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LONG NON-CODING RNA: AN EMERGING MOLECULAR TOOL FOR BIOTIC STRESS MANAGEMENT IN CROP PLANTS

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ABSTRACT

Biotic stresses caused by fungi, bacteria, viruses, nematodes and insect pests are among the major constraints affecting crop productivity, quality and agricultural sustainability. Plants have evolved sophisticated defence mechanisms involving molecular signalling, gene regulation and activation of resistance-associated pathways to overcome these biological challenges. In recent years, long non-coding RNAs (lncRNAs) have emerged as important regulatory molecules in plant defence and stress-responsive gene expression. These RNA molecules, generally longer than 200 nucleotides and lacking conventional protein-coding potential, regulate gene expression at transcriptional, post-transcriptional and epigenetic levels. They participate in plant immune responses by interacting with microRNAs, transcription factors, chromatin-modifying proteins and other regulatory components. Furthermore, advances in transcriptome sequencing, bioinformatics and molecular biotechnology have facilitated the identification and functional characterization of stress-responsive lncRNAs. Understanding these regulatory mechanisms offers new opportunities for developing disease-resistant crop varieties through molecular breeding, genetic engineering and RNA-based technologies. This article highlights the molecular mechanisms, potential applications and future prospects of lncRNAs in biotic stress management for sustainable crop production.

Keywords: Long Non-Coding RNAs (lncRNAs), Plant Biotic Stress, Molecular Plant Defence

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1. INTRODUCTION

Agricultural crop production is continuously challenged by various biotic stresses, including fungal, bacterial and viral pathogens, insect pests and plant-parasitic nematodes. These biological factors cause considerable yield losses, deteriorate crop quality and threaten global food security. Conventional management strategies, such as chemical pesticides, resistant cultivars and biological control, have contributed significantly to crop protection. However, the emergence of pesticide-resistant pest populations, pathogen variability and environmental concerns has increased the demand for innovative and sustainable approaches to plant disease and pest management.

Plants possess complex innate immune systems that recognize invading pathogens and activate a series of biochemical and molecular defence responses. These responses involve pathogen recognition receptors, calcium signalling, reactive oxygen species (ROS) production, mitogen-activated protein kinase (MAPK) cascades and the expression of defence-related genes. In addition to protein-coding genes, non-coding RNAs have recently gained considerable attention as important regulators of plant immunity. Among them, long non-coding RNAs (lncRNAs) represent an emerging class of regulatory molecules involved in controlling plant growth, development and responses to environmental and biological stresses (Sharma et al., 2022). Long non-coding RNAs are generally defined as RNA transcripts exceeding 200 nucleotides that possess little or no conventional protein-coding capacity. Unlike messenger RNAs, their primary biological significance is associated with their regulatory functions rather than protein synthesis. They can influence gene expression through interactions with DNA, RNA and proteins, thereby controlling several cellular and molecular processes. Recent research has demonstrated that lncRNAs participate in plant–pathogen interactions and influence the activation or suppression of plant defence mechanisms (Huang et al., 2023). The identification of stress-responsive lncRNAs has opened new possibilities for understanding the molecular basis of plant resistance. Their ability to regulate multiple defence-associated pathways makes them promising candidates for molecular crop improvement. Therefore, understanding the functional diversity and regulatory mechanisms of lncRNAs is important for developing advanced strategies for sustainable biotic stress management.

