ADAPTATION OF FOOD CROPS TO BIOTIC STRESS

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ABSTRACT

Major food crops such as soybean (*Glycine max*) and maize (*Zea mays*) play an important role in global food security. However, their productivity is often threatened by biotic stresses, including attacks by pathogens, pests, and parasites. This article reviews plant defense mechanisms through multi-omics and biochemical adaptation approaches. Multi-omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, allow the identification of genes and metabolic pathways that contribute to plant resistance. Meanwhile, biochemical mechanisms such as the role of jasmonic acid (JA), antioxidants, defense enzymes, and antimicrobial compounds enhance plant resistance to biotic stresses. This understanding is important in developing biotic stress-resistant varieties through biotechnology and conventional breeding that are useful for supporting global agricultural sustainability.

Keywords: Adaptation; Biotic stress; Maize; Soybean

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INTRODUCTION

Food crops are strategic commodities that are the main source of food needs for the community. However, food crop production is often hampered by various biotic stresses, such as pests and diseases (Paradise et al., 2022). Biotic stresses can significantly reduce crop yields, making it a major challenge in maintaining food security. Therefore, it is very important to study the mechanisms of food crop adaptation to biotic stresses. Adaptation of food crops to biotic stresses can occur independently (autonomous adaptation) or planned (planned adaptation) (Sumaryanto, 2016). Independent adaptation involves the ability of plants to adapt naturally to the biotic stresses faced, while planned adaptation is carried out through human intervention, such as the development of superior varieties that are resistant to pests and diseases. Understanding these two adaptation mechanisms can provide valuable information in efforts to increase the resilience of food crops to biotic stresses.

Biotic stresses can come from various sources, including pests, pathogens, and weeds, which can significantly reduce crop yields. Pests such as aphids (*Aphis glycines*) and caterpillars (*Spodoptera* spp.) can cause direct damage to plants, while pathogens such as fungi (*Fusarium* spp.) and bacteria (*Pseudomonas syringae*) can cause diseases that are fatal to plant growth (Copley et al., 2017; Liu et al., 2016). In addition, the presence of weeds in the cultivation environment competes for water and nutrients. This competition can inhibit growth and reduce yield potential (Fu et al., 2024). Therefore, a deep understanding of the various types of biotic stresses is essential to design effective and sustainable management strategies. Several studies have examined the adaptation of food crops to biotic stresses, both in rice plants (Paradisa et al., 2022), corn (Syah et al., 2019), soybeans (Lestari et al., 2021; Rosawanti, 2016), and other horticultural crops. However, information on the comprehensive adaptation of food crops is still limited. Therefore, this review aims to examine the adaptation mechanisms of food crops to biotic stress based on reputable international journal references.

SPECIFIC INTERACTIONS OF PATHOGENS AND SOYBEAN VARIETIES

Biotic stress in food crops is generally caused by many pathogens with different attack mechanisms. These pathogens are nematodes, pests, viruses, bacteria, and fungi. One of the most damaging pathogens to soybeans is the Soybean cyst nematode (SCN) (*Heterodera glycines*) (Yan & Baidoo, 2018). Rotation of susceptible soybean varieties with nematode-resistant soybean varieties (PI88788) can delay further aggressiveness of the SCN population, thereby reducing crop losses (Thapa et al., 2022). Specific interactions between soybean varieties and SCN have been the focus of research to understand resistance mechanisms and develop more resistant varieties. Plants have their own adaptation mechanisms to biotic stress. When plants sense an attack, stress signals are sent throughout the plant through hormones such as jasmonic acid and salicylic acid, which regulate the plant's defense response. Pattern Recognition Receptors (PRRs) are pattern receptors on the cell surface that plants use to detect biotic stress (Chen & Zhao et al., 2021). These receptors recognize pathogen-associated molecular patterns (PAMPs), also known as pathogen-associated molecular patterns. Then, they trigger a number of early defense responses, which are part of the plant's innate immunity. In addition, plant interactions with certain microbes activate induced defense mechanisms such as Induced Systemic Resistance (ISR), which enhance the overall plant defense against biotic attacks. After initial detection, plants activate biochemical signaling pathways, resulting in the production of a number of defense compounds. With the help of this pathway, antimicrobial compounds, defense proteins, and enzymes, including polyphenol oxidase, are formed, which strengthen the cell wall and stop further penetration of pathogens. By combining rapid detection through PRR and activation of signaling pathways that induce defense responses, plants can respond to various biotic threats in different ways.

