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The Role of MicroRNAs in Plant Growth and Development

Saira Sameen

ABSTRACT

This study explores the crucial role of microRNAs (miRNAs) in plant growth and development. MicroRNAs, small non-coding RNAs ranging from 19 to 25 nucleotides in length, modulate gene expression through mRNA degradation or inhibition of translation. miRNAs, small non-coding RNAs typically 19–25 nucleotides long, regulate gene expression by mRNA degradation or translation suppression. The biogenesis of miRNAs involves RNA polymerase II transcription and processing using the Dicer-like 1 enzyme. MicroRNAs impact diverse developmental procedures, including plant growth, reproductive improvement, and pressure responses. Key miRNAs like miR156 and miR172 adjust floral organ improvement and flowering time, emphasizing how miRNAs interact with transcription elements, maintain meristems, and signal hormones. It also examines the impact of miRNAs on fruit development, specifically in grapevines, affecting characteristics such as taste, size, and shape. This study examines the characteristics of miRNAs in abiotic and biotic strain responses and how they affect defense mechanisms and stress-effector genes. Moreover, it affords insights into the role of miRNAs in retaining nutrient balance by highlighting their effect on transporters that cope with nutrients and adjust to specific conditions resulting from nutrient deficiencies. The study delineates the specificity of miRNAs in plant biology, their crucial role in improved flora, and increased stress tolerance in plants.

Keywords: MicroRNAs in plants, Gene regulation, Plant development, Stress responses, MiRNA biogenesis

Introduction

MicroRNAs (miRNAs) are a class of small, non-coding RNAs that are crucial for regulating gene expression in plants. These linear molecules, usually extended from 19–25 nucleotides, were found to be conserved across various plant species and are involved in a wide range of developmental approaches, including plant maturation, organ formation, and stress responses.^{1,2} The biogenesis of plant miRNAs involves several steps, starting with the transcription of miRNA genes by RNA polymerase II, followed by the processing of the primary miRNA transcript into a precursor miRNA (pre-miRNA) using the enzyme Dicer-like 1. The precursor miRNA is then exported to the cytoplasm, wherein DCL1 processes it to generate the mature miRNA.¹

The life cycle of seed plants consists of distinct developmental stages, which include vegetative structure expansion, reproductive development, and seed/embryo formation. The microRNAs primarily attach themselves to complementary sequences inside the messenger RNA (mRNA) of the gene of interest, causing the target mRNA to degrade or suppress translation.³

Regulation of gene expression at the transcriptional and RNA levels is essential for the growth,

improvement, and defense mechanism of vegetation.⁴ Current research has highlighted the essential role of microRNAs (miRNAs) in regulating gene expression at some point in plant morphogenesis. Genome-extensive mapping and analysis of miRNAs and their potential gene of interest were conducted in numerous plant species, revealing their sizable effect on gene regulation.¹

The feature of miRNAs in controlling developmental transitions is significant to **miR172**. For instance, miR156 and miR172 significantly regulate the growth of floral organs and flowering time. Through interacting with critical transcription elements that manipulate those techniques, these miRNAs mitigate plants and make an appropriate transition from the vegetative to the reproductive levels. Moreover, the HD-ZIP III-miR165/166 direction is vital for each vascular development and leaf polarity, demonstrating how particular miRNA pathways can manage wonderful developmental traits.^{5,6}

The establishment and protection of meristem traits, crucial for plant structure, are other characteristics of miRNAs. It is far obtrusive that miRNAs can impact the general form and structure of flora because they mediate the modulation of axillary meristems through unique transcription elements, including ZF-HD TFs.^{6,7}

Furthermore, the interaction between miRNAs and hormones plays a significant role in coordinating increased responses; miRNAs can modulate hormone signaling pathways to facilitate speedy adjustments to developmental cues.^{5,8}

Moreover, the integration of RNA interference technology, which uses small RNAs like miRNAs, has been explored significantly for crop development. Figure 1 depicts the role of microRNAs in cellular mechanisms, developmental processes, and applications in different fields.

