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Plant miRNAs: Micro Structure and Macro Character

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Editorial

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INTRODUCTION

MicroRNAs are small, endogenous, conserved, non-coding single-stranded RNAs (~21 to 24 nucleotides in length), initially thought to be an oddity of nematode biology and now are regarded as the regulators and master-coordinators of posttranscriptional or translational gene expression in plants, animals, viruses and unicellular eukaryotes (*Chlamydomonas reinhardtii*) with the exception of *Saccharomyces cerevisiae* [1-3]. The first ever miRNAs to be discovered are lin-4 and let-7 in *Caenorhabditis elegans* and 16 miRNAs in *Arabidopsis thaliana* [4]. Before 16 years, none had even heard of microRNAs and today more than 48885 miRNAs from 271 species are registered in the miRBASE (http://www.mirbase.org/) and 10,000 miRNAs from 121 plant species are registered in plant miRNA database (PMRD, http://bioinformatics.cau.edu.cn/PMRD). The number of miRNAs vary in diverse plant species e.g.; *Arabidopsis thaliana* (199), *Oryza sativa* (447), *Medicago truncatula* (375), *Zea mays* (170), *Sorghum bicolor* (148), *Vitis vinifera* (137) etc. Plant miRNAs are evolutionarily conserved across angiosperms, gymnosperms and mosses [5] and now their discovery in algae opines of their evolution from a common unicellular ancestor of algae and higher plants. Lot many angiospermic miRNAs were expressed and identified in a gymnosperm, miR160 and miR390 in a pteridophyte and miR160 from *Polytrichum juniperinum*. Genome has genes that code for miRNAs and most plants have over 100 miRNA genes (MIR) (117 in *Arabidopsis*, 90-120 in *C. elegans*, 178 in *Oryza sativa*, 97 in *Zea mays*) located mainly in the intergenic regions of genome known as **intergenic miRNAs**. Other categories of miRNAs are the **intronic miRNAs** located in the intron region (Less in number) and the **extronic miRNAs** (rarely present) [6] located in the exon region of protein coding or non-coding transcripts.

BIOGENESIS

The biogenesis of miRNA is completed mainly in 4 steps of **Transcription** of Primary-miRNA few kilo bases in size encapsulated with 5' cap and a poly-A tail at two ends from miRNA gene by RNA polymerase II or in few cases by RNA polymerase III which bind to the 3'UTR of mRNA, **Processing** of Primary-miRNA into stem-loop pre-miRNAs in nuclear processing centers called D-bodies, Pre-miRNAs produced by DCL1 is then exported to the cytoplasm from the nuclear pores of nucleus by Exportin 5 ortholog HASTY and other unknown factors. **Maturation** of stem-loop pre-miRNAs into double stranded- mature RNA transcripts (miRNA/miRNA*, where miRNA is the guide strand and miRNA* is the passenger strand) by DCL enzymes with distinct sizes: 21 nucleotides for DCL1 and DCL4, 22 nucleotides for DCL2, and 24 nucleotides for DCL3 in the cytoplasm and mature RNA duplexes are methylated by HEN1, to protect these from exonuclease activity of SMALL RNA DEGRADING NUCLEASE (SDN). Finally **Execution** of silencing reaction of target mRNA sequence usually transcription factors by guide strand of miRNA by incorporation into AGO proteins so as to generate the effector complex miRISC RNA-induced silencing complex (RISC). The miRNA hinders the expression of mRNAs chiefly in two ways of posttranscriptional silencing depending on the degree of complementarity between miRNA and their target i.e.; **translation inhibition** or **mRNA cleavage** [7]. When mRNA has near-perfect complementarity to a miRNA then mRNA is cleaved while with less complementarity mRNA translation is attenuated. Other mechanisms like translational inhibition at the level of initiation and elongation, rapid degradation of the nascent peptide and mRNA degradation are also reported. Several Computational tools for miRNA prediction are MiRscan, proMiRII, mir-abela,triplet-SVM, Vmir, RNA micro, Hertel and Stadler, Bayes MiRNAFind, and One-Class MirnaFind. TargetScanS, miRanda, PicTar, RNA hybrid, Diana-microT, RNA22, MicroTar, TargetBoost, TargetScan and MicroInspector are few miRNA Target prediction tools.

