as flavonoids, 3-deoxyanthocyanins), and antimicrobial peptides. For example, WRKY22 and WRKY33 will continuously rise in aphid resistant sorghum, helping with signal transduction and the accumulation of defense products (Rashad et al., 2022). In addition, the expression changes of transcriptional repressor factors like JAZ also remind us that sorghum actually requires a fine balance between "growth" and "defense".

4 The Main Defense-related Genes and Metabolic Pathways of Sorghum

4.1 Disease-resistant related (PR) genes

During the disease resistance process of sorghum, many PR genes will be significantly upregulated, such as Sobic.001G401200, Sobic.005G169200, etc. The proteins encoded by these genes include defensins, antimicrobial peptides, some receptor kinases, etc. They can directly suppress the growth of pathogens and also initiate more immune responses below. The higher the expression of the PR gene, the stronger the resistance of sorghum to diseases such as valley mold and aphids is usually (Mutinda et al., 2022). Furthermore, some NLR genes (such as ARG1) are also involved in resistance. They are often regulated at the epigenetic and transcriptional levels, thereby enabling sorghum to acquire a relatively broad-spectrum fungal resistance (Lee et al., 2022).

4.2 Phenylpropane pathway and secondary metabolites

The phenylpropane pathway is a very important metabolic route in sorghum defense, capable of synthesizing resistant substances such as lignin, flavonoids, and 3-deoxyanthocyanins. Genes such as PAL, CCoAOMT, and DFR3 are significantly upregulated in disease-resistant varieties, helping to accumulate more lignin and antibacterial components (Khasin et al., 2021). Some of these 3-deoxyanthocyanins (such as apigeninidin, luteolinidin) show strong effects in antifungal and pest resistance. Transcription factors such as MYB also regulate the expression of these metabolic genes, thereby affecting the amount and mode of accumulation of resistant substances.

4.3 Structural barriers and cell wall modification

Sorghum enhances resistance by strengthening the cell wall structure, such as thickening the cell wall, depositing more lignin, β-glucan and callose, etc. (Mutinda et al., 2022). Genes such as CCoAOMT, COMT, and CAD regulate lignin synthesis, making the cell wall stronger and more capable of blocking pathogen entry (Grover et al., 2024). In varieties with high resistance, these genes are usually upregulated more quickly after pathogen infection, making the cell wall stronger and thereby limiting pathogen spread.

4.4 Small rnas and post-transcriptional regulation

Small Rnas (such as miRNA, siRNA) and natural antisense transcripts (NAT) are also important in the defense regulation of sorghum, and they mainly act in the post-transcriptional stage (Govintharaj et al., 2025). For example, the expression of the *ARG1* gene is regulated by its corresponding NAT (CARG), which affects the splicing situation and epigenetic status of ARG1, and thereby influences the resistance of sorghum (Lee et al., 2022). In addition, non-coding RNA and small RNA can further affect the expression of defense genes by regulating the stability and translation efficiency of mRNA, enabling sorghum to respond to different pathogens such as fungi and parasitic plants.

5 The Molecular Defense Mechanisms of the Main Diseases of Sorghum

5.1 Anthrax (*Colletotrichum sublineolum*)

The defense of sorghum against anthracnose mainly relies on epigenetic regulation, resistance genes (such as ARG1), PR protein, as well as phenylpropane and flavonoid metabolic pathways. The *ARG1* gene can function in multiple ways, such as being regulated by the natural antisense transcript CARG and also affected by histone methylation, so it can bring about a relatively broad-spectrum resistance. After the pathogen enters, the phenylpropane and flavonoid pathways will be rapidly activated, generating many antifungal 3-deoxyanthocyanins, such as apigeninidin and luteolinidin. In addition, receptor kinases such as BAK1/SERK4 can trigger PAMP immunity and also promote programmed cell death, thereby enhancing defense (Vela et al., 2025). Some post-transcriptional regulatory modalities (such as alternative splicing) can also affect the expression levels of defense genes.

5.2 Charcoal rot (*Macrophomina phaseolina*)

The charcoal rot pathogen can induce the upregulation of genes related to the cell wall degrading enzyme (CWDE) in sorghum itself, which makes the cell wall more vulnerable to damage and makes susceptible varieties more susceptible to the disease. However, resistant varieties can inhibit the upregulation of these enzymes, thereby maintaining the cell wall structure. In resistant materials, some antifungal genes (such as chitinase and styrene synthase) are expressed more frequently, which can effectively limit the spread of pathogens. Susceptible materials often experience more severe oxidative stress after infection, with excessive accumulation of ROS and RNS, leading to cell death and making the disease even more severe. Resistant varieties can enhance the activity of antioxidant enzymes, such as peroxidase and catalase, thereby reducing damage.