Methodology

This review incorporated a systematic examination of peer-reviewed literature from databases including PubMed, Web of Science, and Google Scholar, focusing on the role of miRNAs in plant growth and stress responses. Relevant studies on miRNA synthesis, regulatory functions, and applications were meticulously examined to synthesize information regarding their mechanisms and agricultural implications. This assessment highlights the critical role of miRNAs in regulating plant growth and stress responses. miR21 enhances pressure tolerance by altering signaling pathways, whereas miR156 and miR172 are valuable for vegetative-to-reproductive transitions and play a crucial role in optimizing plant growth and promoting sustainable agriculture. These consequences underscore the role of miRNAs in sustainable agriculture and their importance in enhancing plant development.



Fig 1 | The role of microRNAs in cellular mechanisms, developmental processes, and applications in different fields

Cross-Talk Between MicroRNAs and Other Regulatory Pathways

MicroRNAs are intricately concerned with complex regulatory networks, interacting with diverse cell pathways to optimize gene expression. Figure 2 depicts one key aspect of miRNA characteristics, specifically their interaction with transcription factors. miRNAs can alter the expression of transcription factors, creating comment loops that keep cellular homeostasis.⁹

For example, the NF-κB pathway generates a regulatory circuit that controls inflammatory responses through interactions with miR-146a and miR-21. The PI3K/AKT pathway indicates sizable interaction with miRNAs. miR-21 has been proven to inhibit apoptosis by regulating the PI3K/AKT/NF-κB signaling pathway in non-small cellular lung cancer cells.¹⁰ This interplay demonstrates how miRNAs impact the pathways that lead to cell survival and proliferation. The precise regulation of miRNAs is likewise stimulated by using epigenetic procedures. Histone adjustments and DNA methylation can affect miRNA expression, and miRNAs can impact the epigenetic equipment. This reciprocal connection complicates gene manipulation and cell reactions to environmental stimuli. The interplay among miRNAs and RNA-binding proteins (RBPs) represents another critical regulatory mechanism. RBPs can compete with or synergize with miRNAs for binding to mRNAs, influencing the final results of miRNA-mediated regulation. This competition or cooperation can result in an adjustment of manipulation of gene expression in response to the internal mechanism of the cell. miRNAs additionally interact with other non-coding RNAs, along with lncRNAs. lncRNAs can act as competing endogenous RNAs (ceRNAs) through sponging miRNAs, thereby modulating their availability to adjust target mRNAs.¹¹

This interplay adds other advantages to the regulatory network and affects numerous cell procedures. The MAPK signaling pathway is crucial in miRNA-mediated regulation. miRNAs and miR-181 have been determined as a primary component of the MAPK pathway, affecting cellular proliferation and survival. Conversely, MAPK signaling can impact miRNA expression, growing a reciprocal regulatory courting. In the context of apoptosis, miRNAs develop interaction with key regulators such as Bcl-2 proteins. miR-181 has been proven to target Bcl-2, influencing the stability among pro-apoptotic and anti-apoptotic elements. This interplay demonstrates the function of miRNAs in modulating cell death pathways.¹⁰

Glycine-rich RNA-binding proteins had been validated to serve distinguished features in plant defense against the pathogen *Pectobacterium carotovorum*. A diffusion of RNA-binding proteins and microRNAs manipulate posttranscriptional activities, consisting of pre-mRNA splicing, mRNA delivery, mRNA balance, and translation.⁴

MicroRNAs and Floral Development

Floral development is a complex process that requires the coordinated expression of multiple genes and

