

Review**Non-invasive assessment in MASLD: From biomarker discovery to clinical pathway integration**

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Abstract

Metabolic dysfunction-associated steatotic liver disease (MASLD) is one of the leading causes of chronic liver disease worldwide. Although liver biopsy remains the histological reference standard for assessing steatohepatitis, fibrosis stage, and therapeutic response, its invasiveness, sampling variability, and limited suitability for repeated monitoring have driven the development of non-invasive approaches. Clinical



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scores based on routine variables, omics-derived biomarkers, quantitative imaging techniques, and multimodal integrative models have substantially expanded the landscape of MASLD assessment.

This review summarizes current progress in non-invasive evaluation of MASLD from a clinically oriented perspective, covering traditional blood-based and clinical tools, omics approaches, quantitative imaging, and multimodal integration. Particular attention is given to how these tools may serve different clinical purposes, including targeted screening or case-finding, specialist referral, fibrosis stratification, prognostic assessment, longitudinal monitoring, and precision, risk-stratified care.

At the same time, major translational barriers remain, including the predominance of technology-driven instead of clinically driven study designs, the imperfect nature of biopsy-based reference standards, insufficient head-to-head comparisons across modalities, limited external validation of high-dimensional models, and uncertainty regarding real-world implementation. We argue that the future of non-invasive assessment in MASLD lies not in identifying a universally superior single modality, but in developing a clinical-context-specific, stepwise, and biologically interpretable framework that aligns non-invasive tools with distinct clinical needs and decision points.

Keywords: MASLD, non-invasive assessment, blood-based biomarkers, omics, quantitative imaging, multimodal models, precision medicine

INTRODUCTION

Metabolic dysfunction-associated steatotic liver disease (MASLD) is currently one of the leading causes of chronic liver disease worldwide, affecting approximately 32% of adults^[1]. Numerous studies have confirmed that the incidence of MASLD continues to rise, placing a substantial burden on healthcare systems globally^[2-5]. A study based on

cohorts from eight countries projected that the total number of MASLD cases would increase by as much as 30% between 2016 and 2030^[6]. At present, the three most important features in the assessment of MASLD are steatosis, inflammatory activity, and fibrosis stage. Among the histological characteristics of MASLD, the degree of liver fibrosis is the feature most closely associated with liver-related outcomes and mortality risk. Therefore, the central goal of non-invasive evaluation is not merely to identify steatosis, but to achieve accurate stratification of high-risk fibrosis and disease progression^[7-9].

Liver biopsy remains the reference standard for histological assessment of MASLD. However, biopsy is associated with invasive risks, including internal bleeding, complications, and even life-threatening events, making it unsuitable as a tool for long-term, real-time monitoring of disease progression^[10]. In addition, each biopsy samples only about 1/50,000 of the liver, and such a limited specimen cannot adequately represent the condition of the entire organ, thereby leading to sampling error^[11-13]. Finally, liver fibrosis is a dynamic process, whereas fibrosis staging based on biopsy is only semi-quantitative and cannot satisfactorily capture disease progression^[14-17]. Because of these limitations, together with the substantial clinical demand, there is an urgent need for non-invasive assessment methods, as biopsy is not suitable for large-scale, repeated, dynamic use in clinical management. Over the past several decades, a wide range of non-invasive approaches has emerged. The analysis of omics and imaging data has led to the development of numerous techniques with promising diagnostic performance to assist clinicians in the evaluation of MASLD.

Rather than seeking a single best-performing tool, the key to non-invasive assessment of MASLD lies in building a stratified, interpretable, and clinically translatable framework that aligns with different clinical scenarios and management goals. In this context, this article reviews non-invasive assessment strategies for MASLD with emphasis not only on diagnostic performance, but also on their utility in screening, risk stratification,

prognosis, and long-term monitoring. Because primary care and specialist liver centers differ substantially in clinical goals and available resources, this review focuses on what each of these settings actually needs. It also emphasizes methods that are interpretable and translatable, rather than covering end-to-end deep learning models in detail. The following sections are organized accordingly, beginning with current clinical tools, then progressing to emerging omics and imaging approaches, and finally exploring their future applications in the precision management of MASLD.

Unlike most previous reviews that focus on diagnostic accuracy of individual non-invasive tests, this review focuses on the clinical positioning of non-invasive tools across different MASLD care pathways. We emphasize how blood-based scores, omics-derived biomarkers, quantitative imaging, and multimodal models may be deployed differently for population screening, referral prioritization, fibrosis stratification, prognostic assessment, longitudinal monitoring, and precision management. A summary of the potential roles of these tool categories across major clinical tasks is provided in Table 1.