Various studies have identified quantitative loci (QTL) associated with SCN resistance, such as rhg1 and Rhg4. A genome-wide association study (GWAS) on 120 Chinese soybean cultivars identified 13 SNPs in 7 genomic regions significantly associated with SCN resistance, including rhg1 and Rhg4 (J. Zhang et al., 2017). In addition, another study found that the variety 'Pingliang xiaoheidou' harbored a novel QTL qSCN-PL10 that contributed to SCN resistance (Guo et al., 2020). The mechanism of soybean SCN resistance involves complex interactions between plant resistance genes and pathogen effectors. Studies have shown that silencing of vital SCN genes through host-induced RNA interference (RNAi) can enhance soybean SCN resistance (Y. Zhang et al., 2022). These studies highlight the potential of genetic manipulation in improving soybean plant resistance to nematodes. Biotic stress, such as pests, can interfere with the vegetative and generative phases, significantly decreasing yield. Based on the mechanism of insect pest attacks, they can be categorized into four, namely sucking pests, leaf eaters, and stem and pod borers. Pest attacks such as Spodoptera litura eat leaves, disrupting the photosynthesis process. Machado et al. (2020) reported that genetic modifications expressing the Cry1Ac/Cry1F protein in soybeans resulted in longer development times and lower larval, egg, and imago survival rates. In addition, various studies have identified biochemical responses to pest attacks with increased production of defense enzymes, such as peroxidase and polyphenol oxidase, in Bemisia tabaci (Harish et al., 2023), Spodoptera Littoralis (Mohamed et al., 2021), and Euschistus heros (Victor et al., 2022). Adequate nutrition with biochar application, soil urease and sucrase activity, and trypsin protease inhibitors can gradually increase polyphenol oxidase activity (de Almeida Barros et al., 2022). The use of resistant varieties and adequate nutrition reduces the impact of yield losses due to pest attacks.

BIOCHEMICAL ADAPTATION TO BIOTIC STRESS

The Role of Jasmonic Acid (JA) in Plant Defense

The main phytohormone that helps plants protect themselves from biotic stress is jasmonic acid (JA), which is synthesized through a complex biosynthetic pathway that begins with linolenic acid, a fatty acid that accumulates in plant cell membranes (Dai et al., 2022). This complex biosynthetic pathway then produces jasmonate as the end product of a stepwise oxidation process. Enzymes such as lipoxygenase (LOX) and allene oxide synthase (AOS) are essential for the early stages of JA formation, which occurs when plants are damaged or attacked by pathogens or herbivores. JA is a primary signal that activates the expression of defense genes in the plant defense system. When JA is triggered, various types of antimicrobials and enzymes are produced, such as polyphenol oxidases and protease inhibitors.

These compounds protect plant tissues from further damage by herbivorous insects or pathogens. This mechanism limits the spread of pathogens and discourages herbivores from reaching plant tissues. JA also controls the immune response by triggering the formation of secondary metabolites. These secondary metabolites protect and deter pathogens. The interaction of JA with other hormones, such as salicylic acid (SA) and ethylene, is essential to ensure an appropriate defense response to a particular stress. JA usually counteracts herbivory stress, while SA usually activates pathogen infection. However, the inhibitory interaction between JA and SA allows plants to adjust their immune system to deal with various threats. Ethylene also helps to enhance the JA response, especially under herbivore attack conditions, and accelerates the activation of systemic defenses in uninfected tissues. Through this dynamic interaction, JA helps maize plants adapt effectively to various damaging biotic stresses. However, the inhibitory interaction between JA and SA allows plants to adjust their defenses to deal with various threats. Ethylene also helps maize plants adapt to various damaging biotic stresses by enhancing the JA response, especially under herbivore attack situations. It accelerates the activation of systemic defenses in uninfected tissues.