Table 1 | Summary of key microRNAs involved in plant development and stress responses

| miRNA | Function | Target Genes | Role in Development/Stress Response |
|------------|---|--|--|
| miR156 | Regulates vegetative-to-reproductive transition. ^{5,6} | SPL genes | Influences flowering time and floral organ development. ^{5,6} |
| miR172 | Affects flowering time. ^{5,6} | APETALA2 | Coordinates floral organ growth. ^{5,6} |
| miR165/166 | Vascular development and leaf polarity. ^{5,6} | HD-ZIP III genes | Essential for leaf formation and vascular tissue. ^{5,6} |
| miR21 | Stress resilience. ¹¹ | Various apoptosis-related genes. ¹¹ | Modulates responses to stress, including apoptosis. ¹¹ |
| miR393 | Drought response. ³² | Auxin transporters. ³² | Enhances drought tolerance. ³² |
| miR827 | Nutrient uptake. ^{27,28} | Phosphate transporters. ^{27,28} | Regulates phosphate homeostasis. ^{27,28} |

Table 1 depicts the functions, goal genes, and importance of every miRNA in reacting to abiotic pressure, highlighting the involvement of miRNAs in plant growth. Each miRNA mentioned in this list is essential for controlling vital features like pressure tolerance, vascular growth, and flowering. For instance, although miR21 will increase strain tolerance through enhancing signaling pathways, miR156 and miR172 are essential for controlling flowering time. A higher grasp of the complicated connections between miRNAs and their organic roles in plant life is made feasible via this methodological approach.

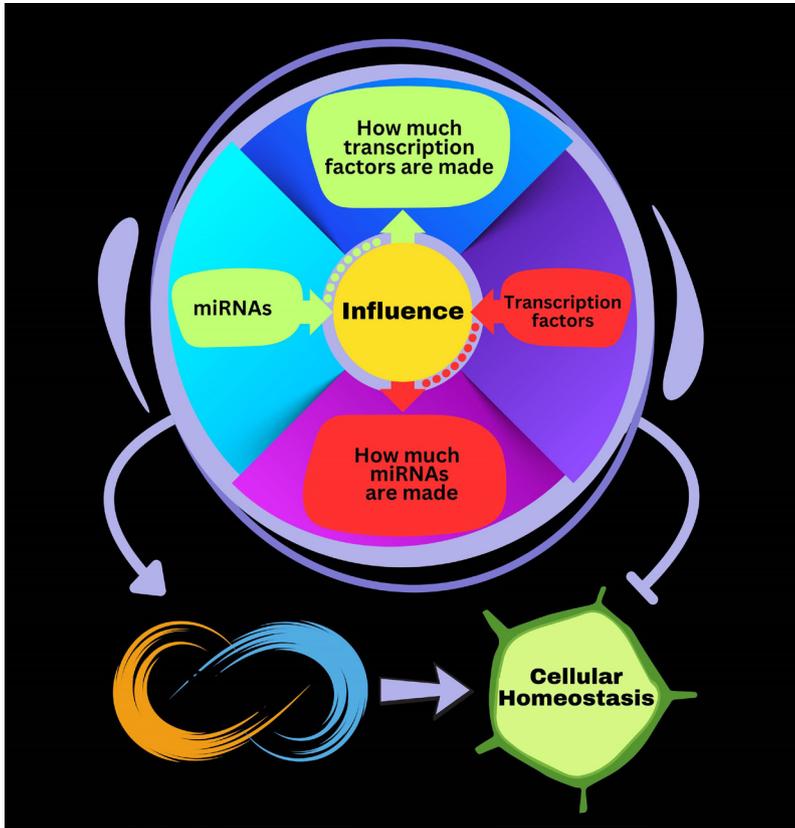


Fig 2 | Key aspect of miRNA characteristics, specifically their interaction with transcription factors

