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Commentary

Plant MicroRNA Precursors: A Bioinformatics Study of Structural Patterns

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DESCRIPTION

The RNA world theory proposes that RNAs store genetic material and stimulated chemical processes which plays a major role in the emergence of present living things. In recent years, scientists have examined this diversity of molecules, concentrating, for example, on tiny non-coding regulatory RNAs. Among them, a 19–24 microRNA molecule with a long evolutionary history is of particular interest (miRNA). miRNA is involved in the growth and development process as well as the response to stressful circumstances in plants. Primary transcripts (pre-miRNA), which are encoded in the nuclear genome, are the source of microRNAs. They develop from progenitors of single-stranded stem-loop RNA with hairpin structures. Computational approaches to biological problem-solving have shown potential in a number of fields. MicroRNAs are a group of small, non-coding, single-stranded RNAs with a length of 22 nt that play a role in the post-transcriptional control of gene expression. These compounds are widely distributed in both plant and animal genomes. MicroRNAs originate from primary transcripts (pre-miRNAs) encoded in the nuclear genome. They are processed from single-stranded stem-loop RNA precursors containing hairpin structures. RNA polymerase II performs the main miRNA (pre-miRNA) transcription process in the nucleus, where miRNA biogenesis begins. With both single- and double-stranded sections, the transcript forms a long hairpin loop shape Single mismatches (i.e., noncomplementary nucleotides), internal loops, and bulges can all be found throughout double-stranded regions. Animals' Drosha enzyme further processes pre-miRNA (ribonuclease III endonuclease). The RNA-binding protein and Drosha work together to cleave the miRNA primary transcript into its 70 nt long precursors, or pre-miRNA. This is the final phase of the nuclear stage in mammals. The newly formed stem-loop structure is transported to the cytoplasm, where another enzyme known as Dicer splits the pre-miRNA into a miRNA:miRNA duplex. As a molecular ruler, ribonuclease Dicer measures the distance between the 3′ or 5′ end and the cleavage point before making the cut that releases the miRNA:miRNA duplex. The miRNA maturation process differs differently in plants.

After the production of plant pre-miRNA, the nuclear cap-binding complex aids a complex made up of the Dicer Like 1 enzyme (DCL1), the double-stranded RNA-binding protein HYL1 (hyponastic leaves 1), and the zinc-finger protein SE (serrate) in cleaving pre-miRNA to pre-miRNA. At least two cleavages are carried out by DCL1 to liberate the miRNA:miRNA duplex from the precursor structure before it is delivered to the cytoplasm. In plants, there are two miRNA cleavage processes. The lower stem region receives the first cut in the base-to-loop cleavage process, whereas the higher (loop) region receives the second cut. DCL1 cuts in the opposite direction in the loop-to-base mechanism. The duplex is moved outside the nucleus after being cleaved.

A primary transcript maturation step led to the formation of this double-stranded miRNA:miRNA duplex. MiRNA is found on the complementary strand, which is made up of one strand. The primary protein of the RNA-induced silencing complex (RISC) and Argonaute (AGO), is then responsible for separating these two strands. After being separated from miRNA, miRNA is often destroyed. After producing mature single-stranded miRNA and embedding it in the complex (resulting in a mi-RISC complex), miRNA uses the complementary sequence to direct the complex to mRNA. Degradation of the target mRNA or blockage of the translation process is made possible by mi-RISC. Plant miRNA maturation still has some unresolved problems compared to the synthesis of miRNA in animals, which is better understood. A microprocessor complex made up of the proteins DCL1, HYL1, and SE recognises the miRNA:miRNA duplex in the miRNA precursor as one of them. The release of the miRNA:miRNA duplex (miRNA on one strand and complementary sequence of miRNA on the other strand) from the pre-miRNA molecule requires at least two cuts from this microprocessor complex. The significance of miRNA neighbouring areas where the DCL1 enzyme begins cleaving has already been made the experimental confirmed on the secondary structural level. Therefore, we assume that dysregulations in primary and secondary structures might serve as a cue for DCL1 to begin cleaving. Recent studies on miRNAs have suggested that the microprocessor complex proteins HYL1 and SE have a role in miRNA recognition. It also revealed how important mismatches are in the double-stranded parts of the miRNA:miRNA duplex. Mismatches can result in either longer or shorter molecules, which can affect the mature microRNA's length. It has been proven that miRNA genes can have introns and that these introns are directly related to the synthesis and correct operation of the host miRNAs. Nevertheless,

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despite having so much knowledge about plant miRNAs, we still do not understand how the microprocessor complex enzyme detects the miRNA:miRNA duplex within its precursor.