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Non-Coding RNAs as Emerging Biomarkers for Cardiometabolic Diseases: A New Frontier in Diagnostics

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Introduction

Non-coding RNAs (ncRNAs), which are RNA molecules that do not translate into proteins, have emerged as critical regulators in various biological processes, including gene expression, cellular development, and metabolism. Recent advancements have highlighted the significant role of ncRNAs in the pathophysiology of Cardiometabolic Diseases (CMD), including cardiovascular diseases, diabetes, and obesity. These diseases are a leading cause of morbidity and mortality globally, and their prevalence continues to rise with changing lifestyles and environmental factors. ncRNAs, particularly MicroRNAs (miRNAs), Long Non-Coding RNAs (lncRNAs), and Circular RNAs (circRNAs), have been shown to influence crucial biological pathways involved in inflammation, lipid metabolism, glucose homeostasis, and vascular function. Their ability to regulate gene expression and signaling pathways makes them potential biomarkers for early diagnosis, prognosis, and therapeutic intervention in CMD. Numerous studies have reported altered ncRNA profiles in individuals with CMD, offering new insights into disease mechanisms and highlighting their diagnostic and therapeutic potential [1].

The potential of ncRNAs as biomarkers for CMD has attracted significant attention due to their tissue-specific expression, stability in body fluids, and correlation with disease stages. These molecules can be detected in easily accessible samples such as blood, urine, and saliva, making them attractive candidates for non-invasive diagnostic approaches. ncRNAs are capable of providing crucial information about disease progression, therapeutic responses, and individualized treatment regimens, positioning them as valuable tools in personalized medicine. Studies have demonstrated that miRNAs, in particular, are involved in the regulation of key genes associated with inflammation, lipid metabolism, and glucose control, which are central to CMD. Furthermore, ncRNAs such as lncRNAs and circRNAs have been identified as important regulators of cardiovascular function, adipogenesis, and insulin resistance. Their involvement in the intricate molecular networks underlying CMD offers new avenues for therapeutic intervention and the development of innovative diagnostic platforms [2].

Description

In recent years, research on ncRNAs has revealed their potential as both diagnostic biomarkers and therapeutic targets in CMD. MicroRNAs, a class of small ncRNAs, have garnered attention for their ability to regulate genes involved in critical processes such as endothelial dysfunction, atherosclerosis, and insulin resistance. Numerous studies have demonstrated that circulating miRNAs are altered in individuals with CMD, providing a snapshot of the molecular changes occurring within the body. For instance, miR-1, miR-133, and miR-155 have been shown to play pivotal roles in regulating cardiovascular function and inflammation, making them potential diagnostic markers for cardiovascular diseases. Furthermore, miRNAs such as miR-33 and miR-142 are involved in lipid metabolism and obesity, which are closely linked to the development of diabetes and atherosclerosis. The ability to detect these miRNAs in blood samples offers a promising approach to the early detection of CMD and monitoring of disease progression [3].

Long Non-Coding RNAs (lncRNAs), another class of ncRNAs, have also emerged as critical regulators in CMD. LncRNAs are involved in various cellular processes, including gene expression modulation, chromatin remodeling, and cellular signaling. Their dysregulation has been associated with the development and progression of cardiovascular diseases, diabetes, and obesity. For example, the lncRNA MALAT1 has been implicated in vascular remodeling and atherosclerosis, while lncRNA H19 plays a role in adipogenesis and insulin resistance. The expression levels of specific lncRNAs in plasma or serum samples have been shown to correlate with disease severity, offering potential for their use in disease prognosis and therapeutic monitoring. Additionally, lncRNAs such as HOTAIR and ANRIL have been associated with the regulation of inflammation and fibrosis, which are key processes in the pathogenesis of CMD. Therefore, lncRNAs may offer a new dimension to the molecular understanding and diagnosis of CMD [4].

Circular RNAs (circRNAs) are another emerging class of ncRNAs that have recently gained attention for their potential role in CMD. Unlike linear RNAs, circRNAs form a covalently closed loop structure, making them highly stable and resistant to degradation. This stability, combined with their tissue-specific expression, makes circRNAs promising candidates for use as biomarkers in the diagnosis and monitoring of CMD. Recent studies have identified several circRNAs that are differentially expressed in CMD, including circRNA-ITCH and circRNA-SIRT1. These circRNAs are involved in regulating key processes such as inflammation, vascular remodeling, and insulin resistance. Given their high stability and tissue specificity, circRNAs can serve as valuable biomarkers for early disease detection and therapeutic response monitoring. Further research is needed to understand the precise molecular mechanisms through which circRNAs influence CMD, and to explore their potential as therapeutic targets [5].

Conclusion

The role of ncRNAs as emerging biomarkers for cardiometabolic diseases represents a promising frontier in diagnostic medicine. These molecules, including miRNAs, lncRNAs, and circRNAs, are critical regulators of the molecular networks underlying the pathophysiology of CMD. Their expression profiles offer insights into disease progression, therapeutic responses, and personalized treatment approaches. Non-invasive detection of ncRNAs in body fluids such as blood, urine, and saliva holds significant promise for early disease detection and monitoring, offering a less invasive alternative to traditional diagnostic methods. While research in this area is still in its early stages, the growing body of evidence supports the potential of ncRNAs as diagnostic biomarkers for CMD. Future studies focusing on large-scale clinical trials, along with the development of robust technologies for ncRNA detection, will be essential for translating these findings into clinical practice. Moreover, the identification of novel ncRNAs and their molecular pathways could open up new therapeutic avenues for the treatment of CMD. As the field progresses, ncRNAs may play a key role in reshaping the landscape of cardiovascular and metabolic disease diagnostics and therapies.

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