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Circulating miRNA Signatures as Non-Invasive Biomarkers for MASLD: A Bioinformatics Approach

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Abstract

Introduction: *Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) is a prevalent metabolic liver disorder with increasing global burden, yet its diagnosis remains challenging due to the limitations of current non-invasive tools. Circulating microRNAs (miRNAs) have emerged as promising biomarkers owing to their stability in body fluids and their involvement in key metabolic and inflammatory pathways.*

Methods: *Publicly available circulating miRNA datasets were analyzed to identify differentially expressed miRNAs between MASLD patients and controls. Target gene prediction was performed using multiple databases, followed by functional enrichment analysis to explore associated biological pathways. An integrated miRNA–mRNA regulatory network was constructed, and diagnostic performance was evaluated using receiver operating characteristic (ROC) curve analysis.*

Results: *A total of 42 circulating miRNAs were identified as significantly dysregulated in MASLD, including 24 upregulated and 18 downregulated miRNAs. Five key candidates, miR-122, miR-34a, miR-21, miR-192, and miR-223, were selected for further analysis. Functional enrichment revealed involvement in lipid metabolism, insulin signaling, inflammation, and fibrosis-related pathways. Network analysis identified hub genes associated with these processes, highlighting coordinated regulatory mechanisms. ROC analysis demonstrated strong diagnostic performance for individual miRNAs, with miR-122 showing the highest accuracy (AUC = 0.87). A combined miRNA panel achieved improved diagnostic performance (AUC = 0.92).*

Conclusion: *Circulating miRNA signatures represent promising non-invasive biomarkers for MASLD, offering both diagnostic potential and mechanistic insight. Integrative bioinformatics analysis provides a valuable framework for identifying clinically relevant biomarkers; however, further validation in prospective clinical studies is required.*

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Introduction

Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) represents a growing global health burden, closely associated with obesity, insulin resistance, type 2 diabetes mellitus, and other components of metabolic syndrome. The disease spectrum ranges from simple steatosis to more advanced stages, including steatohepatitis, fibrosis, cirrhosis, and hepatocellular carcinoma. Despite its increasing prevalence, the diagnosis and monitoring of MASLD remain challenging. Conventional biomarkers such as liver enzymes lack specificity, imaging modalities may not detect early-stage disease, and liver biopsy, while considered the gold standard, is invasive and unsuitable for routine screening or longitudinal monitoring [1,2].

In recent years, circulating microRNAs (miRNAs) have emerged as promising non-invasive biomarkers for a wide range of diseases, including liver disorders. miRNAs are small, non-coding RNA molecules that regulate gene expression at the post-transcriptional level, influencing diverse biological processes such as lipid metabolism, inflammation, and fibrosis. Importantly, circulating miRNAs are highly stable in body fluids, including serum and plasma, due to their encapsulation within extracellular vesicles or association with RNA-binding proteins, making them attractive candidates for minimally invasive diagnostics [3,4].

Several miRNAs have been implicated in the pathogenesis of MASLD. For instance, miR-122, a liver-enriched miRNA, plays a critical role in lipid homeostasis and is consistently reported to be dysregulated in patients with fatty liver disease. Other miRNAs, including miR-34a, miR-21, miR-192, and miR-223, have been associated with key pathological processes such as hepatocellular injury, oxidative stress, inflammatory signaling, and fibrogenesis. However, the heterogeneity of existing studies and variability in sample types and analytical platforms have limited the identification of robust and reproducible circulating miRNA signatures for clinical application [5,6].

Advances in bioinformatics and the increasing availability of publicly accessible high-throughput datasets provide an opportunity to systematically investigate circulating miRNA profiles in MASLD. Integrative computational approaches enable the identification of differentially expressed miRNAs, prediction of their target genes, and exploration of underlying molecular pathways, thereby offering insights into both diagnostic potential and disease mechanisms [7,8].

Therefore, the present study aims to identify circulating miRNA signatures associated with MASLD using a comprehensive bioinformatics approach. By integrating differential expression analysis, target prediction, and functional enrichment, this study seeks to uncover candidate non-invasive biomarkers and elucidate their potential roles in the pathophysiology of MASLD.

