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Role of Long Non-Coding RNA in Plant Disease Resistance

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SUMMARY

This article examines the crucial role of long non-coding RNAs (lncRNAs) in plant disease resistance. As regulatory molecules exceeding 200 nucleotides, lncRNAs influence plant immunity through diverse mechanisms, including chromatin remodeling, R-loop formation, and serving as miRNA precursors. They modulate key defense pathways like PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI), regulating resistance gene expression. While some lncRNAs are evolutionarily conserved, their stress-responsive expression varies across plant species, indicating both shared and specialized functions. The study highlights lncRNA biogenesis, classification, and molecular interactions that shape plant stress responses. These findings advance our understanding of lncRNA-mediated gene regulation and open new possibilities for developing disease-resistant crops through targeted genetic strategies. Future research should explore species-specific lncRNA functions and their practical applications in sustainable agriculture to enhance crop resilience against pathogens.

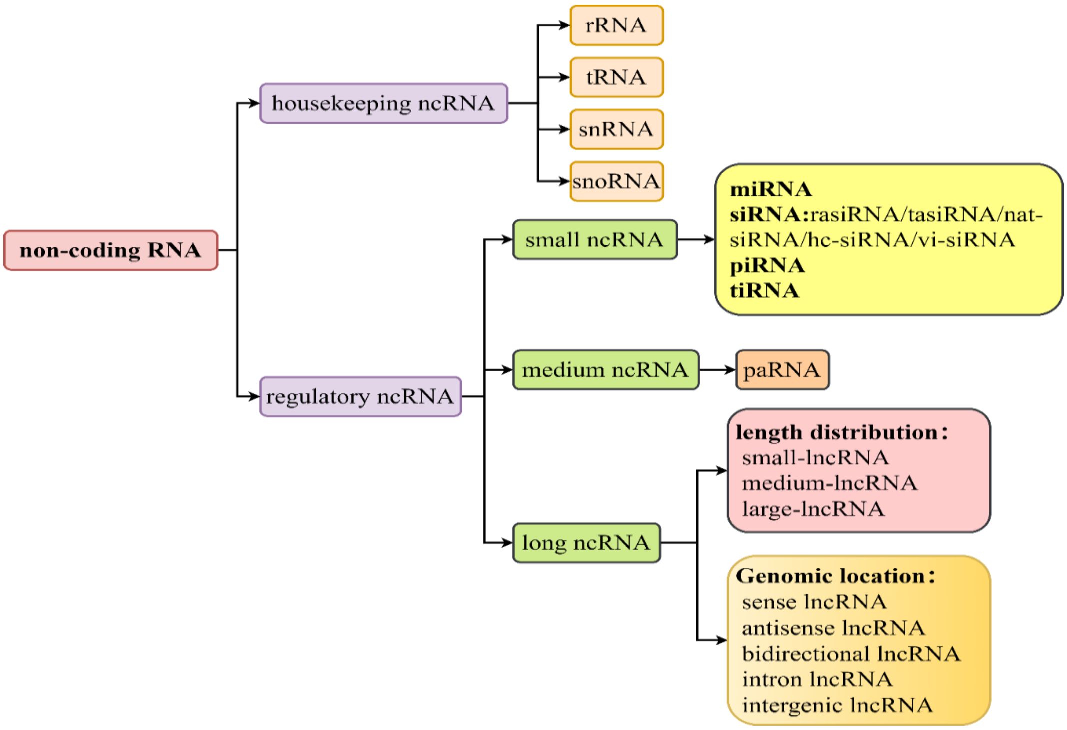
INTRODUCTION

RNA (Ribonucleic Acid) is a nucleic acid similar to DNA but with several key differences. It is typically single-stranded and plays crucial roles in coding, decoding, regulation, and expression of genes. RNA molecules are composed of nucleotides, which consist of a ribose sugar, a phosphate group, and a nitrogenous base. The primary types of RNA are involved in various cellular processes, particularly protein synthesis.

