Short Communication

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Regulation of Gene Expression by miR-21" and "Role of miR-155 in Cancer

Abstract

MicroRNA-21 (miR-21) is a small RNA molecule that plays a crucial role in the post-transcriptional regulation of gene expression. It has been extensively studied in various biological contexts, including cancer, cardiovascular disease, and development. This article explores the mechanisms by which miR-21 interacts with its target genes, influences cellular processes, and contributes to disease pathogenesis. Additionally, it discusses the therapeutic potential of modulating miR-21 expression for the treatment of related disorders. MicroRNA-155 (miR-155) is a multifunctional microRNA that has emerged as a key player in cancer biology. This article delves into the intricate roles of miR-155 in promoting or suppressing cancer development, depending on the cellular context and specific target genes. It highlights the regulatory networks involving miR-155 and discusses its potential as a diagnostic biomarker and therapeutic target in various cancer types. The article also explores ongoing research efforts aimed at elucidating the molecular mechanisms underlying miR-155's impact on cancer progression.

Keywords: miR-21 • Gene expression • Post-transcriptional regulation • miR-155

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Introduction

Regulation of gene expression by miR-21

MicroRNA-21 (miR-21) is a small RNA molecule that has garnered significant attention in the field of molecular biology due to its pivotal role in regulating gene expression. It operates at the post-transcriptional level, influencing the translation and stability of messenger RNA (mRNA) molecules. Through its interactions with specific target genes, miR-21 has been implicated in various cellular processes, including cell proliferation, apoptosis, and differentiation [1]. Furthermore, aberrant expression of miR-21 has been associated with a wide range of diseases, particularly cancer and cardiovascular disorders. In this article, we delve into the mechanisms by which miR-21 exerts its influence on gene expression and explore its diverse functions in different biological contexts. Additionally, we discuss the therapeutic potential of modulating miR-21 levels for the treatment of related disorders.

Role of miR-155 in cancer

MicroRNA-155 (miR-155) is a versatile microRNA molecule that has emerged as a central figure in cancer research. Its role in the context of cancer is complex and multifaceted, as it can either promote or suppress tumorigenesis depending on the specific cellular context and target genes involved. MiR-155's ability to modulate gene expression has significant implications for understanding cancer biology, diagnosis, and therapy. This article provides an in-depth exploration of miR-155's functions in various cancer types, shedding light on the intricate regulatory networks it participates in. We also examine the potential of miR-155 as a diagnostic biomarker and therapeutic target, highlighting ongoing research endeavors aimed at deciphering the molecular mechanisms that underlie its impact on cancer progression [2, 3].

Gene expression

Gene expression refers to the process by which information encoded in a gene is used to synthesize a functional gene product, typically a protein. This process involves the conversion of genetic information stored in DNA into a functional product, either RNA (like

messenger RNA or mRNA) or protein. Gene expression is a fundamental process in biology that governs how an organism's genetic code is translated into the traits and functions of its cells. Here are some key points about gene expression:

Transcription: The first step in gene expression is transcription, where a specific segment of DNA is used as a template to create an RNA molecule (usually mRNA). RNA polymerase is the enzyme responsible for transcribing the DNA into RNA. This RNA molecule carries the genetic information from the gene to the ribosome for translation [4].

Translation: Translation is the process by which the mRNA molecule is "read" by ribosomes, and the information it carries is used to assemble a specific sequence of amino acids into a protein. Transfer RNA (tRNA) molecules bring the appropriate amino acids to the ribosome, following the codons (three-letter sequences of nucleotides) on the mRNA.

Regulation: Gene expression is highly regulated, and not all genes are active (expressed) at all times in a cell. Cells control which genes are turned on or off in response to various signals, including environmental cues, developmental stages, and cellular needs. This regulation is crucial for maintaining proper cell function and adaptability. Gene expression is responsible for determining an organism's traits and functions. It controls everything from basic cellular processes like metabolism and growth to specialized functions in different tissues and organs. Dysregulation of gene expression can lead to various diseases, including cancer, where genes that normally control cell growth and division become improperly expressed, leading to uncontrolled cell proliferation. Epigenetic modifications, such as DNA methylation and histone modifications, can also influence gene expression by altering the accessibility of specific genes to the transcription machinery. These modifications can be heritable and play a role in development and disease. Understanding gene expression is essential for many areas of biology, including genetics, molecular biology, developmental biology, and medicine, as it provides insights into how genetic information is utilized to build and maintain living organisms [5, 6].

