

Circulating MicroRNAs as Non-Invasive Disease Biomarkers

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ABOVE THE STUDY

Circulating microRNAs (miRNAs) have emerged as one of the most promising classes of non-invasive disease biomarkers in modern molecular medicine. In my opinion, their discovery represents a major shift in diagnostic thinking, moving away from tissue-dependent assessments toward dynamic, minimally invasive molecular profiling. These small, non-coding RNA molecules, typically 18-25 nucleotides in length, regulate gene expression post-transcriptionally and are now recognized not only as intracellular regulators but also as stable, measurable entities in body fluids such as blood, saliva, urine, and cerebrospinal fluid.

One of the most compelling features of circulating miRNAs is their remarkable stability in extracellular environments. Despite the presence of ribonucleases in biological fluids, miRNAs remain intact due to their encapsulation within exosomes, microvesicles, or protein complexes such as Argonaute2. This stability makes them ideal candidates for clinical biomarker development, as they can be reliably detected even in small sample volumes and under varying storage conditions. In my view, this robustness distinguishes miRNAs from many traditional RNA-based biomarkers, which are often unstable and technically challenging to measure.

Circulating miRNAs reflect physiological and pathological states of tissues throughout the body. In cancer, for example, tumor-derived miRNAs can be released into the bloodstream and serve as indicators of oncogenic activity. Specific miRNA signatures have been associated with breast, lung, colorectal, and prostate cancers, often correlating with tumor stage, aggressiveness, and metastatic potential. Importantly, these signatures may appear early in disease progression, making them valuable for early detection when therapeutic interventions are most effective.

Beyond oncology, circulating miRNAs have shown strong potential in cardiovascular diseases. Altered levels of miRNAs such as miR-1, miR-133, and miR-208 are associated with myocardial injury and cardiac remodeling. Similarly, in neurodegenerative disorders, miRNA profiles in cerebrospinal fluid and plasma may reflect neuronal damage and synaptic

dysfunction. In metabolic diseases such as diabetes and obesity, circulating miRNAs are linked to insulin signaling pathways and inflammatory responses, highlighting their role as systemic regulators rather than disease-specific markers alone.

A key advantage of miRNA-based diagnostics is their ability to provide multi-dimensional biological information. Unlike single-protein biomarkers, each miRNA can regulate multiple target genes, and each disease state is associated with complex miRNA networks. This network-based behavior allows circulating miRNAs to capture broader pathophysiological changes rather than isolated molecular events. In my opinion, this systems-level property is what makes them particularly powerful for precision medicine applications.

Technological advances in detection methods have significantly accelerated miRNA biomarker research. Quantitative real-time microarrays, and next-generation sequencing are commonly used platforms for profiling circulating miRNAs. More recently, digital PCR and nanoparticle-based biosensors have improved sensitivity and quantification accuracy. However, standardization remains a major challenge. Variability in sample processing, normalization strategies, and data interpretation often leads to inconsistent results across studies.

Another important consideration is biological complexity. Circulating miRNA levels can be influenced by multiple factors, including age, sex, lifestyle, comorbidities, and even circadian rhythms. This variability complicates the establishment of universal reference ranges. Moreover, distinguishing tissue-specific miRNA signals from background noise in circulation remains a technical hurdle. In my view, integrating miRNA profiles with other omics data such as proteomics and metabolomics may help overcome these limitations and improve diagnostic precision.

From a clinical perspective, circulating miRNAs hold promise not only for diagnosis but also for prognosis and treatment monitoring. Changes in miRNA expression over time can reflect disease progression or therapeutic response, offering a dynamic tool for patient management. For example, declining levels of

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Received: 15-May-2025, Manuscript No. JMPB-25-41753; **Editor assigned:** 19-May-2025, PreQC No. JMPB-25-41753 (PQ); **Reviewed:** 02-Jun-2025, QC No. JMPB-25-41753; **Revised:** 09-Jun-2025, Manuscript No. JMPB-25-41753 (R); **Published:** 16-Jun-2025. DOI: 10.35248/jmpb.25.6.215.

Citation: Yusuf A (2025). Circulating MicroRNAs as Non-Invasive Disease Biomarkers. *J Mol Pathol Biochem*.6:215.

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oncogenic miRNAs after treatment may indicate tumor regression, while persistent elevation could signal recurrence.

Despite their promise, several barriers must be addressed before widespread clinical adoption. These include assay standardization, validation in large cohorts, and development of cost-effective, high-throughput platforms. Additionally, regulatory frameworks for miRNA-based diagnostics are still evolving, requiring clear guidelines for clinical implementation.

In conclusion, circulating microRNAs represent a powerful and versatile class of non-invasive biomarkers with broad applications across multiple disease domains. In my opinion, their integration into clinical practice has the potential to transform early diagnosis, disease monitoring, and personalized treatment strategies. However, realizing this potential will require continued technological refinement, rigorous validation, and a deeper understanding of their biological complexity within human disease systems.