What is Non-Coding RNA….?

The term non-coding RNA (ncRNA) is commonly employed for RNA that does not encode a protein. In human 97–98% of the transcriptional output =non coding RNA. Short non-coding RNA (sncRNA) is a non-coding RNA smaller than 200 nucleotides in length. Long non-coding RNA (lncRNA) is a non-coding RNA greater than 200 nucleotides in length. LncRNA lack of a complete specific open reading frame, and has no function of a coding protein.

Classification of Non-coding RNA



The DNA sequence from which a functional ncRNA is transcribed is often called an RNA gene. Abundant and functionally important types of non-coding RNAs include tRNAs, rRNAs, small ncRNAs such as microRNAs, siRNAs, piRNAs, snoRNAs, snRNAs, exRNAs, and the long ncRNAs such as XIST (X-Inactive Specific Transcript) and HOTAIR (HOX-AntisenseIntergenic RNA). LncRNAs can regulate gene expression at transcription and post-transcription, epigenetic level. According to whether it has the function of encoding protein, the scientists divide RNA into two categories: non-coding RNA (ncRNA) and coding RNA (Djebali et al. 2012). To distinguish it from well-known small RNAs (miRNAs and siRNAs) with less than 200 nt, the term lncRNA swere introduced.

Biogenesis of lncRNA:

The biogenesis of lncRNAs involves several intricate steps, which include transcription, processing, degradation, and maturation.

1.Transcription:

lncRNAs are primarily transcribed by RNA polymerase II, although RNA polymerases III, IV, and V can also be involved. This transcription process may produce various truncated or extended transcripts.

2.Processing:

Post-transcriptional modifications play a crucial role in lncRNA processing. These modifications include capping, splicing, and polyadenylation, which are typical for RNA polymerase II transcripts. However, some transcripts produced by RNA polymerases IV and V may skip these steps.

3.Degradation:

The premature transcripts of lncRNAs are subject to degradation by the RNA exosome and the exonuclease XRN2. If mutations occur, they can lead to the accumulation of faulty transcripts, disrupting normal cellular function.

4.Maturation:

Once processed, lncRNAs undergo maturation to become fully functional molecules. Mature lncRNAs can function in various roles, such as decoys, scaffolds, or guides. These roles enable them to interact with other molecules within the cell and regulate gene expression at multiple levels.

Functional Roles:

Mature lncRNAs have diverse functional roles. They are known to regulate gene expression at transcriptional and post-transcriptional levels and influence numerous biological processes, including stress responses and disease resistance in plants.

For example, in plants, lncRNAs are involved in responding to biotic and abiotic stresses, thereby playing a critical role in the organism's overall stress response mechanism.

Origin of lncRNA

The origins of lncRNAs are categorized based on their genomic location and their relationship to nearby genes:

- ✓ Sense lncRNA: These overlap with the sense strand of protein-coding genes.
- ✓ Antisense lncRNA: These overlap with the antisense strand of protein-coding genes.
- ✓ Intronic lncRNA: These are transcribed entirely from the introns of other genes.
- ✓ Intergenic lncRNA: These are located between protein-coding genes and do not overlap with any nearby coding sequences.
- ✓ Enhancer lncRNA: These are transcribed from enhancer regions associated with protein coding genes.

Functional Mechanism of LncRNA in plants

Chromatin Remodelling

Long non-coding RNAs (lncRNAs) can modify chromatin structure by engaging with chromatin modifying proteins, which leads to histone modifications and alterations in chromatin accessibility. This process can either enhance or inhibit gene transcription.

Examples: COLDAIR, COLDWRAP, LAIR, AG-incRNA4, MAS: These lncRNAs facilitate the recruitment of proteins that are involved in histone modifications, resulting in changes to chromatin structure and subsequent gene expression.

R-loop Formation

LncRNAs are capable of forming R-loops, which are three-stranded structures made up of an RNA-DNA hybrid along with a displaced single-stranded DNA.

