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Non-Coding RNAs: Gene Regulators in Health and Disease

Tomasz Kowalczyk*

Department of Genomics and DNA Analysis, Baltic Science University, Gdańsk, Poland

Introduction

Non-coding RNAs (ncRNAs) are now understood to be crucial regulators of gene expression, far beyond their initial dismissal as mere transcriptional byproducts. This review delves into the multifaceted ways ncRNAs, including microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs), modulate gene activity at transcriptional, post-transcriptional, and epigenetic levels. Their pervasive roles in fundamental cellular processes such as development and differentiation, as well as their involvement in disease pathogenesis, are highlighted, underscoring their significance as potential diagnostic biomarkers and therapeutic targets. [1]

MicroRNAs (miRNAs) represent a well-characterized class of ncRNAs that predominantly exert their regulatory functions by binding to the 3' untranslated regions (3'-UTRs) of target messenger RNAs (mRNAs). This interaction typically leads to either translational repression or mRNA degradation, thereby fine-tuning protein output. This review explores the complex regulatory networks orchestrated by miRNAs across diverse cellular contexts and their critical implications in diseases such as cancer and cardiovascular disorders. [2]

Long non-coding RNAs (lncRNAs) constitute a vast and heterogeneous collection of transcripts exceeding 200 nucleotides in length. These molecules execute their regulatory roles through a variety of mechanisms, including acting as scaffolds, decoys, and guides for chromatin-modifying complexes. This paper provides a comprehensive discussion of the emerging roles of lncRNAs in epigenetic regulation, the maintenance of gene imprinting, and the preservation of genome stability. [3]

Circular RNAs (circRNAs) are a distinct class of covalently closed RNA molecules formed through a process known as back-splicing. Unlike their linear counterparts, circRNAs generally exhibit enhanced stability and can function as microRNA sponges, decoys for RNA-binding proteins, or even encode small peptides. This article offers a thorough review of circRNA biogenesis, their diverse functions, and their involvement in various biological processes and disease states. [4]

The intricate interplay between ncRNAs and the epigenome is a rapidly advancing field of scientific inquiry. This study specifically investigates how lncRNAs facilitate the recruitment of epigenetic modifiers, such as Polycomb repressive complexes and histone deacetylases, to particular genomic loci. This recruitment process profoundly influences chromatin structure, leading to either gene silencing or activation. [5]

The potential for ncRNAs in cancer diagnosis and therapy is substantial. This review critically examines how the dysregulated expression of miRNAs, lncRNAs, and circRNAs contributes to the initiation of tumors, their spread (metastasis), and resistance to therapeutic agents. Furthermore, it discusses their utility as biomarkers for cancer detection and as targets for the development of novel treatment strategies. [6]

Post-transcriptional regulation mediated by ncRNAs, particularly miRNAs, is a highly refined cellular process. This study meticulously investigates the molecular mechanisms by which miRNAs interact with their target mRNAs, resulting in either translational inhibition or mRNA destabilization. It further explores the downstream consequences of these interactions on the cellular levels of specific proteins. [7]

Long non-coding RNAs are increasingly recognized for their diverse and complex roles in cellular processes that extend beyond simple gene silencing. This research highlights the capacity of lncRNAs to serve as scaffolds, bringing together proteins and nucleic acids to facilitate the assembly of functional molecular complexes. These complexes are essential for intricate processes like gene regulation and signal transduction. [8]

The impact of ncRNAs on development and differentiation is profound and far-reaching. This review elucidates how specific miRNAs and lncRNAs orchestrate the complex gene expression programs that are fundamental to cell fate decisions, the proper development of tissues, and the critical maintenance of stem cell pluripotency. [9]

Circular RNAs are emerging as key regulators of gene expression through a variety of sophisticated mechanisms, including their function as microRNA sponges and their ability to bind to RNA-binding proteins. This paper delves into the regulatory landscape influenced by circRNAs and explores their integral involvement in numerous cellular functions and disease contexts, emphasizing their promise as therapeutic targets. [10]

Description

Non-coding RNAs (ncRNAs) have transcended their former perception as mere transcriptional noise, now recognized as central players in gene regulation across various biological levels. Their diverse mechanisms of action, encompassing transcriptional, post-transcriptional, and epigenetic modulation, involve critical classes such as microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs). These molecules are integral to fundamental cellular activities like development and differentiation, and their dysregulation is implicated in disease pathogenesis, marking them as significant diagnostic and therapeutic targets. [1]

