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NON-CODING RNA BASED GENE REGULATION IN PLANT ABIOTIC STRESS TOLERANCE

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ABSTRACT

Plants are continuously exposed to abiotic stresses such as drought, salinity, heat, and nutrient deficiency, which significantly affect growth and productivity. Unlike mobile organisms, plants rely on intricate molecular regulatory systems to adapt and survive. Recent advances in plant genomics have revealed that non-coding RNAs (ncRNAs), which do not encode proteins, play a crucial role in regulating gene expression under stress conditions. These molecules, including microRNAs, small interfering RNAs, long non-coding RNAs, and circular RNAs, act at transcriptional and post-transcriptional levels to fine-tune stress-responsive pathways. Understanding ncRNA-mediated regulation provides new opportunities for developing climate-resilient crops through advanced biotechnological interventions.

KEYWORDS: Abiotic stress, Gene regulation, lncRNA, miRNA, Non-coding RNA

INTRODUCTION

Agricultural productivity is increasingly threatened by abiotic stresses such as drought, salinity, extreme temperatures, and nutrient limitations. These stresses disrupt physiological and biochemical processes, ultimately reducing crop yield and quality. Since plants are sessile organisms, they have evolved highly sophisticated molecular mechanisms to perceive stress signals and initiate adaptive responses.

Traditionally, research in plant stress biology has focused on protein-coding genes; however, recent discoveries have highlighted the importance of non-coding regions of the genome. A substantial proportion of plant transcripts do not encode proteins but instead function as regulatory molecules. Among these, non-coding RNAs (ncRNAs) have emerged as key regulators of gene expression, modulating stress responses at multiple levels. Their ability to control complex gene networks makes them central players in plant adaptation to adverse environmental conditions.

NON-CODING RNAS: DEFINITION AND TYPES

Non-coding RNAs are RNA molecules that are transcribed from DNA but are not translated into proteins. Despite lacking coding potential, they regulate gene expression at transcriptional, post-transcriptional, and epigenetic levels. Based on their size and function, ncRNAs are broadly classified into several categories, including microRNAs (miRNAs), small interfering RNAs (siRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs).

These molecules act as molecular regulators that control when and how genes are expressed, enabling plants to respond rapidly and efficiently to environmental changes. Their regulatory roles are particularly critical under stress conditions, where precise modulation of gene expression determines plant survival and productivity.

CLASSES OF NON-CODING RNAS AND THEIR FUNCTIONS

MICRO RNAS (MIRNAS)

MicroRNAs are short RNA molecules, typically 21–24 nucleotides in length, that regulate gene expression by binding to complementary sequences in messenger RNAs (mRNAs). This interaction leads to mRNA degradation or inhibition of translation, thereby reducing protein synthesis.

In plants, miRNAs are among the most extensively studied ncRNAs and are known to play critical roles in abiotic stress responses. Under conditions such as drought or salinity, specific miRNAs are either upregulated or downregulated, leading to the modulation of stress-responsive genes. Many miRNAs interact with hormone signaling pathways, particularly abscisic acid (ABA), which regulates stomatal closure and water balance. Additionally, miRNAs target transcription factors that control large gene networks, enabling coordinated stress responses at the cellular and whole-plant levels.

SMALL INTERFERING RNAS (SIRNAS)

Small interfering RNAs are another important class of regulatory RNAs that primarily function in gene silencing through RNA interference (RNAi). They are involved in RNA-directed DNA methylation and chromatin modification, leading to transcriptional gene silencing.

siRNAs play a significant role in epigenetic regulation, allowing plants to switch stress-related genes on or off depending on environmental conditions. This mechanism can also contribute to stress memory, where prior exposure to stress enhances the plant’s ability to respond to subsequent stress events. Such epigenetic modifications provide an additional layer of regulation that complements transcriptional and post-transcriptional control mechanisms.

LONG NON-CODING RNAS (LNCRNAS)

Long non-coding RNAs are transcripts longer than 200 nucleotides that exhibit diverse regulatory functions. Unlike miRNAs and siRNAs, lncRNAs act through multiple mechanisms, including serving as molecular scaffolds, guides, or decoys for proteins and other RNA molecules.