Example: APOLO: This lncRNA creates R-loops that can affect the local chromatin structure and gene expression.

Alternative Splicing

LncRNAs can influence alternative splicing by interacting with splicing factors or pre-mRNA, which leads to the generation of various mRNA isoforms from the same gene. Example: ASCO-lncRNA: This lncRNA plays a role in modulating the splicing of pre-mRNA, resulting in the production of different transcript variants.

Transcription Regulation

LncRNAs can regulate transcription by interacting with the transcription machinery or by attracting transcription factors to specific genomic locations.

Examples: ELENA1, VAS: These lncRNAs engage with the transcription initiation complex to influence gene transcription.

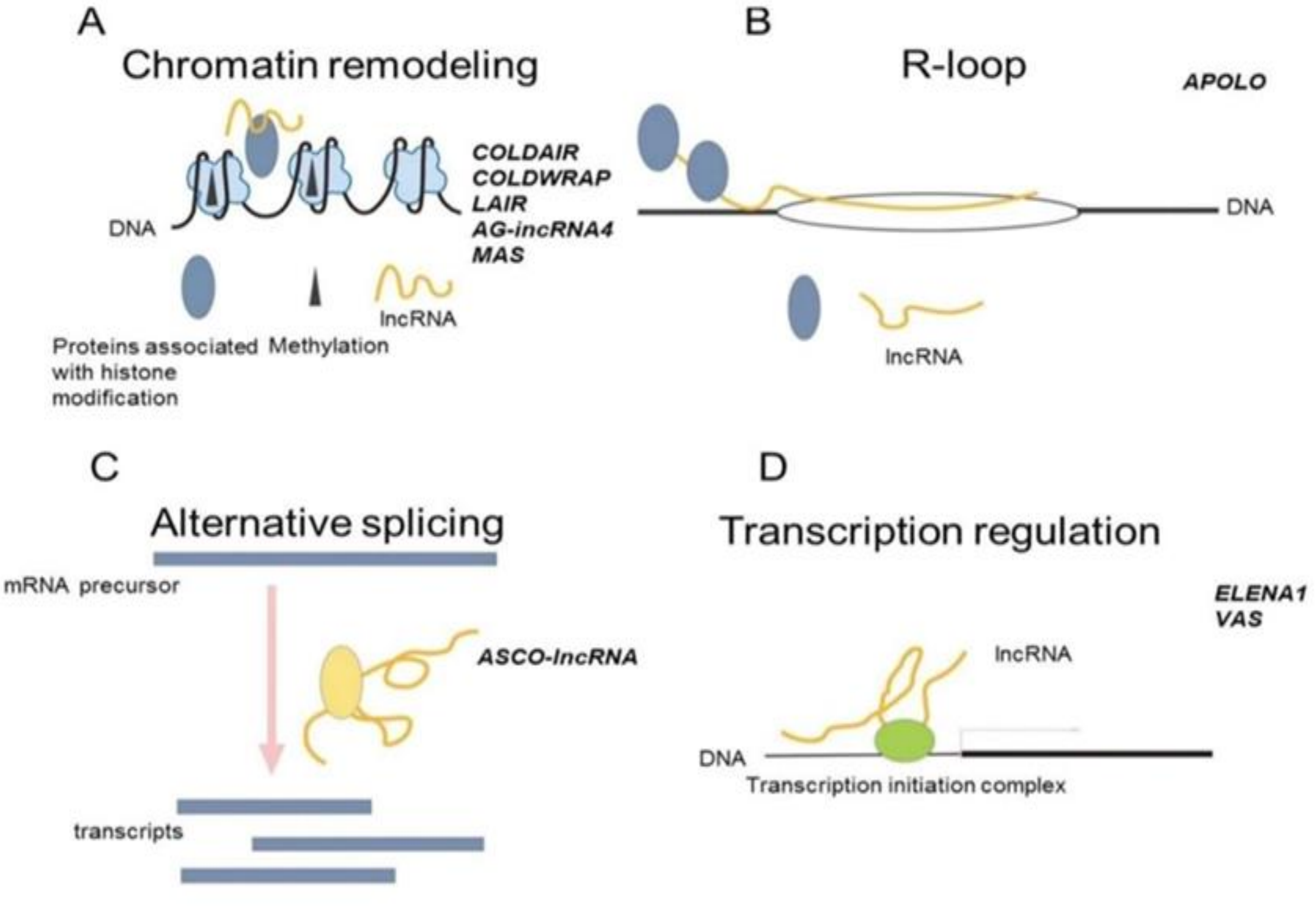
siRNA and miRNA Precursor

LncRNAs can act as precursors for small interfering RNAs (siRNAs) and microRNAs (miRNAs), which are critical for post-transcriptional gene silencing.

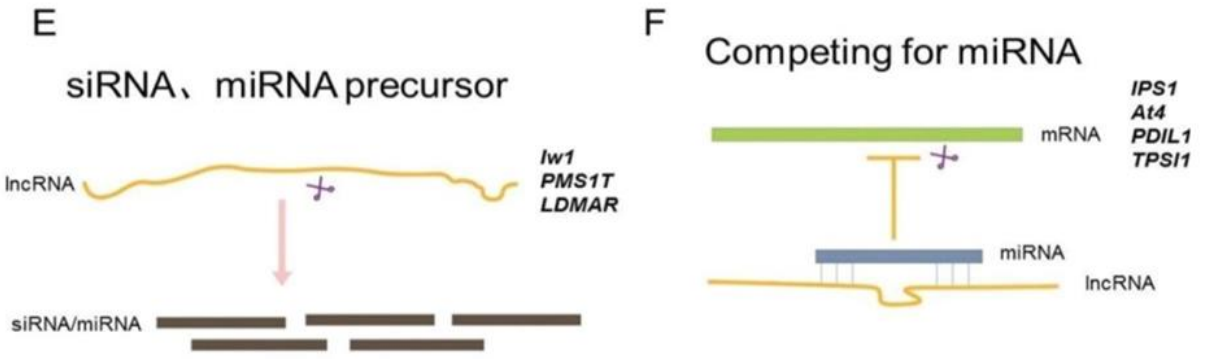
Examples: lwi, PMS1T, LDMAR: These lncRNAs are processed into siRNAs or miRNAs, which guide the RNA-induced silencing complex (RISC) to degrade target mRNAs or inhibit their translation.

Competing Endogenous RNA (ceRNA)

LncRNAs can function as competing endogenous RNAs (ceRNAs) by sequestering miRNAs, preventing these miRNAs from binding to and repressing their target mRNAs. Examples: IPS1, At4, PDL1, TPS1:



These lncRNAs bind to miRNAs, thereby inhibiting their interaction with target mRNAs and relieving the repression of those mRNAs.



Molecular Mechanism of LncRNA in three major biotic stresses.