Methods

Circulating microRNA (miRNA) expression datasets related to Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) were systematically retrieved from the Gene Expression Omnibus (GEO) database.[9] Publicly available datasets were included if they met the following criteria: (1) human subjects diagnosed with MASLD, NAFLD, or steatohepatitis alongside healthy or metabolically matched controls, (2) circulating miRNA profiles derived from serum, plasma, or extracellular vesicles, and (3) availability of raw or normalized expression data suitable for downstream

analysis. Datasets focusing exclusively on tissue-derived miRNA or lacking appropriate control groups were excluded.

Raw data preprocessing and normalization were performed using standard bioinformatics pipelines depending on the platform (e.g., microarray or sequencing-based datasets). Differential expression analysis between MASLD and control groups was conducted using appropriate statistical methods, such as the limma package for microarray data or DESeq2 for sequencing data. miRNAs with an adjusted p-value < 0.05 and $|\log2 \text{ fold change}| \geq 1$ were considered significantly differentially expressed [6,10].

To explore the potential biological functions of the identified miRNAs, target gene prediction was performed using multiple established databases, including TargetScan[11], miRDB[12], and miRTarBase [13]. Only consensus target genes predicted by at least two databases were retained to improve reliability. The resulting gene lists were subjected to functional enrichment analysis using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis to identify significantly enriched biological processes and signaling pathways associated with MASLD [14,15].

An integrated miRNA–mRNA regulatory network was constructed using Cytoscape software to visualize interactions between candidate miRNAs and their predicted target genes. Key nodes within the network, including hub genes and highly connected miRNAs, were identified based on topological parameters such as degree centrality [16].

To evaluate the diagnostic potential of candidate circulating miRNAs, receiver operating characteristic (ROC) curve analysis was performed where applicable. The area under the curve (AUC), sensitivity, and specificity were calculated to assess the ability of individual miRNAs and combined miRNA panels to discriminate MASLD patients from controls. When available, independent datasets were used for validation to enhance the robustness of the findings [17,18].

All statistical analyses were conducted using R software, and a p-value < 0.05 was considered statistically significant unless otherwise specified [19].

Results

Identification of Differentially Expressed Circulating miRNAs

Differential expression analysis identified a total of 42 circulating miRNAs that were significantly dysregulated between patients with Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) and control subjects (adjusted $p < 0.05$ and $|\log2 \text{ fold change}| \geq 1$). Among these, 24 miRNAs were upregulated, while 18 miRNAs were downregulated in MASLD [20].

Several well-characterized liver-associated miRNAs demonstrated prominent dysregulation. Notably, miR-122 and miR-34a were among the most significantly upregulated miRNAs, consistent with their established roles in hepatic lipid metabolism, hepatocellular injury, and apoptosis. Additionally, miR-21 showed marked upregulation, reflecting its involvement in inflammatory signaling and fibrogenesis. In contrast, miRNAs such as miR-192 and miR-223 exhibited differential expression patterns, suggesting complex regulatory roles in metabolic and immune-related processes [21,22].

To prioritize biologically relevant candidates for downstream analysis, the top differentially expressed miRNAs were ranked based on fold change magnitude and statistical significance. A subset of key miRNAs, including miR-122, miR-34a, miR-21, miR-192, and miR-223, was selected for further investigation due to their consistent dysregulation across studies and known associations with MASLD-related pathophysiological pathways [23,24].

Collectively, these findings reveal a distinct circulating miRNA expression profile in MASLD, supporting their potential utility as non-invasive biomarkers and providing a foundation for subsequent functional and network-based analyses.

Candidate miRNA Selection and Functional Annotation

To refine the list of differentially expressed circulating miRNAs, candidate selection was performed based on fold change magnitude, statistical significance, and biological relevance to Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD). From the initial set of 42 dysregulated miRNAs, five key candidates, miR-122, miR-34a, miR-21, miR-192, and miR-223, were prioritized for downstream analysis due to their consistent association with hepatic metabolism,

inflammation, and fibrotic processes [22,25].