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FUNCTIONS

Plants live a sedentary life with less chance of escaping when ecological conditions become adverse and lack strong immune system to battle against the biological invasions by pathogens so have developed very sophisticated methods to evade abiotic and biotic stresses [4], out of which the plant modulated miRNA machinery is the foremost. Specific functions of all miRNAs are mysterious as only few have been functionally characterized. Micro-RNAs are an imperative piece of puzzle that is gene regulation. Majority of microRNAs regulate other genes by binding to complementary sequences in the target gene and negatively regulate protein-coding genes through translational repression or mRNA cleavage or can cause their methylation. It has been estimated that more than 30% of protein-coding genes can be regulated by microRNAs. miRNAs regulate expression of more than one third of genes in animals and have at some point influenced the expression of nearly the entire genome. In plants, the number of known miRNAs and miRNA targets is lower than in animals so the spectrum of miRNA action seems to be extremely wide, counting various aspects of development, several adaptive responses to stresses and the regulation of the miRNA pathway itself. Plant miRNAs act in multiple biological processes and affect almost everything like growth, development, flowering, auxin response, leaf polarity, cell fate/differentiation, maintenance of genome integrity, metabolism, nutrient homeostasis, signaling pathways, hormone homeostasis, immune response, DNA repair, oxidative stress response, circadian rhythm, viral replication, adaptive responses to biotic and abiotic stresses and the miRNA pathway regulation itself [8].

FUTURE PERSPECTIVES

The miRNAs number ranges from 1000 to 60,000/cell, show spatiotemporal distribution, express across diverse organs and each organ has a distinctive miRNA "profile" which may change during plant growth and development and stress conditions. A miRNA can influence expression of numerous target genes and in consequence regulate cell differentiation, proliferation and death. Decoding of all the miRNA targets and their roles will be one of the impending challenges in this promptly promising scientific arena and will act as players of the next generation genetic engineering for augmentation and improvement of various therapeutic plants and crops. Furthermore, the biological effects of Plant- miRNAs for human therapy have been profiled computationally. *Curcuma longa* miRNAs target genes linked with diabetes mellitus type II, cardiovascular disorders, Alzheimer's, cancer and thalassemia and miRNAs of *Gmelina arborea* target genes connected with human cancer, blood borne disorders and urinary infections. Plant derived miRNA (MIR2911) present in decoction of a Chinese herb honeysuckle has ethnobotanical use against influenza. MIR2911 targets influenza A viruses, represses their replication progression, fights influenza infection and thus the miRNAs like this can act as novel bioactive agents for regulation of human health or can target genes connected with the ailments at a very early stage [9]. This could pave a way for artificial synthesis of therapeutic plant-derived miRNAs for treatment of various human syndromes.

REFERENCES

1. Brodersen P, et al. Widespread translational inhibition by plant miRNAs and siRNAs. Science. 2008;320:1185-1190.
2. Zhang B. MicroRNA: a new target for improving plant tolerance to abiotic stress. J Exp Bot. 2015;66:1749-1761.
3. Axtell JM. Classification and comparison of small RNAs from plants. Ann Rev Plant Biol. 2013;64:137-159.
4. Bakhshi B, et al. MicroRNA signatures of drought signaling in rice root. PLoS One. 2016;11: 0156814.
5. Jones-Rhoades MW. Conservation and divergence in plant microRNAs. Plant Mol Biol. 2012;80:3-16.
6. Sunkar R, et al. Cloning and characterization of microRNAs from rice. Plant Cell. 2005;17:1397-1411.
7. Rogers K, Chen X. Biogenesis, turnover, and mode of action of plant MicroRNAs. Plant Cell. 2013;25:2383-2399.
8. Zhang B and Wang Q. MicroRNA-based biotechnology for plant improvement. J Cell Physiol. 2015;230:1-15.
9. Xie W, et al. MicroRNAs as new bioactive components in medicinal plants. Planta Med. 2016;82:1153-1162.