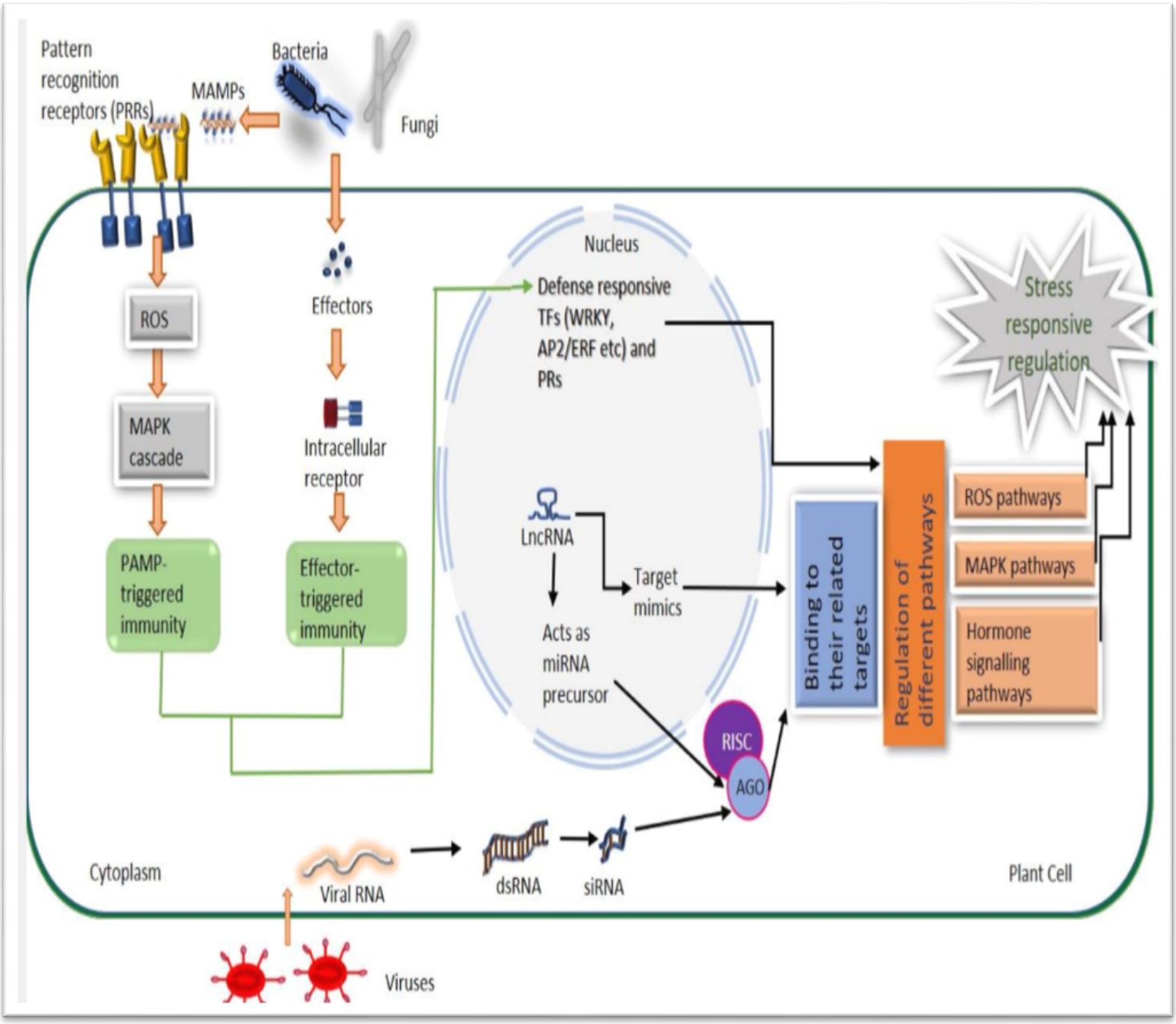