MicroRNAs (miRNAs) are among the most extensively studied ncRNAs, primarily functioning through complementary base pairing with the 3' untranslated regions

(3'-UTRs) of target messenger RNAs (mRNAs). This interaction leads to either the inhibition of translation or the degradation of the mRNA molecule, effectively controlling protein synthesis. This review examines the intricate regulatory networks established by miRNAs in various cellular settings and their substantial contributions to diseases, including cancer and cardiovascular disorders. [2]

Long non-coding RNAs (lncRNAs), defined as transcripts longer than 200 nucleotides, represent a vast and functionally diverse group of molecules. They mediate their regulatory effects through a multitude of strategies, such as acting as scaffolds to bring proteins together, serving as decoys for regulatory factors, or guiding chromatin-modifying complexes to specific genomic locations. This paper discusses the evolving understanding of lncRNAs' roles in epigenetic regulation, gene imprinting, and the maintenance of genomic integrity. [3]

Circular RNAs (circRNAs) are characterized by their unique covalently closed structure, formed via back-splicing events. This structural feature confers greater stability compared to linear RNAs. CircRNAs can act as potent microRNA sponges, sequestering these small regulatory RNAs, or bind to RNA-binding proteins, influencing their availability. They also possess the capacity to encode small peptides. This article provides an overview of circRNA biogenesis, their multifaceted functions, and their involvement in diverse biological processes and pathological conditions. [4]

The intricate relationship between ncRNAs and the epigenome is a dynamic area of active research. This study delves into the mechanisms by which lncRNAs orchestrate epigenetic modifications, notably by recruiting key epigenetic effector complexes like Polycomb repressive complexes and histone deacetylases. This recruitment directly impacts chromatin architecture, leading to precise control over gene expression, including silencing and activation. [5]

The therapeutic and diagnostic potential of ncRNAs, particularly within the context of cancer, is immense and continues to be explored. This review investigates how the aberrant expression of miRNAs, lncRNAs, and circRNAs contributes to the development of cancer, its progression, and the emergence of drug resistance. It further elaborates on their utility as reliable cancer biomarkers and promising targets for the development of innovative therapeutic interventions. [6]

Post-transcriptional gene regulation by ncRNAs, with a particular focus on miRNAs, is a finely tuned and complex process critical for cellular homeostasis. This study provides detailed insights into the molecular mechanisms governing miRNA-mRNA interactions, leading to either translational repression or mRNA destabilization. It further explores the downstream effects of these regulatory events on cellular protein abundance and function. [7]

Long non-coding RNAs are increasingly appreciated for their multifaceted contributions to cellular functions, extending beyond their roles in gene silencing. This research highlights their important function as molecular scaffolds, facilitating the assembly of protein and nucleic acid complexes. These complexes are essential for regulating gene expression and mediating signal transduction pathways, showcasing the dynamic nature of lncRNA action. [8]

The profound influence of ncRNAs on developmental processes and cellular differentiation is undeniable. This review outlines the critical roles that specific miRNAs and lncRNAs play in orchestrating the complex gene expression programs essential for determining cell fate, guiding tissue morphogenesis, and maintaining the pluripotency of stem cells throughout development. [9]

Circular RNAs are rapidly emerging as significant regulators of gene expression through a variety of sophisticated mechanisms. These include their well-established roles as microRNA sponges and their interactions with RNA-binding proteins. This paper systematically explores the regulatory landscape governed by circRNAs and their critical involvement in diverse cellular functions and disease states, emphasizing their considerable potential as therapeutic targets. [10]

Conclusion

Non-coding RNAs (ncRNAs), including microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs), are critical regulators of gene expression at multiple levels. They influence transcriptional, post-transcriptional, and epigenetic processes, playing vital roles in cellular functions such as development and differentiation. Dysregulation of these ncRNAs is implicated in various diseases, particularly cancer, highlighting their potential as diagnostic biomarkers and therapeutic targets. miRNAs primarily act by targeting mRNA 3'-UTRs for translational repression or degradation. lncRNAs exhibit diverse functions, acting as scaffolds, decoys, or guides for chromatin modifiers, impacting epigenetic regulation. circRNAs, characterized by their stability, can function as miRNA sponges or interact with RNA-binding proteins. Research continues to uncover the complex regulatory networks and therapeutic applications of these versatile RNA molecules.

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Conflict of Interest

None.

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Address for Correspondence: Tomasz, Kowalczyk, Department of Genomics and DNA Analysis, Baltic Science University, Gdańsk, Poland, E-mail: t.kowalczyk@bsu.pl

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