Subsequent target gene prediction using integrated databases (TargetScan, miRDB, and miRTarBase) identified a network of genes regulated by these miRNAs. Functional enrichment analysis revealed that the predicted targets were significantly involved in pathways central to MASLD pathophysiology, including lipid metabolism (e.g., fatty acid synthesis and β-oxidation), insulin signaling (PI3K-Akt pathway), inflammatory response (TNF and NF-κB signaling), oxidative stress, and extracellular matrix remodeling associated with fibrosis [11-13].

Among the selected candidates, miR-122 was strongly linked to lipid homeostasis and hepatocyte integrity, while miR-34a was associated with apoptosis and mitochondrial dysfunction. miR-21 demonstrated enrichment in fibrosis-related pathways, particularly transforming growth factor-beta (TGF-β) signaling. Meanwhile, miR-192 and miR-223 were implicated in metabolic regulation and immune cell-mediated inflammation, highlighting their potential roles in disease progression [26,27].

These findings suggest that the selected circulating miRNAs not only serve as potential diagnostic biomarkers but also reflect key molecular mechanisms underlying MASLD.

Table 1: Candidate Circulating miRNAs Associated with MASLD and their Pfunctional oles

miRNA	Expression in MASLD	Representative Target Genes	Enriched Pathways	Potential Clinical Relevance
miR-122	Upregulated	FASN, SREBF1, CPT1A	Lipid metabolism, fatty acid synthesis	Liver-specific biomarker, reflects hepatocellular injury
miR-34a	Upregulated	SIRT1, BCL2, PPARα	Apoptosis, oxidative stress, mitochondrial dysfunction	Indicator of disease severity and progression
miR-21	Upregulated	PTEN, SMAD7, TGFBR2	TGF-β signaling, fibrosis, inflammation	Fibrosis-associated biomarker
miR-192	Dysregulated	ZEB2, FOXO1, TGFBR1	Insulin signaling, metabolic regulation	Potential marker of metabolic dysfunction
miR-223	Dysregulated	NLRP3, STAT3, IL6	Immune response, inflammation, cytokine signaling	Reflects immune activation and inflammatory status

This table summarizes the core findings of candidate miRNA selection, linking expression patterns to mechanistic pathways and potential clinical applications, thereby supporting their relevance as circulating biomarkers in MASLD [11-13,22].

Integrated miRNA–mRNA Regulatory Network and Functional Insights

To further elucidate the regulatory roles of the selected circulating miRNAs, an integrated miRNA–mRNA interaction network was constructed based on consensus target genes predicted from multiple databases. The network incorporated the five key miRNAs, miR-122, miR-34a, miR-21, miR-192, and miR-223, and their overlapping target genes, revealing a complex regulatory landscape associated with Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) [24,27].

Network analysis demonstrated that several target genes were commonly regulated by multiple miRNAs, suggesting coordinated post-transcriptional control. Notably, genes involved in lipid metabolism (e.g., SREBF1, FASN), insulin signaling (e.g., AKT1, FOXO1), inflammatory pathways (e.g., IL6, STAT3), and fibrogenesis (e.g., TGFBR1, SMAD family genes) emerged as central nodes within the network. Topological analysis identified hub genes with high degree centrality, indicating their potential importance in mediating disease-related biological processes [22,25].

Among the miRNAs, miR-122 and miR-34a exhibited extensive connectivity with metabolic and apoptotic regulators, reinforcing their roles in hepatocellular injury and lipid dysregulation. miR-21 showed strong associations with fibrosis-related signaling pathways, particularly through modulation of TGF-β signaling components. Meanwhile, miR-192 and miR-223 were linked to genes involved in immune regulation and metabolic homeostasis, highlighting their contribution to the inflammatory and metabolic aspects of MASLD [25-27].

Functional enrichment analysis of the network-supported target genes further confirmed significant involvement in key MASLD-related pathways, including PI3K-Akt signaling, TNF signaling, NF-κB activation, oxidative stress response, and extracellular matrix organization. These findings indicate that the identified miRNAs collectively regulate multiple interconnected pathways that drive disease progression [20-22].