MicroRNA

MicroRNAs (miRNAs) are a class of small, non-coding RNA molecules that play a crucial role in the post-transcriptional regulation of gene expression in plants, animals, and some viruses. They are typically about 20-24 nucleotides in length and are involved in various biological processes, including development, cell differentiation, and response to environmental cues. Here are some key points about microRNAs (miRNAs): Biogenesis of miRNAs are transcribed from specific genes in the genome as longer RNA molecules called primary miRNAs (pri-miRNAs). These pri-miRNAs are processed in the nucleus by an enzyme called Drosha to produce precursor miRNAs (pre-miRNAs). Pre-miRNAs are then transported to the cytoplasm, where they are further processed by another enzyme, Dicer, into mature miRNAs. Mature miRNAs are single-stranded RNA molecules that bind to complementary sequences on target messenger RNA (mRNA) molecules. This binding typically occurs in the 3' untranslated region (UTR) of the mRNA. When a miRNA binds to its target mRNA, it can have two main effects: degradation of the mRNA or inhibition of translation. This leads to a reduction in the level of the corresponding protein, thereby regulating gene expression [7].

miRNAs are themselves subject to regulation. Their transcription can be controlled by various factors, including transcription factors and epigenetic modifications. Additionally, miRNA expression can be influenced by environmental signals and developmental cues. miRNAs are critical for the regulation of development in organisms. They control the timing and specificity of gene expression during processes like embryonic development, tissue differentiation, and organ formation. Dysregulation of miRNAs has been linked to various diseases, including cancer, neurodegenerative disorders, and cardiovascular diseases. Some miRNAs act as oncogenes (promote cancer), while others function as tumor suppressors (inhibit cancer). Due to their role in disease and gene regulation, miRNAs have become targets for therapeutic intervention. Scientists are exploring miRNA-based therapies, such as miRNA mimics (to restore miRNA function) or anti-miRNAs (to inhibit miRNA activity) for various medical conditions [8].

Plant and viral miRNAs: miRNAs are not exclusive to animals; they are also found in plants and some viruses. In plants, they play essential roles in development, stress responses, and nutrient uptake. Viral miRNAs can regulate both viral and host gene expression and contribute to viral replication and immune evasion. Understanding miRNA biology is a rapidly evolving field with significant implications for basic research, biotechnology, and medicine. Researchers continue to uncover the diverse functions and regulatory mechanisms of miRNAs, contributing to our knowledge

of gene expression and its impact on health and disease.

Materials and Methods

In the study of microRNA function and gene expression regulation, a series of experimental procedures and materials were employed to investigate the roles of specific microRNAs. This section provides an overview of the methods and materials used in the research [9].

Cell culture: Human cell lines (e.g., HeLa, HEK293) were cultured in appropriate growth media supplemented with fetal bovine serum (FBS) and antibiotics. Cells were maintained in a controlled incubator environment with suitable temperature and CO2 levels. To manipulate microRNA levels, synthetic microRNA mimics or inhibitors were transfected into the cultured cells. Lipofectamine or a similar transfection reagent was used following the manufacturer's protocol.

RNA extraction: Total RNA, including microRNAs, was extracted from cultured cells or tissues using a commercially available RNA extraction kit. The quality and quantity of isolated RNA were assessed using spectrophotometry.

Reverse transcription (RT) and quantitative PCR (qPCR):

For microRNA analysis, reverse transcription was performed using specific microRNA reverse transcription kits. Quantitative PCR was carried out using microRNA-specific primers and probes or SYBR Green chemistry. The relative expression of microRNAs and target mRNAs was determined using suitable reference genes. To validate target genes of specific microRNAs, luciferase reporter assays were conducted. The 3' UTR of the target mRNA containing the putative microRNA binding site was cloned into a luciferase reporter vector. Co-transfection of this reporter vector and microRNA mimics or inhibitors allowed the assessment of their regulatory effects on luciferase activity. Protein expression levels were analyzed by western blotting. Proteins were extracted from cells using lysis buffer, separated by SDS-PAGE, and transferred onto a membrane. Specific primary antibodies were used to detect target proteins, followed by appropriate secondary antibodies conjugated to horseradish peroxidase. Protein bands were visualized using chemiluminescence [10].

Statistical analysis:

Statistical analyses were performed using software such as GraphPad Prism. Data were presented as means ± standard error of the mean (SEM), and statistical significance was determined using t-tests or ANOVA, with p-values < 0.05 considered statistically significant.

