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Gene silencing by small RNAs in plants

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Abstracts

The phenomenon of gene silencing by small non-coding RNAs, i.e., small interfering RNA (siRNA) and microRNA (miRNA) has becoming as one of potential approaches for crop improvement. Gene silencing is generally defined as an epigenetic modification of gene expression leading to inactivation of previously active individual genes or larger chromosome regions. Gene silencing can also occur post transcriptionally due to mRNA degradation and/or repression of its translation. These effects are often mediated by small RNA regulators such as small interfering RNAS (siRNAs), microRNAs (miRNAs) which are generated from different forms of double-stranded RNA (ds RNA) accumulating in cells. Small RNAs, particularly siRNAs can also participate in silencing of genes at the level of transcription. Gene silencing (also known as RNA interference) is a sequence-specific gene inactivation system that down regulates RNA accumulation at the transcriptional or post-transcriptional levels. In eukaryotes, a wide range of biological processes are regulated through gene silencing.

Key words: -small RNAs, gene silencing. transcription.

Introduction

Gene silencing is generally defined as an epigenetic modification of gene expression leading to inactivation of previously active individual genes or larger chromosome regions. Gene silencing can also occur post transcriptionally due to mRNA degradation and/or repression of its translation. These effects are often mediated by small RNA regulators such as small interfering RNAS (siRNAs), microRNAs (miRNAs), or Piwi-associated RNAs (pi RNAs), which are generated from different forms of double-stranded RNA (ds RNA) accumulating in cells. Small RNAs, particularly siRNAs can also participate in silencing of genes at the level of transcription.

In plants, small RNAs are classified as microRNAs (miRNAs) or small interfering RNAs (siRNAs) based on their precursors and biogenesis. miRNAs derive from longer RNA precursors containing a stem-loop or hairpin structure with imperfect base-pairing in the stem region. In contrast, siRNAs derive from longer double-stranded RNAs (dsRNAs) that exhibit nearly perfect sequence complementarity. Typically, multiple siRNA species are generated from a single precursor. Despite the differences in precursors and biogenesis that distinguish the different classes of small RNAs, however, it is important to emphasize that all small RNAs function as sequence-specific guides in target regulation.

What is the difference between siRNA and miRNA?

- miRNA derived from specific genomic loci, while siRNA derived from mRNA, transposons, viruses or heterochromatic DNA.
- Synthesis of miRNA is processed from longer precursor hairpin transcripts (primary nuclear miRNA sequence by RNase III endonuclease), whereas that of siRNA processed from long bimolecular RNA duplexes.
- Each miRNA hairpin precursor molecule produces single miRNA duplex, whereas each siRNA precursor molecule produces multiple siRNA duplexes.
- siRNA sequences are rarely conserved, while miRNA sequences are well conserved.
- All bases within siRNA contribute to its target specificity, whereas only 5' half of miRNA contributes to its target specificity.
- miRNA often bind to the 3' untranslated region of target transcripts, whereas siRNAs form complementary duplex anywhere along a target mRNA.

Mechanism of gene silencing

The mechanism of RNAi, by small non-coding RNAs involves a RNA-induced silencing complex (The RNA silencing mechanism starts with the production of 20 to 26 nucleotide (nt) small RNA (sRNAs) through a series of key components, such as Dicer-like protein (DCL), Argonaute (AGO) protein, and RNA-dependent RNA polymerase (RDRs). The DCL proteins generate siRNAs from a dsRNA precursor and then incorporates into RISCs. On the basis of their origin and formation, these sRNAs are divided into siRNAs or microRNAs (miRNAs). AGO proteins perform the large part of RISCs, bind the sRNAs and interact with homologous RNAs, that affect DNA methylation, endonuclease activity, or translational repression of mRNAs. RDR enzymes are responsible for the synthesis of dsRNAs using single-stranded RNAs (ssRNAs) as the templates, which are then further processed by Dicer-like (DCLs) proteins and start a new round of RNA silencing

Gene silencing (also known as RNA interference) is a sequence-specific gene inactivation system that

down regulates RNA accumulation at the transcriptional or post-transcriptional levels. In eukaryotes, a wide range of biological processes are regulated through gene silencing including development, organ formation, and stress responses. Additionally, in plants, nematodes, and insects, gene silencing is an essential for antiviral immunity. Viruses are targeted by gene silencing. To promote infection, viruses of plants, nematodes, and insects encode suppressors of gene silencing. Suppression of gene silencing protects viruses and caused developmental defects perceived as symptoms in infected organisms and also in tomato parthenocarpic fruits developed due to gene silencing by using RNAi (De Jong et al., 2009).

Conclusion and Future prospects

Gene silencing is a down-regulation of gene expression. It as an epigenetic regulation of gene expression and widely used in agriculture and biotechnology. Besides all the types of gen silencing RNAi is most important post transcriptional gene silencing. RNAi is widely used gene silencing method than antisense RNA Technology. It as many advantageous compares to CRISPR and TALEN due to its highly cost-effective nature, ease of experimental setup, ease of experimental validation, high efficiency as a gene knockdown effect and it is useful approach in future therapeutic tool. Selection of appropriate gene targets is an important parameter in the potential success of gene silencing by these small RNAs. The potential for transcriptional and post transcriptional gene silencing is an exciting possibility of application of RNAi.

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