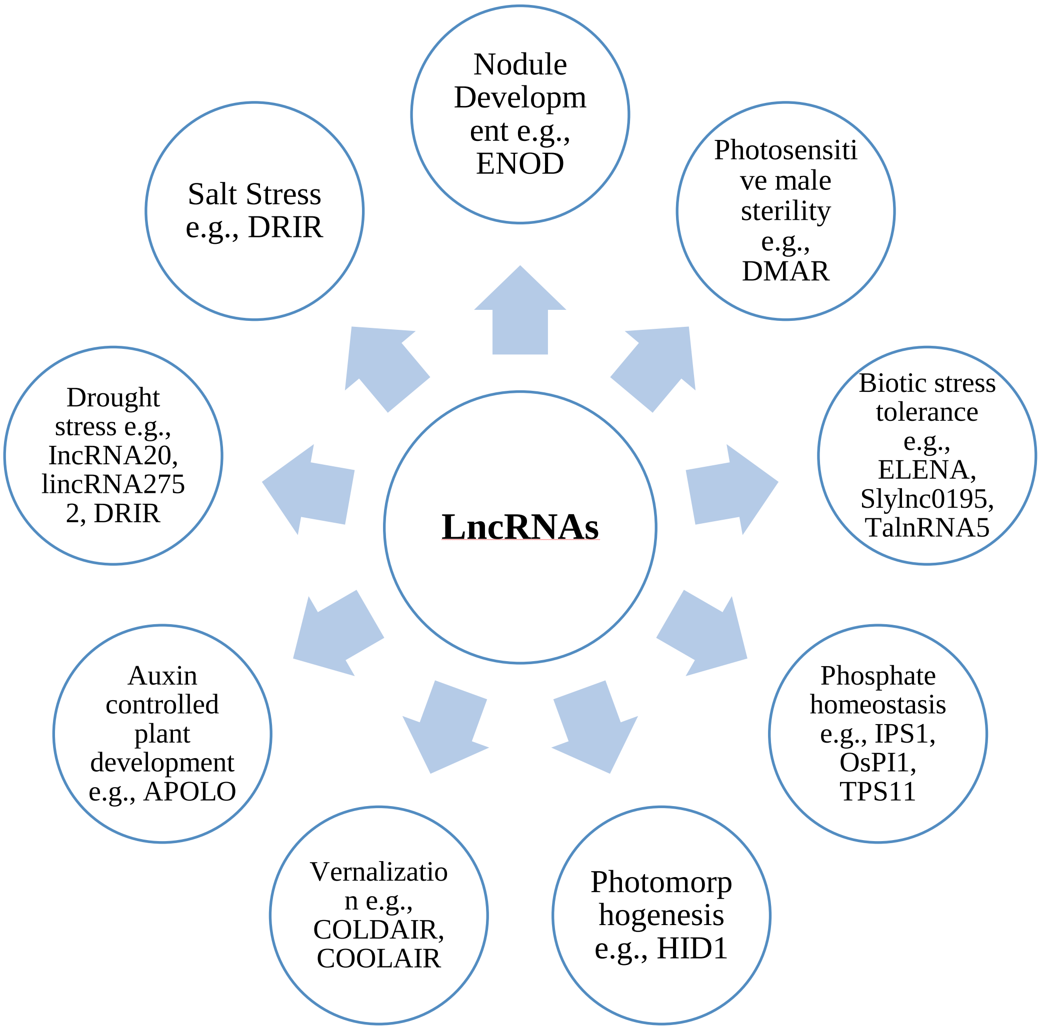