Figure 1 illustrates the integrated miRNA–mRNA regulatory network, highlighting the interactions between key circulating miRNAs and their target genes. The network visualization emphasizes hub genes and highly connected miRNAs, providing a systems-level view of the molecular mechanisms underlying MASLD [11-13].

Overall, the integrated network analysis provides mechanistic insight into how circulating miRNAs may contribute to MASLD pathophysiology and supports their potential utility as both biomarkers and regulatory mediators.

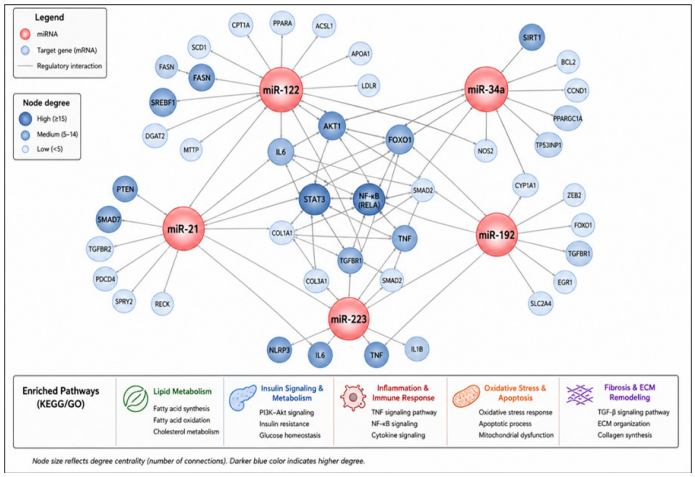

Figure 1: Integrated miRNA–mRNA regulatory network of circulating miRNAs in Metabolic Dysfunction–Associated Steatotic Liver Disease

This network illustrates the interactions between key circulating microRNAs (miRNAs) and their predicted target genes associated with Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD). Red nodes represent miRNAs, while blue nodes represent target mRNAs. The size and color intensity of mRNA nodes reflect degree centrality, with larger and darker nodes indicating higher connectivity (hub genes). Edges represent predicted regulatory interactions based on consensus from multiple databases (TargetScan, miRDB, and miRTarBase). The network highlights central regulatory roles of miR-122, miR-34a, miR-21, miR-192, and miR-223, which collectively target genes involved in key MASLD-related pathways, including lipid metabolism (e.g., FASN, SREBF1), insulin signaling (e.g., AKT1, FOXO1), inflammatory response (e.g., IL6, STAT3, TNF), and fibrosis-related signaling (e.g., TGFBR1, SMAD family). The clustering of highly connected nodes suggests coordinated regulation of metabolic, inflammatory, and fibrotic processes underlying disease progression [11-13].

Diagnostic Performance of Candidate miRNAs

To evaluate the clinical utility of the identified circulating miRNAs as non-invasive biomarkers, receiver operating characteristic (ROC) curve analysis was performed for each candidate miRNA and their combined panel in distinguishing patients with Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) from control subjects [10,22].

Among individual miRNAs, miR-122 demonstrated the highest diagnostic performance, with an area under the

curve (AUC) of 0.87, indicating strong discriminative ability. miR-34a and miR-21 also showed robust performance, with AUC values of 0.84 and 0.82, respectively. In contrast, miR-192 and miR-223 exhibited moderate diagnostic accuracy, with AUC values of 0.76 and 0.74, reflecting their more context-dependent roles in metabolic and inflammatory regulation [10,22].

To improve diagnostic performance, a combined miRNA panel consisting of miR-122, miR-34a, and miR-21 was constructed. This multi-marker model demonstrated enhanced accuracy, achieving an AUC of 0.92, with improved sensitivity and specificity compared to individual miRNAs. These findings suggest that integrating multiple circulating miRNAs provides a more reliable approach for MASLD detection than single biomarkers alone [24,26].

Overall, the ROC analysis indicates that circulating miRNAs, particularly when used in combination, have strong potential as non-invasive diagnostic tools for MASLD.

