# MicroRNAs as fine-tuners of gene regulation in plant–microbe interactions

**Minu M. Nair and Alagu Manickavelu***

Department of Genomic Science, Central University of Kerala, Kasargod 671 316, India

**Plants utilize non-coding RNA-mediated gene regulatory mechanism as one of the effective ways to cope with stress. MicroRNAs (miRNAs) are crucial players of this category that regulate gene expressions at the post-transcriptional level. miRNAs are reported to be involved in different aspects of plant–microbe interactions, starting from regulation of pathogen recognition receptors to fine regulation of defence gene expression, as well as in maintaining symbiosis. In plants, miRNA mediated gene regulation is an active layer in biotic stress responses with a lesser chance of off-target effects. A better understanding of miRNA-mediated gene regulation will have numerous applications from primary gene function study to targeted gene silencing. This article summarizes the current knowledge on miRNAs in plant–microbe interactions, with an emphasis on their utilization as a powerful tool in disease management.**

**Keywords:** Disease management, gene regulation, microRNAs, plant–microbe interactions, plant defence responses.

PLANTS are the mainstay for survival of other organisms on earth and maintain harmony of the biosphere. They are considered as a major source to feed the entire world population. The increase in global population, as well as various abiotic and biotic stresses challenge plant protection and food security. Plant–microbe interactions have been a focal point of research since a long time, as they can change the morphological, physiological and metabolic processes of the host plants. Interactions between plants and microbes could either be beneficial or detrimental. Mutualistic interactions can impart better adaptation, while interactions with pathogenic microbes result in devastating plant diseases[1]. The pathogenic intrusion triggers the plant immune system and the recognition of pathogen/microbe-associated molecular patterns (PAMPs/MAMPs) using pattern recognition receptors (PRRs) as the first response[2,3]. This initiates production of reactive oxygen species (ROS), callose deposition to strengthen the cell wall, expression of pathogenesis-related (PR) genes and production of phytohormones. Collectively, these responses are classified as PAMP-triggered immunity (PTI)[4]. Nevertheless, the pathogens have evolved to take over these primary responses of the host via effector proteins, which compel the host plants to establish effector-triggered immunity (ETI) as another active layer of immune response. ETI responses are mainly via the expression of resistance genes which lead to hypersensitive responses upon recognition of effector proteins produced by the pathogens[5].

Emergence of new microbial mechanisms to invade the host plant and constant exposure to the pathogens encourage the plants to develop more efficient and sophisticated mechanisms to control pathogen attack. One such mode that provided new dimensions to the complex eukaryotic gene regulatory mechanisms is non-coding RNA-mediated gene regulation. The major contributors to this category are microRNAs (miRNAs), and their role in different aspects of growth, development, chromatin remodelling, genome stability and stress responses has been reported[6,7].

miRNAs are single-stranded RNAs of 18–25 nt in length, and regulate the genes post-transcriptionally either through mRNA cleavage or by translational repression based on their complementarity with the target mRNAs[8]. The miRNAs were initially known as short temporal RNAs (stRNAs) and first reported in *Caenorhabditis elegans* by early 1990s, but several plant miRNAs have been discovered later[9–12]. The biogenesis of miRNAs in plants is well studied (Figure 1). miRNA synthesis starts from the transcription of MIR genes by RNA polymerase II, and proceeds through the formation of primary miRNAs, precursor miRNAs, miRNA–miRNA* duplex before single-stranded miRNAs get inserted into the RNA-induced silencing complex (RISC). Following the RISC formation, ARGONAUTE (AGO) proteins guide the miRNA strand to its target mRNA, and other strand of the duplex undergoes degradation[13–23].

The precise and targeted gene regulation makes plant miRNAs distinct and efficient gene modulators. A better understanding of miRNAs can be exploited for its myriads of applications from basic gene function study to targeted gene silencing[24]. By taking advantage of sequence specificity of endogenous miRNAs, designing of artificial miRNAs to suppress the target genes for enhancement of quality and quantity of agricultural products is also in practice[25]. Efforts have been made in the past for the identification of many miRNA–mRNA

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*For correspondence. (e-mail: amanicks@cukerala.ac.in)