Figure: A general model of stress-responsive regulation by regulatory lncRNAs.After stress signal perception, PAMP-triggered immunity (PTI) is activated through the production of signal transducers such as reactive oxygen species (ROS). Pathogen-specific effector-triggered immunity (ETI) is activated by NB-LRR resistance (R) genes after effectors such as the virulence factor of pathogens enter into the plant cells.PTI and ETI both lead to activation of defense-related pathways.

Roles of some of the functionally characterized lncRNAs in different biological processes.



CONCLUSION

Non-coding RNAs (ncRNAs) play pivotal roles in regulating plant responses to biotic stresses through complex interactions with target genes and proteins. While many ncRNAs are evolutionarily conserved, their expression patterns often vary across plant species under similar stress conditions, reflecting specialized adaptation mechanisms. This study systematically examines ncRNA classification, biogenesis, and functional mechanisms, with particular emphasis on long non-coding RNAs (lncRNAs) in plant immunity. The findings enhance our understanding of how ncRNAs modulate defense pathways like PTI and ETI, offering new insights into plant stress adaptation. Future research should focus on elucidating species-specific regulatory networks and exploring practical applications in crop improvement. By leveraging ncRNA-mediated gene regulation, we can develop innovative strategies to engineer stress-resistant crops, contributing to sustainable agriculture and global food security in the face of climate change and emerging plant diseases.

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