2. CLASSIFICATION AND MOLECULAR MECHANISMS OF LNCRNAS

Based on their genomic location and relationship with neighbouring protein-coding genes, plant lncRNAs are broadly classified into long intergenic non-coding RNAs (lincRNAs), antisense lncRNAs, sense lncRNAs, intronic lncRNAs and bidirectional lncRNAs. Each category possesses distinct regulatory characteristics and may influence gene expression through different molecular mechanisms. LncRNAs regulate gene expression through both cis-acting and trans-acting mechanisms. Cis-acting lncRNAs generally influence the expression of neighbouring genes, whereas trans-acting lncRNAs regulate distant target genes through interactions with transcription factors, chromatin-modifying complexes and other regulatory proteins. Some lncRNAs also function as molecular decoys by binding microRNAs and preventing them from suppressing their target messenger RNAs. This mechanism, commonly described as competing endogenous RNA (ceRNA) activity, contributes to the regulation of plant defence-associated genes (Huang et al., 2023). Another important mechanism involves the interaction of lncRNAs with chromatin-modifying proteins, which can influence histone modifications and transcriptional activity. Certain lncRNAs also act as precursors of small interfering RNAs, contributing to RNA-mediated gene silencing. These multiple regulatory mechanisms enable lncRNAs to coordinate different components of plant immunity and provide flexibility in responding to pathogen attacks.

3. ROLE OF LNCRNAS IN PLANT DEFENCE AGAINST BIOTIC STRESS

3.1 Resistance Against Fungal Pathogens

Fungal diseases caused by pathogens such as Phytophthora infestans, Botrytis cinerea and other economically important fungi significantly affect crop productivity. Recent investigations have revealed that lncRNAs participate in regulating plant resistance against fungal infections by controlling defence-related genes and molecular signalling

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pathways. In tomato, lncRNA23468 has been reported to function as an endogenous target mimic of miR482b, thereby reducing miRNA-mediated suppression of nucleotide-binding leucine-rich repeat (NLR) resistance genes and enhancing resistance against Phytophthora infestans. Similarly, tomato lncRNA16397 has been associated with the regulation of reactive oxygen species accumulation and expression of the neighbouring glutaredoxin-related gene, contributing to resistance against late blight disease (Huang et al., 2023). These findings indicate that lncRNAs can regulate disease resistance by modifying the expression of important immune-related genes. Their involvement in ROS regulation and resistance-gene expression provides promising opportunities for developing fungal disease-resistant crop varieties through molecular approaches.

3.2 Defence Against Bacterial Pathogens

Bacterial pathogens cause several economically important diseases, including bacterial blight, bacterial wilt and leaf spot diseases. Plants recognize bacterial-associated molecular patterns through pattern recognition receptors, which subsequently activate defence signalling pathways. An important example is ELENA1 (ELF18-INDUCED LONG NON-CODING RNA1), an Arabidopsis lncRNA associated with resistance against Pseudomonas syringae pv. tomato DC3000. ELENA1 interacts with the mediator complex protein MED19a and promotes the expression of the pathogenesis-related gene PR1, thereby contributing to plant defence responses. This interaction demonstrates how lncRNAs can influence transcriptional machinery and regulate the expression of disease-resistance-associated genes (Huang et al., 2023). Furthermore, research on Arabidopsis has demonstrated that pathogen-associated molecular patterns, such as bacterial flagellin and elongation factor Tu, can alter lncRNA expression. These findings suggest that lncRNAs participate in early immune signalling and subsequent defence-related transcriptional responses.

3.3 Regulation of Viral Disease Resistance

Plant viruses cause serious economic losses in crops such as rice, maize, tomato, cotton and several horticultural species. Viral infections frequently interfere with host gene expression and manipulate cellular defence mechanisms to facilitate their multiplication and spread. LncRNAs may contribute to antiviral defence by regulating RNA silencing pathways, interacting with microRNAs and influencing the expression of resistance-associated genes. Their involvement in endogenous and cross-kingdom RNA regulatory networks provides an additional dimension to plant–virus interactions. Although the functional characterization of virus-responsive lncRNAs remains relatively limited compared with other regulatory RNAs, their potential involvement in antiviral immunity represents an important area for future investigation (Sharma et al., 2022; Bhar and Roy, 2023).

