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Short Communication

The Importance of Human miRNA Repertoire in Understanding Human Health and Diseases

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DESCRIPTION

In the intricate landscape of human biology, microRNAs (miRNAs) have emerged as critical players in gene regulation. These small non-coding RNA molecules, typically 20-25 nucleotides in length, wield immense power to modulate gene expression, making them key regulators of various biological processes. In recent years, extensive research efforts have focused on unraveling the complexity of the human miRNA repertoire and understanding their roles in health and disease. This article provides an overview of miRNAs, their biogenesis, functions, and the importance of deciphering the vast and diverse human miRNA repertoire.

miRNA biogenesis

miRNAs are transcribed from specific genes into primary miRNA transcripts (pri-miRNAs) by RNA polymerase II or III. The pri-miRNAs undergo a series of processing steps mediated by the Drosha and Dicer enzymes, resulting in the generation of mature miRNAs. Following the cleavage of the pri-miRNA by Drosha in the nucleus, the resulting hairpin-shaped precursor miRNA (pre-miRNA) is exported to the cytoplasm, where Dicer cleaves it further to produce the mature miRNA duplex. One strand of the duplex, called the guide strand, is incorporated into the RNA-Induced Silencing Complex (RISC), while the other strand, known as the passenger strand, is typically degraded [1].

Regulatory functions of miRNAs

Once incorporated into the RISC, mature miRNAs exert their regulatory functions by base-pairing with target messenger RNA (mRNA) molecules [2]. This interaction can lead to mRNA degradation or translational repression, thereby controlling the expression of target genes. Due to their ability to target multiple mRNAs, miRNAs can influence various cellular processes, including cell proliferation, differentiation, apoptosis, and development.

The human miRNA repertoire

The human genome harbors thousands of miRNA genes, and the catalog of known miRNAs continues to expand. Early studies relied on experimental methods, such as cloning and sequencing, to identify miRNAs [3]. However, advances in high-throughput sequencing technologies and bioinformatics have facilitated the discovery of numerous novel miRNAs. The miRBase database serves as a comprehensive repository for miRNA sequences and annotation.

Diversity and regulation of miRNA expression

miRNA expression is highly dynamic and cell-specific, allowing for fine-tuned gene regulation. Multiple factors influence miRNA expression, including transcriptional regulation, epigenetic modifications, and post-transcriptional processing. Various diseases, such as cancer and neurological disorders, are associated with dysregulation of miRNA expression. Studying the diversity and regulation of miRNA expression is crucial to unravel their functional significance and potential as therapeutic targets.

Clinical implications and future perspectives

The emerging understanding of miRNA biology has opened up new avenues for diagnostics, prognostics, and therapeutics. miRNAs hold promise as biomarkers for disease detection, prognosis, and response to treatment. Additionally, manipulating miRNA expression using synthetic miRNA mimics or inhibitors shows potential for therapeutic interventions [4]. However, further research is needed to fully comprehend the complexity of the human miRNA repertoire and its relevance to human health and disease.

CONCLUSION

The study of human miRNA repertoire has unveiled the extraordinary complexity and regulatory potential of these small RNA molecules. They act as intricate orchestrators of gene expression, influencing diverse biological processes.

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Understanding the intricacies of the miRNA repertoire is key to deciphering human biology and advancing our knowledge of diseases. With ongoing advancements in genomic technologies and bioinformatics, researchers continue to explore the vast miRNA landscape, bringing us closer to unlocking the full potential of these small yet mighty regulators.

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