

Role of microRNAs (miRNAs) in Plant Improvement

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ABSTRACT

Plant gene expression is controlled by microRNAs (miRNAs), which are small, non-coding RNA molecules with a length of 20–22 nucleotides. They function by either inhibiting translation or cleaving messenger RNA (mRNA) to silence particular target genes after transcription. miRNAs function as fine-tuners of plant growth, development, flowering, root formation and reactions to the environment because they regulate numerous crucial genes. According to recent studies, miRNAs are crucial to plant improvement initiatives. They improve nutrient uptake (nitrogen, phosphorus and sulfur); help crops withstand abiotic stresses like drought, salinity, heat and cold; offer resistance against diseases caused by bacteria, fungi and viruses; and enhance yield-related traits like grain number, plant architecture and flowering time. Improved crop varieties are currently being developed using miRNA-based techniques like overexpression, knockdown (STTM/MIM), CRISPR-based editing of MIR genes and miRNA markers. Using examples from significant miRNA families like miR156, miR159, miR396, miR399 and miR482, this article summarizes the contributions and uses of plant miRNAs in crop improvement while providing a straight forward explanation of their biogenesis and activities.

INTRODUCTION:

A significant problem is feeding the world's expanding population in the face of climate change. For many

years, conventional plant breeding has improved crops, but development is gradual and frequently constrained by the genetic

variation that is accessible. The importance of tiny RNA molecules in regulating plant genes is one of the most fascinating discoveries of the past 20 years, and modern biotechnology offers new methods (Bartel, 2004).

Tiny RNAs called microRNAs (miRNAs) do not code for proteins. Rather, they govern (control) other genes. Each miRNA attaches itself to a target messenger RNA (mRNA) and either cuts it or prevents it from being translated into a protein. According to Jones-Rhoades *et al.* (2006), a single miRNA can thereby regulate whole networks of genes related to growth, blooming, stress response, and nutrition utilization.

Thousands of miRNAs have been discovered by plant scientists in crops like rice, wheat, corn, cotton and tomatoes. Many of these miRNAs have a direct impact on qualities that breeders aim to enhance such as nutrient efficiency, disease resistance, drought and salt tolerance and yield (Tang and Chu, 2017). The synthesis and function of miRNAs are briefly described in this overview, followed by a discussion of their function and uses in plant improvement.

1. WHAT ARE miRNAs AND HOW DO THEY WORK?

MIR genes are the genes that generate miRNAs. The MIR gene is first converted into a lengthy primary transcript (pri-miRNA) in the nucleus. This transcript is broken into a hairpin-shaped precursor (pre-miRNA) and a brief miRNA/miRNA* duplex of roughly 20–22 nucleotides by the enzyme Dicer-like 1 (DCL1). One strand (the mature miRNA) joins the RISC complex, which is led by the Argonaute 1 (AGO1) protein, following modification by the enzyme HEN1 and export to the cytoplasm. Through complementary base pairing, the miRNA directs this complex to target mRNAs. The target mRNA is primarily cut and destroyed in plants due to

near-perfect matching; occasionally, translation is prevented (Jones-Rhoades *et al.*, 2006). Figure 1 summarizes this entire procedure.

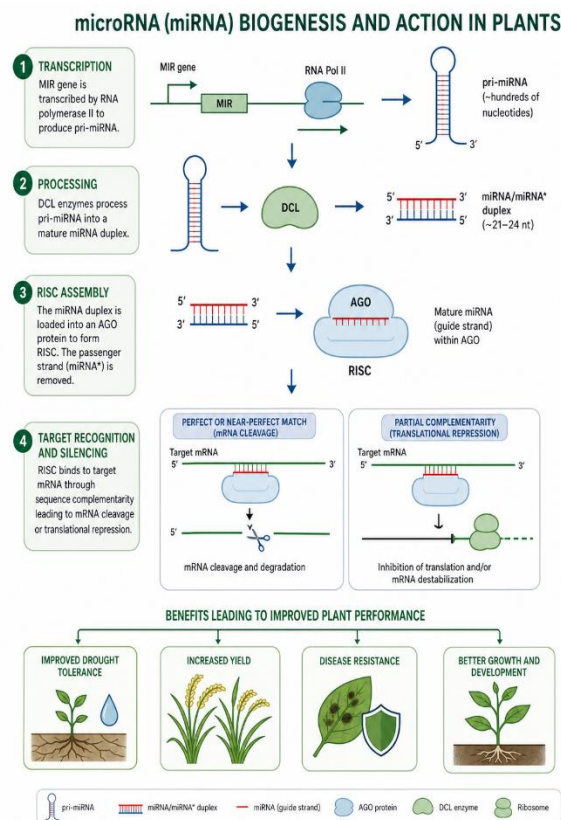


Figure 1. Simplified miRNA biogenesis in plants — from MIR gene transcription through DCL processing, AGO loading and RISC action, leading to practical crop outcomes (drought handling, yield, defense).

