

Exploring the Roles of Non-Coding RNAs in Agriculture: Unveiling Gene Regulation and Potential for Crop Improvement

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Abstract:

Non-coding RNAs (ncRNAs) represent a rapidly expanding field of research that is transforming our understanding of gene regulation in plants. ncRNAs, including microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs), are crucial regulators of genetic expression, having significant implications for crop improvement, stress tolerance, and disease resistance. This article explores the emerging roles of these ncRNAs in agriculture, examining their involvement in plant growth, defense mechanisms, and their potential as targets for biotechnological applications. With sequencing technologies and computational biology advancements, the agricultural sector is poised to harness these molecules to drive future innovations in sustainable food production.

Introduction

Non-coding RNAs (ncRNAs) are RNA molecules that, unlike messenger RNAs (mRNAs), do not encode proteins but instead function as critical regulators of gene expression. In recent years, the agricultural research community has begun to recognize the importance of ncRNAs in regulating plant development, stress responses, and defense mechanisms against pathogens. While the majority of genomic research in agriculture has traditionally focused on protein-coding genes, it is now evident that ncRNAs, particularly miRNAs, lncRNAs, and circRNAs, play indispensable roles in fine-tuning gene networks involved in plant adaptation to biotic and abiotic stresses.

This article highlights the significance of ncRNAs in agriculture, discusses the current state of research on their roles in gene regulation, and explores their potential applications for

crop improvement through genetic engineering and breeding programs. The ability of ncRNAs to modulate gene expression at the post-transcriptional level opens new avenues for designing crops more resilient to environmental stressors and diseases, ultimately contributing to global food security.

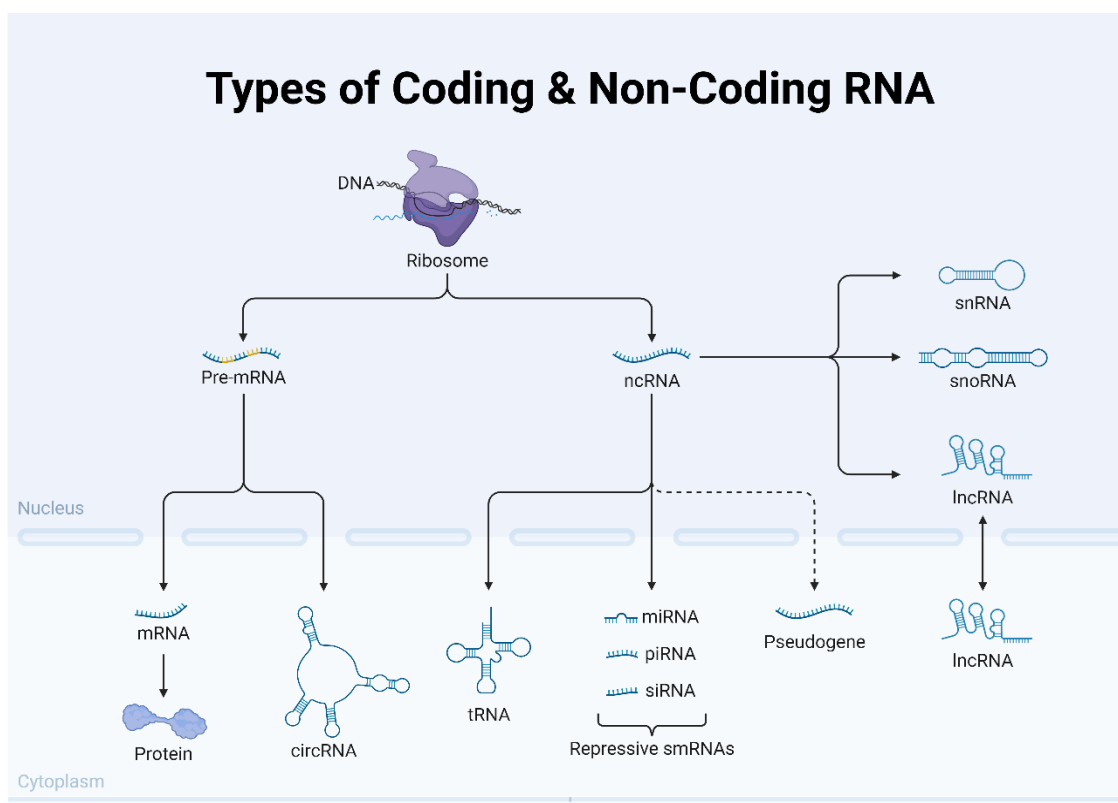


Figure 1. Types of non-coding RNA

MicroRNAs in Crop Development and Stress Tolerance

MicroRNAs (miRNAs) are short, non-coding RNA molecules, typically 21-24 nucleotides long, that regulate gene expression by binding to complementary sequences in target mRNAs, leading to their degradation or translational inhibition. Since discovering miRNAs in plants, their roles in crop development and environmental stress responses have been extensively studied.