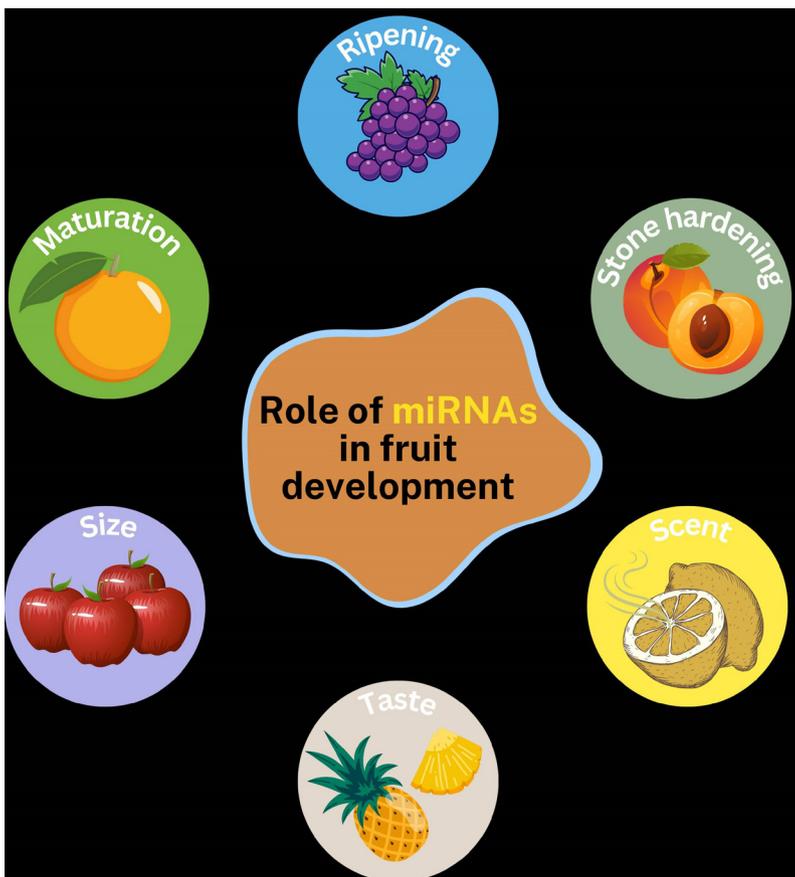


Fig 3 | Role of miRNAs in fruit development

regulatory elements.^{1,2} Researchers have explored the involvement of miRNAs in regulating crop advancement. The expression of precise miRNAs has been identified as vital for developing and differentiating floral organs and the ovary, oviduct, uterus, and cervix. The growth cycle of seed flowers, which includes the vegetative developmental phase and the reproductive increase segment, is also heavily stimulated by the moves of miRNAs and their target genes.²

For example, miRNAs play an essential role during the female reproductive cycle, altering gene expression and contributing to organ improvement and characteristics. The significance of miRNAs in various aspects of mammalian reproduction, from germ cellular commitment to peri-implantation.¹²

Furthermore, the research on miRNAs and their putative genes in grapevine confirmed the sizeable impact of small regulatory RNAs on plant growth and development, consisting of floral development. Likewise, manipulating developmental segment transitions via miRNAs in seed flowers supplied precious insights into the regulatory mechanisms involving miRNAs and their objectives throughout the vegetative-to-reproductive transition and floral organ formation.²

MicroRNAs and Fruit Development

Recent research has reflected the role of miRNAs in fruit development together with the ripening and maturation of fleshy culmination, indicating their involvement in several physiological and biochemical pathways (Figure 3). Researchers examined the expression of miRNAs and their goal genes at some point of the stone-hardening level of grape berry improvement, figuring out 161 conserved and 85 species-specialized miRNAs, with 30 being tissue-specialized and associated with stone hardening.¹³

Furthermore, research has elucidated the appropriate strategies through which miRNAs influence fruit development. The regulation of grapevine flower development is significantly influenced by miR172, with several participants displaying particular spatio-temporal expression patterns and regulatory mechanisms.^{2,13,14}