5.3 Valley mold complex

The resistance of trichoderma oryzae is regulated by multiple genes, involving pathogen recognition receptors (such as SbLYK5), PR protein, defensins, MAPK signaling pathway, and the production of antibacterial secondary metabolites such as 3-deoxyanthocyanins. MYB transcription factors (such as Y1 and Y3) regulate some flavonoid genes (such as DFR3), thereby affecting the accumulation of resistant substances (Nida et al., 2021). In varieties with high resistance, genes such as PR protein, defenin and antimicrobial peptide are rapidly upregulated after Aspergillus oryzae infection, enhancing the physical and chemical defense of grains. Some grain-specific proteins, such as KAFIRIN and LEA3, are also considered to be related to resistance.

5.4 Bacterial stripe disease (*Xanthomonas vasicola*)

The defense of sorghum against bacterial stripe disease is mainly achieved by regulating the cell wall structure and metabolic signals. Pathogens secrete various cell wall degrading enzymes (CWDE) to assist in infection, while sorghum strengthens the cell wall barrier by up-regulating lignin synthesis genes such as Bmr12 (also known as COMT) (Wang et al., 2025). The Bmr12 mutant is more susceptible to diseases, indicating that lignin metabolites (such as sinapaldehyde) have a direct inhibitory effect on the pathogen. Meanwhile, in the resistance response, the expression of the PR gene and some defense metabolites increases, and some of these metabolites can also suppress the pathogenic factors of the pathogen (Wang et al., 2021).

5.5 Viral diseases (MDMV, SCMV)

The defense of sorghum against viral diseases (such as MDMV and SCMV) involves PR genes, phenylpropane metabolism, hormone signaling (especially salicylic acid), and small RNA regulation. After the administration of salicylic acid, the expression of defense genes such as PR1, NPR1, and PAL will increase significantly, thereby enhancing resistance (Lu et al., 2023; Zhou et al., 2024). Viral infection can affect signaling pathways such as Ca^{2+}, ROS, and ethylene, and also alter the expression of transcription factors like WRKY and ERF. Small Rnas (such as mirnas) are also involved in early immune regulation and affect resistance levels by regulating the expression of target genes (Su et al., 2022).

6 Comprehensive Molecular and Breeding Strategies to Enhance Sorghum Resistance to Anthracnose: Case Analysis

6.1 Case background

Sorghum anthracnose (*Colletotrichum sublineola*) is one of the significant issues affecting global sorghum production, especially in warm and humid regions where the reduction in production is very obvious. The effects of traditional prevention and control methods are unstable, so the use of disease-resistant varieties has always been regarded as the most economical and sustainable approach. In recent years, with the development of molecular genetics and genomics, more disease-resistant genes have been discovered, which has also promoted the molecular breeding of anthracnose resistant sorghum (Lemu et al., 2021).

6.2 Discovery of resistance sites

Researchers used methods such as GWAS, linkage mapping and population genetics to identify multiple QTLS and resistance genes related to anthracnose resistance in many different sorghum germplasms. For example, NLR genes such as ARG4 and ARG5 have been identified in various materials, and most of them can provide broad-spectrum resistance (Cruet-Burgos et al., 2020; Cuevas et al., 2023; Habte et al., 2023). Further studies have found that these resistance genes are often concentrated in regions such as chromosome 5 and 9, and there are abundant allelic variations and copy number differences. These variations provide more options for breeding (Birhanu et al., 2024).

6.3 Transcriptomic insights

Transcriptome studies have shown that resistant sorghum will re-regulate many genes in the early stage of pathogen infection. Immune receptors, MAPK pathways, WRKy-like transcription factors, and genes related to secondary metabolism will all be rapidly activated. In addition, many NLR genes, antifungal related kinases and stress proteins are also significantly upregulated. Meanwhile, the small RNA network is also involved in regulating resistance (Fu et al., 2020; Zhang et al., 2025). Some physical barrier genes (such as those regulating epidermal wax) are also elevated, making it more difficult for pathogens to break through the plant surface (Xiong et al., 2023).

6.4 Application of molecular-assisted breeding

Based on the identified QTLS and candidate genes, researchers have developed a variety of molecular markers such as SNPS, SSRS, and AFLP for MAS and gene aggregation. These tools can significantly improve breeding efficiency and also help combine multiple resistance genes into the same material (Lemu et al., 2021; Habte et al., 2023). With the popularization of genome-wide selection technology and high-throughput typing tools, the speed of seeking resistance resources and utilizing these resources is also getting faster and faster (Birhanu et al., 2024).

6.5 Experience summary

The outcome of this case indicates that integrating molecular genetics, genomics and traditional breeding can significantly enhance sorghum's resistance to anthracnose. The aggregation of polyclonal resistance genes, the use of molecular markers, and the application of transcriptome data all provide reliable support for the improvement of disease-resistant varieties. However, the pathogenic bacteria themselves can change, and environmental factors can also affect the resistance effect. Therefore, the breeding work still needs to be constantly updated and evaluated, and verified at multiple locations. In the future, it is still necessary to continue to explore new resistance resources and conduct more systematic research on resistance mechanisms (Mekonen et al., 2025).