Regulation of Plant Development

In crops, miRNAs regulate critical developmental processes such as leaf morphogenesis, root architecture, flowering, and seed development. For instance, miR156 and miR172 are well-known regulators of plant transition from the juvenile to adult phase. Overexpression of miR156 has been shown to delay flowering in rice and maize, while miR172

promotes floral development (Chuck et al., 2007). Similarly, miR319 has been implicated in leaf shape and size regulation in crops like tomato and Arabidopsis (Palatnik et al., 2007).

Role in Abiotic Stress Responses

MiRNAs also play crucial roles in plant adaptation to environmental stresses such as drought, salinity, and temperature extremes. For example, miR398 is downregulated during oxidative stress, allowing for increased expression of copper/zinc superoxide dismutase (CSD1 and CSD2), which scavenges harmful reactive oxygen species (ROS) (Sunkar et al., 2006; Nozawa et al., 2021). In rice, miR393 modulates drought stress tolerance by targeting the TIR1 auxin receptor, altering the plant's hormonal response to water-deficit conditions (Xia et al., 2015; Chen et al., 2021).

Table 1: Key miRNAs in Plant Development and Stress Responses

| miRNA | Function | Target Genes | Crop Examples | References |
|--------|------------------------------------|--|---------------------|--|
| miR156 | Juvenile-to-adult phase transition | SPL (SQUAMOSA promoter-binding protein-like) | Maize, Rice | Chuck et al., 2007; Zhang et al., 2017 |
| miR172 | Floral development | AP2-like transcription factors | Wheat, Rice | Chen et al., 2010; May et al., 2013 |
| miR398 | Oxidative stress tolerance | Superoxide dismutases (CSD1, CSD2) | Arabidopsis | Sunkar et al., 2006; Nozawa et al., 2021 |
| miR393 | Drought stress tolerance | TIR1 (auxin receptor) | Rice | Xia et al., 2015; Chen et al., 2021 |
| miR319 | Leaf morphogenesis | TCP transcription factors | Tomato, Arabidopsis | Palatnik et al., 2007; Wang et al., 2020 |

Long non-coding RNAs: A New Frontier in Crop Research

Non-coding RNAs (lncRNAs) are a diverse class of ncRNAs, typically longer than 200 nucleotides, that regulate gene expression through various mechanisms, including chromatin remodeling, transcriptional interference, and post-transcriptional regulation. Although the

study of lncRNAs in crops is still in its infancy compared to miRNAs, recent findings suggest that lncRNAs may play essential roles in plant growth, development, and stress responses.

- ✚ **Involvement in Plant Defense Mechanisms:** lncRNAs have been implicated in regulating plant immunity against pathogens. For instance, lncRNA973 has been shown to enhance resistance to *Phytophthora infestans* in cotton by modulating the expression of defense-related genes (Zhang et al., 2019; Qiao et al., 2021). Similarly, in *Arabidopsis*, the lncRNA induced by phosphate starvation (IPS1) competes with miR399 to regulate phosphate homeostasis, highlighting the intricate interplay between lncRNAs and miRNAs in nutrient sensing and response (Franco-Zorrilla et al., 2007).
- ✚ **Regulation of Abiotic Stress Tolerance:** In response to abiotic stress, lncRNAs can modulate gene networks, enabling plants to adapt to unfavorable environmental conditions. In rice, the drought-induced lncRNA DROUGHT (DRIR) promotes drought tolerance by upregulating stress-responsive genes and enhancing root growth (Qin et al., 2020). This suggests that lncRNAs could serve as promising targets for engineering crops with enhanced tolerance to drought and other abiotic stresses (Rui et al., 2023).

Circular RNAs: Emerging Players in Gene Regulation

Circular RNAs (circRNAs) are a unique ncRNAs formed through back-splicing exons or introns, resulting in covalently closed-loop structures. CircRNAs are more stable than linear RNAs due to their resistance to exonucleases. Recent studies have begun to uncover the roles of circRNAs in gene regulation in plants, although much remains to be explored.

- ✚ **Potential Functions in Plant Growth and Development:** CircRNAs can act as molecular sponges for miRNAs, preventing miRNAs from binding to their target mRNAs. This miRNA sequestration can influence gene expression patterns during plant growth and development. In rice, several circRNAs have been identified that may regulate key developmental pathways by interacting with miRNAs involved in root and shoot growth (Ye et al., 2017; Zuo et al., 2022).
- ✚ **Response to Biotic and Abiotic Stresses:** There is growing evidence that circRNAs regulate stress responses in crops. For instance, circRNAs responsive to salt stress have been identified in soybeans, suggesting that these molecules may play a role in salinity tolerance (Zhao et al., 2019; Zang et al., 2021). The stability and regulatory capacity of



circRNAs make them attractive candidates for further investigation as potential tools for enhancing crop resilience (Chen et al., 2023).

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