3.4 Role in Insect Pest and Nematode Resistance

Apart from microbial pathogens, plants are frequently attacked by insect pests and plant-parasitic nematodes. These organisms damage plant tissues, interfere with nutrient transport and alter normal physiological processes. Plant responses to insect herbivory involve complex signalling networks associated with jasmonic acid, salicylic acid and other defence-related compounds. LncRNAs may participate in regulating these signalling networks and modulating the expression of genes associated with plant defence. Their involvement in plant–insect interactions has also been highlighted in recent investigations of plant immunity. However, the precise molecular functions of individual lncRNAs in insect and nematode resistance require further experimental validation (Huang et al., 2023; Othman et al., 2024).

4. APPLICATIONS OF LNCRNAS IN MOLECULAR CROP IMPROVEMENT

The growing understanding of lncRNA-mediated gene regulation offers several opportunities for improving crop resistance against biotic stresses. High-throughput RNA sequencing (RNA-seq), transcriptome profiling and computational analysis can be employed to identify differentially expressed lncRNAs under pathogen or insect infestation. These technologies help identify potential regulatory molecules associated with resistant and susceptible crop genotypes.

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Functional characterization through gene silencing, overexpression studies, CRISPR-based genome editing and molecular interaction analysis can further establish the biological functions of candidate lncRNAs. Once validated, beneficial lncRNAs or their regulatory regions may be explored as molecular targets for developing resistant crop varieties.

Another promising approach involves integrating lncRNA information with marker-assisted selection and genomic selection programmes. The identification of lncRNA-associated molecular markers may help researchers understand the genetic basis of complex resistance traits and facilitate the selection of desirable genotypes. Furthermore, emerging RNA-based technologies may provide opportunities to manipulate specific regulatory pathways involved in plant defence. However, the application of lncRNAs in practical crop improvement is still at an early stage. Their expression may vary according to crop species, developmental stages, environmental conditions and pathogen populations. Therefore, functional validation under controlled and field conditions is essential before their wider application in commercial agriculture.

5. FUTURE PROSPECTS AND RESEARCH CHALLENGES

Despite considerable progress in identifying plant lncRNAs, several challenges remain in understanding their biological functions. One major limitation is their relatively low sequence conservation across plant species, which makes the identification of functionally equivalent lncRNAs difficult. Additionally, their tissue-specific and condition-dependent expression patterns create challenges in accurate characterization. Future research should focus on identifying stress-specific lncRNAs in important agricultural crops, including rice, maize, wheat, pulses, oilseeds and horticultural plants. Integration of transcriptomics, proteomics, metabolomics and advanced bioinformatics will help establish comprehensive regulatory networks associated with plant immunity. Artificial intelligence and machine learning may also support the prediction of lncRNA structures, target interactions and potential regulatory functions. An emerging research direction is the investigation of interactions between plant-derived and pathogen-derived non-coding RNAs. Understanding such cross-kingdom RNA communication may provide new insights into host–pathogen relationships and identify novel opportunities for disease management. The integration of lncRNA research with precision breeding, genome editing and RNA-based biotechnology could eventually contribute to the development of climate-resilient and disease-resistant crop varieties (Othman et al., 2024).

6. CONCLUSION

Long non-coding RNAs have emerged as important molecular regulators of plant immunity and represent a promising research frontier in biotic stress management. Their involvement in transcriptional regulation, microRNA interactions, chromatin modification and defence signalling highlights their importance in controlling plant responses against fungal, bacterial and viral pathogens. Evidence from studies involving tomato and Arabidopsis demonstrates that specific lncRNAs can influence resistance-associated genes and contribute to the activation of plant defence mechanisms. The application of advanced sequencing technologies, bioinformatics, genome editing and molecular breeding can accelerate the identification and functional characterization of these regulatory molecules. Nevertheless, further research is necessary to understand their specificity, stability and practical effectiveness under field conditions. Integrating lncRNA-mediated regulatory mechanisms into modern crop improvement programmes could provide innovative opportunities for developing disease-resistant varieties, reducing dependence on chemical pesticides and promoting sustainable agricultural production. Thus, lncRNAs represent a promising molecular resource for the next generation of precision-based plant protection strategies.

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