7 Frontier Technologies and Future Directions of Molecular Defense Mechanisms against Major Sorghum Diseases

7.1 Genomics and pan-genomics

The genomic sequencing of sorghum and major pathogenic bacteria has enabled us to have a clearer understanding of the disease resistance mechanism. Since the release of the sorghum reference genome in 2009, the genomes of different sorghum genotypes and some pathogenic bacteria (including the anthrax pathogen *Colletotrichum sublineola*) have also been sequenced successively. This provides a basis for the discovery of disease-resistant genes, QTLS and defense-related genes (Birhanu et al., 2024). Pan-genomics research has also enabled us to observe genetic differences among different sorghum varieties, including some new resistance alleles. These resources can be further used for disease-resistant breeding.

7.2 CRISPR/Cas genome editing

Gene editing technologies such as CRISPR/Cas9 have brought significant breakthroughs to disease-resistant sorghum breeding. By precisely modifying disease-resistant genes or susceptibility genes, resistance can be more accurately enhanced. For instance, after knocking out the related SL biosynthesis genes in sorghum with CRISPR/Cas9, the resistance of sorghum to the parasitic weed Striga was significantly enhanced (Weldemichael et al., 2024). Furthermore, the CRISPR/Cas system can also be used to regulate stress-resistant genes, disease defense pathways, and even achieve simultaneous improvement of multiple traits (Srivastava et al., 2025).

7.3 Multi-omics integration

Multi-omics analysis (such as genomics, transcriptomics, proteomics, and metabolomics) has become an important method for studying the disease resistance of sorghum. Looking at these data together can help us more systematically identify disease-resistant genes, signaling pathways and key metabolites, and understand the relationships among them. For example, after the combined analysis of transcriptome and metabolome, it can be seen that sorghum will focus on activating pathways such as flavonoid and phenylpropyl metabolism when responding to fungal diseases and abiotic stresses (such as salt, cadmium, drought) (Ren et al., 2022; Jiao et al., 2023; Yue et al., 2025). Multi-omics also helps to discover new disease-resistant markers and candidate genes, which can accelerate the breeding process (Birhanu et al., 2024; Ahn et al., 2025).

7.4 Microbiome assisted defense

The microbial communities on the roots and leaves of sorghum also play a significant role in the process of disease resistance. Studies have found that diseases such as anthracnose can alter the composition and network structure of the leaf surface and endophytic microbiome of sorghum, and this change can instead enhance the plant's own resistance (Chen et al., 2024). Some beneficial microorganisms (such as Trichoderma, Bacillus, PGPR, etc.) can also assist sorghum in various ways, such as inducing systemic resistance, secreting antibacterial substances, and improving nutrient absorption, thereby making sorghum more disease-resistant and growing better (Yadav et al., 2023). With the development of microbiome engineering and biocontrol products, green management methods for sorghum diseases will become more diverse (Chen et al., 2024).

8 Conclusions and Prospects

The defense of sorghum against major diseases (such as anthracnose, valley mold, aphids, etc.) relies on multi-level molecular mechanisms. These mechanisms include recognizing the PAMP signals of pathogens, initiating multiple signaling pathways (such as MAPK and hormone pathways), expressing a large number of disease-resistant genes (such as NLR receptors, PR proteins, and antimicrobial peptides), and generating metabolites such as 3-deoxyanthocyanins. These reactions together enable sorghum to have a strong defense against fungi, bacteria and insects.

Technologies such as molecular marker-assisted selection (MAS), GWAS, QTL mapping and genome editing have significantly accelerated the discovery and utilization of disease-resistant genes. For instance, in-depth research on NLR genes such as ARG1 and the precise localization of multiple QTLS have provided reliable evidence for breeding in areas like anthracnose resistance and aphid resistance. Meanwhile, the joint analysis of multiple omics (transcriptomics, metabolomics, proteomics) helps us gain a more comprehensive understanding of the resistance regulatory network and also provides more clues for the discovery of new resistance genes.

The joint advancement of traditional breeding methods (such as field resistance screening and germplasm utilization) and molecular techniques (such as marker-assisted selection, gene editing and transgenic) is the key path to enhancing the broad-spectrum resistance of sorghum. By conducting large-scale screening of resistant resources, aggregating polyresistant genes with molecular markers, and integrating systems biology and precise phenotypic analysis, the breeding efficiency and resistance stability of disease-resistant varieties can be significantly enhanced.

Although considerable progress has been made in the molecular research on the disease resistance of sorghum, there are still many issues that need to be further explored. The key directions for the future include: further research on the interaction patterns between sorghum and different pathogens, especially the defense characteristics under the combined action of multiple pathogens; Search for more new resistance genes and regulatory elements by using pan-genome and multi-omics technologies; Strengthen the research on the functions of antagonistic genes and their regulatory patterns, and also pay attention to the influence of epigenetic modifications; Promote the application of cutting-edge technologies such as gene editing and microbiome engineering in breeding; At the same time, the resistance performance of the varieties should be repeatedly evaluated in different ecological environments to ensure their stability and persistence. Further research on the defense mechanism of sorghum, combined with the integration of multiple technologies, will provide more solid support for ensuring food security and promoting sustainable agriculture.

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Conflict of Interest Disclosure

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

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