An assessment of small regulatory RNAs in fruit plants underscores the influence of miRNAs on the size, shape, color, aroma, and flavor of various fruits. A crucial factor influencing these capabilities is the interaction of miRNAs with hormone-signaling pathways, including auxin and gibberellin. This illustrates how miRNA-mediated regulation includes essential characteristics for horticultural practices and their developmental roles.^{5,15}

MicroRNAs and Abiotic Stress Responses

miRNAs are essential translational regulators that modify gene expression to adapt to environmental stressors, including high heat, salinity, and drought. A complex regulatory network in which particular miRNAs can both promote or avoid the expression of target genes connected with stress resilience proved with research showing changes in miRNA expression across several plant species under abiotic pressure

conditions. Studies have established that based on different types of abiotic pressure experienced, the expression of precise miRNAs is considerably improved or declined. In Arabidopsis, dryness causes miR156, miR319, and miR393 to be upregulated, while different miRNAs, including miR169, are downregulated within the identical situation.^{16,17}

MicroRNAs have been proven to target various stress-responsive genes, influencing techniques like antioxidant defense, osmotic adjustment, and the activation of strain-signaling pathways.^{18,19} For example, the GhMAP3K62-GhMCK16-GhMPK32 kinase cascade has been classified as a crucial element during the drought tolerance response, with the downstream activation of the GhEDT1 transcription issue.¹⁹ Furthermore, manipulating enzymatic and non-enzymatic antioxidants has emerged as a promising strategy to increase the pressure tolerance of plants.²⁰

MicroRNAs can switch from repressing to activating gene expression in response to mobile stressors like nutrient deficiency. For instance, miR-10 will increase ribosomal protein translation during amino acid shortage.¹¹

MicroRNAs and Biotic Stress Responses

MicroRNAs are concerned with the post-transcriptional regulation of target mRNAs, influencing plant defense mechanisms through various pathways in pathogenic environments and other biotic challenges. For example, unique miRNAs, including miR161, miR164, and miR396, were shown to be downregulated in Arabidopsis in response to *Heterodera schachtii* contamination, indicating their capacity as biomarkers for biotic strain responses. Furthermore, in soybeans, a comprehensive examination diagnosed 101 miRNAs belonging to 40 families that respond to the soybean cyst nematode *Heterodera glycines*, besides assisting the idea that miRNAs play essential roles in plant defense.²¹

In addition to silencing genes, miRNA regulatory mechanisms can induce translational repression and mRNA degradation. Plant life may also efficiently adapt their responses to distinctive illnesses. The extent of complementarity between miRNAs and their target mRNAs determines whether the contact consequences are translational inhibition or direct cleavage.¹⁷

Recent advancements have shown new miRNA-mediated regulatory pathways that enhance plant resilience towards biotic stresses by modulating the expression of transcription factors and practical enzymes crucial for defense responses.²²

Moreover, studies have indicated that miRNAs respond to individual pathogens and can also be a part of a broader regulatory community that integrates indicators from multiple stressors. This adaptability is crucial for flora undergoing diverse environmental challenges because it allows them to optimize their shielding techniques.²³

The evolutionary conservation of these regulatory systems inside the kingdom Plantae is highlighted by

the discovery of unique miRNA families connected to biotic pressure responses in numerous species.²⁴

This increasing understanding of miRNA capabilities in biotic stress responses highlights their importance as an objective for enhancing infection resistance in crops. By manipulating miRNA expression profiles, researchers proposed to develop plants with advanced resilience in opposition to pathogens, which is essential for sustainable agricultural practices under food safety concerns worldwide.²⁵

MicroRNAs and Nutrient Homeostasis

In the present years, the clinical network has witnessed a developing interest in the elaborate relationship between miRNAs and nutrient homeostasis.