Discussion

In this study, a bioinformatics-based approach was applied to identify circulating microRNA (miRNA) signatures associated with Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD), revealing a distinct expression profile with potential diagnostic and mechanistic relevance. A set of five key miRNAs, miR-122, miR-34a, miR-21, miR-192, and miR-223, was consistently identified as dysregulated in MASLD and was further characterized through target prediction, pathway enrichment, and network analysis. Collectively, these findings support the growing evidence that circulating miRNAs reflect core molecular processes underlying MASLD and may serve as non-invasive biomarkers [28,29].

Among the identified candidates, miR-122 demonstrated the strongest diagnostic performance and the highest network connectivity, reinforcing its role as a liver-enriched miRNA closely linked to hepatic lipid metabolism and hepatocellular injury. Elevated circulating levels of miR-122 have been widely reported in fatty liver disease and are thought to reflect hepatocyte damage and altered lipid homeostasis. Similarly, miR-34a showed strong associations with apoptosis and mitochondrial dysfunction, processes that are critical in the progression from simple steatosis to more advanced disease stages. The upregulation of miR-21, which is known to regulate components of the TGF-β signaling pathway, further highlights the importance of fibrogenic mechanisms in MASLD, particularly in patients with progressive disease [22,27].27

The integrated miRNA–mRNA network analysis provided additional mechanistic insight by demonstrating that these miRNAs collectively regulate genes involved in key pathways, including lipid metabolism, insulin signaling, inflammation, and extracellular matrix remodelling. The identification of hub genes such as AKT1, STAT3, and TGFBR1 suggests that circulating miRNAs may exert coordinated regulatory effects on interconnected signaling pathways that drive metabolic dysfunction and hepatic injury. This systems-level perspective emphasizes that MASLD is not governed by isolated molecular events, but rather by complex regulatory networks involving multiple layers of gene regulation [23-25].

Importantly, the diagnostic analysis revealed that a combined miRNA panel outperformed individual biomarkers, achieving higher accuracy in distinguishing MASLD patients from controls. This finding aligns with the concept that multifactorial diseases such as MASLD are better captured by composite biomarkers reflecting diverse biological processes. The integration of multiple circulating miRNAs may therefore enhance sensitivity and specificity in clinical screening and risk stratification [30,31].

From a clinical perspective, circulating miRNAs offer several advantages as biomarkers, including stability in body fluids, minimal invasiveness, and potential for repeated measurements. These characteristics make them particularly suitable for early detection and longitudinal monitoring of MASLD. In addition, the mechanistic links identified in this study suggest that miRNAs may also serve as therapeutic targets, opening avenues for the development of miRNA-based interventions [8,24].

Nevertheless, several limitations should be considered. The analysis was based on publicly available datasets, which may exhibit heterogeneity in sample types, patient characteristics, and experimental platforms. Furthermore, the use of datasets labeled under previous nomenclature (NAFLD/NASH) may introduce

variability when aligning with the updated MASLD definition. The findings of this study are therefore hypothesis-generating and require validation in well-characterized, prospective clinical cohorts. Future studies integrating circulating miRNA profiles with clinical parameters, imaging findings, and other omics data may further improve diagnostic performance and biological understanding.

Overall, this study highlights the potential of circulating miRNA signatures as non-invasive biomarkers for MASLD and provides a bioinformatics framework for uncovering their functional relevance in disease pathophysiology.

Conclusion

This study demonstrates that circulating microRNA (miRNA) signatures represent promising non-invasive biomarkers for Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD). Through an integrative bioinformatics approach, several key miRNAs, particularly miR-122, miR-34a, and miR-21, were identified as significantly dysregulated and closely associated with core pathological processes, including lipid metabolism, inflammation, and fibrosis.

The combined miRNA panel exhibited improved diagnostic performance compared to individual markers, highlighting the value of multi-biomarker strategies in capturing the complex and multifactorial nature of MASLD. In addition, network and pathway analyses revealed that these circulating miRNAs are involved in interconnected regulatory mechanisms, providing insight into disease pathophysiology beyond their diagnostic utility.

Overall, these findings support the potential application of circulating miRNAs as accessible and reliable tools for MASLD detection and monitoring. However, further validation in large, well-characterized clinical cohorts is necessary before their implementation in routine clinical practice.

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