Antioxidants in Overcoming Oxidative Stress

Excessive production of reactive oxygen species (ROS), such as hydrogen peroxide and superoxide, is often caused by biotic stress in corn plants. ROS can damage important cellular structures such as DNA, membrane lipids, and proteins. If not controlled, this accumulation of ROS causes oxidative stress, which can accelerate cell death. Although plants use ROS as an initial signal to activate defenses, oxidative damage caused by ROS can weaken plant resistance to further stress. Therefore, plants are also protected by neutralizing ROS, protecting cells from more severe oxidative damage. Various antioxidant compounds produced by corn plants include catalase (CAT), peroxidase (POD), and superoxide dismutase (SOD) enzymes that function to reduce the amount of ROS in cells (Zhang et al., 2021). These enzymes work together to detoxify ROS, converting them into less reactive molecules. This reduces damage to plant tissues attacked by pathogens or herbivores. In addition to antioxidant enzymes, plants also produce non-enzymatic antioxidants such as ascorbic acid and glutathione, which protect cellular components from oxidative damage (Wu et al., 2021). Ascorbic acid and glutathione act as free radical scavengers that neutralize ROS and help maintain redox balance within the cell, essential for supporting other defense responses. With this combination of enzymatic and non-enzymatic antioxidants, maize plants can maintain cellular health and enhance their defenses when faced with biotic stresses. As part of the defense response to biotic stresses, maize plants produce a variety of antimicrobial compounds (Yuan et al., 2023). These compounds are produced through secondary metabolic pathways and include compounds such as phenolics, flavonoids, alkaloids, and terpenoids.

Antimicrobial Compound Production

Plants produce antimicrobial compounds, including saponins, tannins, and isoflavonoids, in response to pathogen attack. Phenolics and flavonoids are often found in areas around wounds or tissues attacked by pathogens, and they function to stop microbial growth and prevent the spread of infection within the plant. In addition, phytochemicals, including tannins and saponins, have antimicrobial properties that help plants fight pathogens (Xiao & Zhang et al., 2022). For example, saponins damage the cell membranes of microbes, preventing them from multiplying in plant tissues. In contrast, tannins bind to microbial proteins, inhibiting their enzymes and slowing pathogen growth. In addition to protecting plant cells from further damage, these phytochemicals also trigger other systemic defense mechanisms, such as the activation of hormonal signals, such as jasmonic acid and salicylic acid. All of these mechanisms are responsible for the overall plant immune response. Corn plants can produce a variety of antimicrobial compounds, which can activate a chemical defense layer that slows or stops pathogen invasion. In addition to supporting the sustainability of plant production in conditions vulnerable to biotic stress, corn plants can also produce a variety of antimicrobial compounds. These compounds protect plant tissues by stopping microbial growth or strengthening cell walls through lignification.

In addition, to combat biotic stress, corn plants produce various defense enzymes. These enzymes are essential for stopping pathogen growth and strengthening cell structures. To strengthen cell walls, enzymes including polyphenol oxidase (PPO), peroxidase (POD), and lipoxygenase (LOX) (Xu et al., 2023). Stop the spread of infection and reduce damage caused by pathogen and insect attacks. For example, polyphenol oxidase helps oxidize phenols into compounds that are toxic to pathogens, increasing the defense of infected tissues against additional invasion. Peroxidase does two things to protect plants: it produces free radicals that are directly antimicrobial and promotes lignin formation in plant cell walls. The formation of lignin strengthens the cell structure, making it difficult for pathogens to penetrate and attack plant tissues deeper (Liu & Wang et al., 2022). Lipoxygenase enzymes perform a variety of important tasks, including breaking down fatty acids in cell membranes, producing signals such as jasmonic acid, triggering the activation of systemic defense genes, and regulating plant immune responses to various biotic stresses. By working together with these enzymes and proteins, plants develop a robust defense system to cope with biotic stresses and maintain their resilience and survival in stressful environments.