One of the key aspects of microRNA features is their potential to govern the uptake and assimilation of vitamins. It's been confirmed that these molecules are crucial for controlling pathogenic bacteria residing in the eukaryotic cells. They impact the interaction between host and pathogen and the bacterium's capacity to react to changes in pH, temperature, or dietary deficiency. Moreover, miRNAs implicated in the modulation of communication between the cells, envelope homeostasis, biofilm formation, and strain reaction in microorganisms might be vital for maintaining nutrient homeostasis.²⁶

The interaction among miRNAs and nutrient transporters is crucial for preserving homeostasis. Researchers showed that unique miRNAs modify the expression of transporter genes responsible for nutrient uptake, thereby influencing the plant's capability to evolve to low nutrient availability. For instance, miR827 has been linked to the phosphate transport system, where its expression is modulated during phosphate deficiency, leading to alterations in transporter gene kinetics.^{27,28}

Furthermore, miRNAs respond to potassium stress. Studies have shown that some miRNAs are differentially expressed in low potassium environments, affecting physiological procedures that include photosynthesis and root growth. For instance, miR160a and miR396c were implicated in objectifying the photosynthetic performance and root structure during potassium deficiency.²⁸

MicroRNAs as Biotechnological Tools

MicroRNAs have emerged as powerful biotechnological tools for crop development and plant research. One of the most promising miRNAs in plant biotechnology programs is using artificial miRNAs (amiRNAs) for centered gene silencing. This method permits researchers to downregulate genes of interest, providing treasured insights into gene characteristics and manipulating advantageous traits.²⁹

The short tandem target mimic (STTM) approach has gained promising attention as a tool for reading miRNA functions in flora. This technique involves engineered RNA molecules that sequester precise miRNAs, efficiently inhibiting their role. STTM has been specifically beneficial in rice studies, which have investigated the roles of miRNAs in diverse agronomic traits. Recent advances in CRISPR/Cas9 technology have featured

new opportunities for miRNA-based crop enhancement. Researchers have efficiently used CRISPR/Cas9 to edit miRNA genes and their active sites, allowing for particular manipulation of miRNA-mediated regulatory networks.³⁰ This approach gives a transgene-free method for crop breeding, confronting concerns related to genetically changed organisms.

Establishing miRNA databases and bioinformatics tools has significantly facilitated research on miRNA in plants. Complete facts on miRNA sequences, targets, and expression profiles may be determined in sources like miRBase and the Plant MicroRNA Database (PMRD).³¹

These databases and advanced computational prediction tools have improved our capacity to identify and signify miRNAs and their targets in diverse plant species.

Clinical Applications of Plant MicroRNAs

Plant miRNAs play a significant role in stress response and disease resistance pathways. In rice, miR528 activates the antiviral pathway by regulating L-ascorbate oxidase and inhibiting ROS accumulation, thereby reducing cell demise and host plant harm. In wheat infected with powdery mildew, the expression of miR156, miR159, and miR164 is upregulated, and miR393, miR444, and miR82 are downregulated, indicating their involvement in disorder resistance.³²

Plant miRNAs have appeared to be effective in treating cancer. The manufacturing of quinoline alkaloids can be motivated via some miRNAs, which include *pso-miR13*, *pso-miR2161*, and *pso-miR408*, which might also have results for treating cancer. Five new miRNAs and four conserved miRNAs were shown to be putative members in terpene trilactone production pathways in *Ginkgo biloba*, which may also have anti-cancer results.³³

Nanotechnology-based delivery structures have shown promising efforts for miRNA-based cancer therapeutics. Such systems can probably restrict most cancer initiation and development procedures. Nevertheless, demanding situations stay within the green transport and concentrate on plant miRNAs for clinical approaches.³⁴

AI and Nanotechnology-Based Delivery System in miRNA Target Prediction

AI and nanotechnology have greatly improved the latest developments in miRNA studies. Technologies like DeepMirTar, which mixes low-level, strategic, and primary data-level capabilities to reinforce predictive accuracy above traditional strategies, have improved AI-driven miRNA goal prediction.³⁵

Mimosa, the other progressive technique, employs the transformer framework to represent non-canonical base-pairing patterns, improving predictive skills by reducing reliance on pre-selected candidate targets.³⁶ Moreover, k-mer splitting and self-supervised neural networks are used by kmerPMTE, a novel framework for plant miRNA-goal prediction, to extract semantic embeddings, improving predictive accuracy across plant datasets.³⁷ Those tendencies open the door to greater

accuracy in treatment strategies by demonstrating the revolutionary capability of using AI in miRNA research.