2. ROLE OF miRNAs IN PLANT IMPROVEMENT

2.1 Growth, development and yield

Plant architecture and yield components are regulated by a number of miRNAs. One of the most well-researched instances is miR156, which targets SPL genes and regulates blooming timing and the transition from the juvenile to the adult phase. In rice and maize, yield-related attributes are enhanced by a moderate decrease in miR156. Through MYB transcription factors, miR159 influences the development of flowers and seeds; miR160

and miR167 change auxin signalling to shape the growth of roots and shoots; miR166 regulates the development of leaves and vessels and miR396 governs cell division and leaf size. Scientists can modify plant form, flowering period, and ultimately grain yield by modifying these miRNAs (Tang and Chu, 2017).

2.2 Abiotic stress tolerance (drought, salt, heat, cold)

Important participants in stress reactions are miRNAs. Stress-protective genes are turned on or off by rapid changes in the amounts of miRNAs including miR169, miR393 and miR398, under drought and salt stress. For instance, rice, tomatoes and wheat are more drought-tolerant when miR169 is manipulated because it targets the NF-YA transcription factor. Superoxide dismutases (CSD genes), which shield cells from oxidative damage brought on by heat, dehydration and heavy metals are regulated by miR398 (Zhang, 2015). Therefore, creating climate-resilient crops by the engineering of these miRNAs is a promising approach.

2.3 Disease and pest resistance

Additionally, miRNAs aid plants in their defense against diseases. NBS-LRR resistance (R) proteins, the plant's first line of defense against bacteria, viruses and fungi, are regulated by members of the miR482/miR2118 family. Modifying miR482 activity in cotton and tomatoes boosts resistance to bacterial and fungal infections. Similarly, by suppressing auxin signalling during pathogen infection, miR393 enhances basal immunity. A useful new method for creating disease-resistant cultivars is miRNA-based resistance (Zhang, 2015).

2.4 Nutrient use efficiency

miRNAs control the uptake and use of nutrients by plants. In low-phosphorus soil,

miR399 enhances phosphate (P) absorption by targeting PHO2. miR169 and miR444 are associated with nitrogen use, while miR395 controls sulfate transporters and sulfur metabolism. Better nutrient-use crops use less fertilizer, which decreases farming costs and lessens pollution in the environment. Table 1 summarizes significant instances of miRNAs and their functions in plant improvement.

Table 1. Important miRNA families and their role in plant improvement

miRNA family	Target gene(s)	Role in plant improvement	Example crop(s)
miR156	SPL transcription factors	Juvenile-to-adult transition, flowering time, tillering, higher yield	Rice, maize, wheat
miR159	MYB / GAMYB	Flower and anther development, seed germination	Rice, wheat, barley
miR160/167	ARF (auxin response factors)	Root and shoot architecture, auxin signalling	Tomato, rice, Arabidopsis
miR166	HD-ZIP III	Leaf development, vascular bundles, shoot branching	Maize, rice
miR169	NF-YA	Drought and salt tolerance, nitrogen response	Rice, wheat, tomato
miR393	TIR1/AFB receptors	Drought, salt, cold tolerance; basal disease immunity	Rice, Arabidopsis
miR396	GRF (growth regulating factors)	Leaf and cell growth, grain size and yield	Rice, wheat, maize
miR398	CSD (superoxide dismutases)	Oxidative, heat and heavy-metal stress tolerance	Wheat, Arabidopsis
miR399	PHO2 (E2 conjugase)	Phosphate uptake and use efficiency	Rice, barley, soybean
miR482/2118	NBS-LRR (R proteins)	Disease resistance against fungi,	Cotton, tomato, wheat

		bacteria, viruses	
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Source: summarised from Jones-Rhoades et al. (2006), Zhang (2015) and Tang & Chu (2017).

CONCLUSION AND FUTURE PROSPECTS

Plant growth, yield, stress tolerance, disease resistance and nutrient utilization are all governed by miRNAs, which are tiny but potent regulators. MiRNA-based engineering provides a versatile and effective means of enhancing complex features that are challenging to manage through traditional breeding alone because a single miRNA can regulate numerous genes simultaneously. In the future, the development of climate-smart, high-yielding and nutrient-efficient crop types will be accelerated by integrating miRNA engineering with genome editing, high-throughput sequencing and speed-breeding.

Thus, a key component of contemporary plant development is comprehending and using miRNAs.

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