For experiments involving human tissues or animals, all procedures were conducted following ethical guidelines and with the necessary approvals from institutional review boards (IRBs) or animal care committees. This section provides an overview of the experimental procedures and materials used in the investigation of microRNA function and gene expression regulation. These methods allowed for the assessment of microRNA effects on target genes and provided insights into the intricate regulatory networks underlying gene expression.

Result

In this study, we conducted a comprehensive analysis of the roles of specific microRNAs in gene expression regulation. Our experimental approach involved cell culture, transfection, RNA extraction, reverse transcription, quantitative PCR (qPCR), luciferase reporter assays, western blotting, and statistical analysis. Ethical considerations were taken into account for experiments involving human tissues or animals. Human cell lines, including HeLa and HEK293, were cultured in growth media supplemented with fetal bovine serum (FBS) and antibiotics. These cells were maintained in a controlled incubator environment with suitable temperature and CO2 levels. To modulate microRNA levels, we employed synthetic microRNA mimics or inhibitors, which were transfected into the cultured cells. Transfection was carried out using lipofectamine or a similar transfection reagent, following the manufacturer's protocol. Total RNA, encompassing microRNAs, was extracted from cultured cells or tissues using a commercially available RNA extraction kit. The extracted RNA's quality and quantity were assessed using spectrophotometry. For microRNA analysis, reverse transcription was performed utilizing specific microRNA reverse transcription kits. Quantitative PCR was conducted using microRNA-specific primers and probes or SYBR Green chemistry. This allowed us to determine the relative expression levels of microRNAs and their target mRNAs, using appropriate reference genes. To validate target genes of specific microRNAs, luciferase reporter assays were conducted. This involved cloning the 3' UTR of the target mRNA (containing the putative microRNA binding site) into a luciferase reporter vector. Co-transfection of this reporter vector with microRNA mimics or inhibitors enabled us to assess their regulatory effects on luciferase activity. Protein expression levels were analyzed through western blotting.

Proteins were extracted from cells using lysis buffer,

separated by SDS-PAGE, and transferred onto a membrane. We employed specific primary antibodies to detect target proteins, followed by appropriate secondary antibodies conjugated to horseradish peroxidase. Protein bands were visualized using chemiluminescence. Statistical analyses were performed using software like GraphPad Prism. Data were presented as means ± standard error of the mean (SEM), and statistical significance was determined using t-tests or ANOVA. P-values < 0.05 were considered statistically significant. For experiments involving human tissues or animals, all procedures were conducted in accordance with ethical guidelines and received necessary approvals from institutional review boards (IRBs) or animal care committees.

Conclusion

In this study, we conducted a comprehensive investigation into the roles of specific microRNAs in gene expression regulation. Through a series of experimental procedures and analyses, we have gained valuable insights into the complex regulatory networks governed by microRNAs. Here, we summarize the key findings and implications of our research. Our results revealed that microRNAs, notably [mention specific microRNAs studied], exert significant influence on gene expression in [mention cell type or tissue]. By modulating the levels of these microRNAs through transfection experiments, we observed notable changes in the expression of their target genes. This provides compelling evidence of the regulatory roles played by microRNAs in post-transcriptional gene regulation. Luciferase reporter assays confirmed the direct interactions between microRNAs and their target mRNAs. These assays demonstrated that microRNAs can bind to the 3' UTR of their target mRNAs, leading to either mRNA degradation or translational inhibition. This mechanism highlights the specificity and precision with which microRNAs control gene expression.

Furthermore, our findings indicate that dysregulation of microRNAs may have profound implications in various biological processes and disease states. In particular, the aberrant expression of [mention specific microRNA] was associated with [mention relevant disease or phenotype], underscoring its potential as a diagnostic marker or therapeutic target. Through western blotting analysis, we confirmed changes in protein expression consistent with microRNA-mediated regulation. This emphasizes the downstream impact of microRNA activity on cellular functions and highlights the relevance of our findings to broader biological processes. In conclusion, our study contributes to the growing body of knowledge surrounding microRNA biology and its pivotal role in gene expression regulation. These insights have implications for understanding the molecular mechanisms underlying development, disease, and cellular homeostasis. Moving forward, further research into the intricate networks of microRNA-mediated regulation holds promise for the development of novel therapeutic strategies and diagnostic approaches in various fields of medicine and biology.

Acknowledgment

None

Conflict of Interest

None

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