Challenges and Future Directions

Despite significant advancements in our understanding of miRNAs in plant growth and development, challenges and potential pathways remain. Due to the predominance of research on model organisms, a common challenge is identifying the specific functions of notable miRNAs in various plant species.^{6,38}

Expanding research to diverse horticultural and crop plant life will offer more comprehensive information on miRNA roles throughout specific species. Another venture is the lack of effective transformation structures in many plant species, hindering the purposeful validation of recognized miRNAs.³⁸

Growing robust transformation strategies for a wider variety of plant life might be crucial for advancing miRNA research. Unraveling the complex regulatory networks related to miRNAs, their goals, and other molecular pathways remains an enormous project.^{5,6}

Future studies must be cognizant of integrating miRNA information with different omics processes to build complete models of plant developmental techniques. The ability of miRNAs in crop improvement and molecular breeding is a thrilling place for future exploration.^{22,38}

Developing miRNA-based technology for enhancing resistance against disease, pressure tolerance, and agronomic trends can be treasured for agriculture. However, this calls for overcoming demanding situations in designing and editing synthetic miRNAs (amiRNAs) and ensuring their solid expression in target vegetation.²²

Novel Direction and Practical Applications

Many techniques can provide new experimental frameworks and close the gaps in miRNA research. It is impossible to ignore the methods in which miRNAs influence their interactions with different regulatory molecules, together with RNA-binding proteins and sequential non-coding RNA. Radical research is required to combine their interconnections to represent how they impair gene expression. Insight into evolutionary conservation and useful range may also be improved by investigating the region of miRNAs in other plant species and during numerous environmental conditions. CRISPR/Cas9 strategy can be used in the experimental setup to adjust precise miRNA genes, permitting practical monitoring of phenotypic alterations and stress reactions. Case studies have demonstrated the effectiveness of miRNAs in enhancing agricultural practices. For example, it has been established that manipulating miR172 can improve the production and flowering time of rice culmination, subsequently boosting agricultural productivity. amiRNAs target unique genes connected to drought resistance in maize, growing the crop's capacity to face water shortages. Those applications show the capability of miRNAs as tools for developing resilient crop genotypes that may survive under abiotic stressors, supporting sustainable farming practices.

Conclusion

MicroRNAs significantly regulate the morphogenesis and development of plants via diverse mechanisms. Those small non-coding RNAs concern vegetation features, including floral improvement, fruit maturation, stress responses, and nutrient homeostasis. By targeting particular mRNAs for degradation or translational repression, miRNAs fine-track gene expression in response to developmental cues and environmental stimuli. The intricate regulatory networks related to miRNAs about their interactions with transcription elements, hormones, and different signaling pathways. These interactions create complex remark loops that maintain cellular homeostasis, allowing flowers to evolve to changing conditions. The function of miRNAs in mediating abiotic and biotic pressure responses is particularly extensive because it offers avenues for enhancing crop resilience and productivity. Recent advances in our information of miRNA features in nutrient homeostasis and fruit improvement have opened new opportunities for agricultural programs. Researchers aim to enhance disease resistance, improve fruit quality, and optimize nutrient utilization in plants by manipulating miRNA expression. As studies in this discipline progress, the capacity for leveraging miRNA-based techniques in plant biotechnology and crop development becomes increasingly apparent. Future research will probably raise awareness of unraveling the complicated interplay among miRNAs and other regulatory factors and growing realistic applications for miRNA-mediated crop enhancement.

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