MULTI-OMIC APPROACHES IN IMPROVING PLANT RESISTANCE

The application of multi-omics in biotic stress management is gaining increasing attention as researchers attempt to improve the resistance of these plants to various pathogens. The main advantage of the multi-omics approach in research is its ability to identify key genes and quantitative trait loci (QTL) associated with biotic stress resistance. One of the widely used genomic applications is genome-wide association analysis (GWAS) (Patel et al., 2024) to explore genetic variation among soybean populations related to resistance to Cercospora leaf spot disease. In addition, Lukanda et al (2023) reported that GWAS analysis also successfully identified a new source of resistance to red spot disease caused by Coniothyrium glycines. Exploiting natural variation with GWAS can provide deeper insights into the genes underlying biotic stress resistance. Transcriptomic analysis has revealed important insights into the gene expression profile of soybean under pathogen attack. Bansal et al. (2015) identified genes such as CYP and TUB4 that showed less expression variation related to gene transcription under biotic stress. A study by Dong et al. (2018) highlighted the role of WRKY transcription factors in mediating plant responses to powdery mildew, suggesting the mechanism by which specific genes are activated or repressed during biotic stress. bZIP transcription factors induced by both biotic and abiotic stress conditions showed different plant defense responses (Zhang et al., 2018). The application of transcriptomics in biotic stress management in soybean plays a vital role in understanding the genetic response of plants to various pathogens. Physiological mechanisms such as metabolomics and proteomics play a role in defense against biotic stresses. Metabolomics studies have identified specific metabolites that accumulate in soybeans under biotic stress. For example, accumulation of flavonoids and isoflavonoids has increased insect herbivores' resistance (Pinheiro et al., 2024; Zhang et al., 2020). In addition, proteomics identification conducted by Wang et al. (2020) using biocontrol agents against nematodes, such as Sinorhizobium fredii, increased the biosynthesis of phenylpropanoids, flavones, flavanols, and isoflavonoids. Metabolomics and proteomics studies correlate with pathogen infection responses leading to the production of antimicrobial compounds (Anzano et al., 2022). Therefore, multi-omics provides a comprehensive understanding of plant responses to biotic stress, thereby facilitating the development of resistant varieties.

RESEARCH APPLICATIONS AND IMPLICATIONS

The multi-omics approach provides great opportunities in the development of crop varieties that are more resistant to biotic stresses. The application of this technology supports plant breeding to increase resistance to pathogens without sacrificing productivity. Through genomic and transcriptomic data, superior varieties can be produced with high efficiency. The use of this technology also allows for reduced dependence on chemical pesticides, thus supporting environmental sustainability. With the integration of multi-omics and biochemical approaches, more adaptive crop production can improve the stability of sustainable agricultural systems.

CONCLUSION

A multi-omics approach and biochemical adaptation mechanisms provide a comprehensive understanding of plant responses to biotic stresses. Utilizing these technologies enables the development of highly efficient resistant crop varieties, supporting global food security. In addition, this approach has the potential to reduce dependence on environmentally damaging chemical pesticides. Further research is needed to integrate multi-omics data into more adaptive plant breeding strategies. Implementation of these technologies can promote the sustainability of global agricultural systems by increasing efficiency and productivity. The combination of these approaches can improve global food needs while maintaining ecosystem balance. The use of multi-omics and biochemical approaches provides innovative solutions to modern agricultural challenges.

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