Recent studies have demonstrated that lncRNAs are actively involved in plant responses to abiotic stress by regulating gene expression, chromatin structure, and hormone signaling pathways. They can modulate antioxidant defense systems, transcriptional activity, and metabolic processes, thereby enhancing stress tolerance. The functional diversity of lncRNAs makes them key components of complex regulatory networks in plants (Huang et al., 2023; Yang et al., 2023).

Furthermore, lncRNAs have been implicated in chromatin remodeling and three-dimensional genome organization, influencing gene accessibility and expression patterns under stress conditions (Feuerstein et al., 2025; Chanwala et al., 2026).

CIRCULAR RNAS (CIRCRNAS)

Circular RNAs are a relatively recent addition to the family of ncRNAs and are characterized by their covalently closed loop structure, which confers high stability. One of their primary functions is to act as “miRNA sponges,” binding to miRNAs and preventing them from interacting with their target mRNAs.

Through this mechanism, circRNAs indirectly regulate gene expression and contribute to the formation of complex regulatory networks. Their stability and regulatory potential make them important players in stress adaptation, although their roles in plants are still being actively explored.

ROLE OF NCRNAS IN ABIOTIC STRESS TOLERANCE

Abiotic stresses negatively affect plant growth by disrupting water relations, nutrient uptake, photosynthesis, and cellular homeostasis. Non-coding RNAs play a central role in mitigating these effects by regulating key physiological and biochemical processes.

For instance, ncRNAs influence root architecture, enabling plants to explore soil more efficiently for water and nutrients under stress conditions. They also regulate stomatal behavior, helping to control water loss during drought. Additionally, ncRNAs modulate osmotic adjustment and antioxidant defense systems, which protect cells from oxidative damage caused by stress.

Another important aspect of ncRNA function is their involvement in coordinating large gene networks. By targeting transcription factors and signaling pathways, ncRNAs enable plants to mount a rapid and integrated response to environmental challenges. This coordinated regulation is essential for maintaining growth and productivity under stress conditions.

TECHNOLOGICAL ADVANCES AND APPLICATIONS

The study of ncRNAs has been greatly facilitated by advances in high-throughput sequencing technologies such as RNA sequencing (RNA-seq), small RNA profiling, and degradome analysis. These tools allow researchers to identify stress-responsive ncRNAs and map their target interactions with high precision.

The integration of multi-omics approaches, including genomics, transcriptomics, and epigenomics, has further enhanced our understanding of ncRNA-mediated regulatory networks. These insights are now being translated into practical applications in crop improvement.

Biotechnological tools such as CRISPR/Cas systems enable precise editing of ncRNA genes, their regulatory elements, or target sites in mRNAs. Additionally, artificial miRNAs and RNA interference strategies can be designed to modulate specific stress-response pathways. These approaches offer significant advantages, as targeting a single ncRNA can influence multiple downstream genes, resulting in more robust and coordinated stress tolerance.

FUTURE PROSPECTS

As climate change continues to intensify environmental stresses, the importance of developing resilient crop varieties cannot be overstated. Non-coding RNA–based regulatory mechanisms provide a promising avenue for achieving this goal.

Future research should focus on integrating ncRNA studies with systems biology approaches to better understand their roles in complex stress responses. The development of advanced bioinformatics tools and databases will further facilitate the identification and functional characterization of ncRNAs.

Moreover, translating laboratory findings into field applications remains a critical challenge. Efforts should be directed toward developing ncRNA-based technologies that are cost-effective, scalable, and suitable for diverse agricultural systems. Harnessing the regulatory potential of ncRNAs will play a pivotal role in ensuring sustainable agriculture and global food security in the face of climate change.

CONCLUSION

Non-coding RNAs have emerged as key regulators of gene expression in plants, particularly under abiotic stress conditions. Through their diverse mechanisms of action, including post-transcriptional regulation, epigenetic modification, and interaction with other regulatory molecules, ncRNAs enable plants to adapt to challenging environments. Their ability to control complex gene networks makes them valuable targets for crop improvement strategies aimed at enhancing stress tolerance and productivity. With ongoing advancements in molecular biology and biotechnology, ncRNA-based approaches are expected to play a central role in the development of climate-resilient crops, contributing to sustainable agricultural systems and long-term food security.

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