Table 1. The potential application of the MASLD non-invasive assessment tool in different clinical tasks.

| Tool category | Screening | Diagnosis/Staging | Risk stratification/Prognosis | Treatment monitoring |
|---|---------------------|---|---|--|
| Clinical scores / blood-based assessment | FIB-4, NFS, APRI | FAST, MEFIB, MAST, Pro-C3-based or other blood-based models | FIB-4 and related blood-based models for liver-related outcomes and mortality risk | Repeated measurement of FIB-4 and related blood-based markers, although value for individual histological monitoring remains inconsistent |
| Single omics | Not established | Genomics, transcriptomics, proteomics, and metabolomics for biomarker discovery and diagnosis | Genomics for long-term risk stratification; other omics for progression and outcome prediction | Potential for treatment-response monitoring, especially for dynamic molecular changes, but not yet implemented in routine clinical practice |

| | | | | |
|-------------------------|-----------------|---|---|--|
| Multi-omics integration | Not established | Multi-omics models for disease classification, fibrosis stratification, and mechanistic subtyping | Potential for prognostic stratification and disease progression prediction | Potential for dynamic monitoring, but clinical implementation remains limited |
| Elastography | US, VCTE | VCTE, SWE, MRE | VCTE, MRE | Repeated liver stiffness measurement but clinical implementation remains limited |
| Quantitative imaging | Exploratory | MRI-PDFF, corrected T1, T1rho, MPF | MRE, MPF and other advanced MRI-based markers with potential prognostic value | Longitudinal MRI-based assessment of steatosis and fibrosis-related change |
| Radiomics | Not established | Radiomics models based on US, CT, or MRI for fibrosis or steatosis assessment | Exploratory; clinical utility remains uncertain | Exploratory |

CLINICAL PARAMETER-BASED NON-INVASIVE TOOLS

Clinical application of non-invasive tools differs between primary care and hepatology specialist settings. In primary care, the main goal is to identify low-risk patients who can be managed without much intervention and high-risk patients who need further tests or specialist referral. In contrast, hepatology clinics focus on more refined diagnostic assessment, fibrosis staging, prognostic stratification, treatment selection, and longitudinal monitoring^[19]. These tasks demand more from non-invasive tools, requiring them to be reliable, robust, and consistent. Assessment based on routine laboratory parameters and simple clinical variables is the common non-invasive strategy in MASLD. These tools are inexpensive, accessible, and scalable, making them particularly suitable for first-line triage and population-level risk stratification. Existing evidence indicates that non-invasive tools such as Fibrosis-4 index (FIB-4), Nonalcoholic fatty liver disease fibrosis score (NFS) and Aspartate aminotransferase-to-platelet ratio index (APRI) are clinically useful in the assessment of patients with MASLD^[20-23]. Because these parameters are derived from routine clinical indicators and the calculations are simple and inexpensive, these methods are highly accessible in large-scale population screening and primary care settings. As a result, they have become the most commonly used first-line screening tools and have been incorporated into clinical guidelines^[24,25].

Studies have moved beyond comparing these models to fibrosis stages and now focus more on their ability to predict liver-related events, hepatocellular carcinoma, and overall mortality^[22,23,26]. However, most conventional scoring systems are based on indirect indicators such as age, aminotransferase levels, platelet count, and metabolism-related parameters. Although they are clinically useful, they remain limited in their ability to capture biological heterogeneity and individualized disease trajectories^[20,27,28]. Particularly in the context of dynamic monitoring, repeated measurement of indices such as FIB-4 has shown some prognostic value in several large population-based studies^[27], but its ability to identify true histological progression in

individual patients is not stable, and findings have even differed across studies^[20,28]. Therefore, conventional non-invasive scores are more suitable for population-level screening and stratification, whereas their utility for precise monitoring and individualized management still requires further improvement.

The assessment of traditional clinical variables has gradually evolved from the use of single diagnostic tools toward multimodal, multilevel integration. On the one hand, the integration of traditional clinical variables with mechanistic information derived from proteomics, metabolomics, and spatial transcriptomics holds promise not only for improving diagnostic and prognostic performance, but also for supporting patient stratification, therapeutic target identification, and treatment response monitoring, thereby promoting the evolution of non-invasive assessment from a clinical adjunct to a precision medicine decision-making platform^[26,28]. On the other hand, composite models represented by FAST, MEFIB, and MAST are more clinically translatable^[29-31]. The FAST model (FibroScan + AST) focuses on identifying active Metabolic Dysfunction-Associated Steatohepatitis (MASH) with significant fibrosis^[29]. The MEFIB model (MRE + FIB-4) is intended to optimize specialist referral for patients with significant fibrosis^[30]. The MAST model further integrates MRE, MRI-PDFF, and AST to enable joint assessment of high-risk MASH activity and fibrosis risk^[31]. Compared with omics-based integrative approaches, these elastography-based composite models are cheaper, easier to use, and more practical for clinics and trial screening; by contrast, omics-driven integrative strategies are better for understanding disease mechanisms and supporting therapeutic development.

Routine clinical scores are easy to scale and access, but they don't reflect much of the underlying biology. Table 2 summarizes the representative studies of blood-based biomarkers, conventional fibrosis scores, and clinically translatable composite models discussed in this section.

Table 2. Representative studies of blood-based biomarkers and clinical scoring systems for non-invasive assessment of MASLD.

| Author(s) | Year | Study design | Sample size | Clinical Task | Biomarker / Model |
|---|-------------|---------------------|--------------------|----------------------|--|
| Srivastava A, <i>et al.</i> ^[21] | 2019 | Prospective | 3,012 | Screening | FIB-4 |
| Siddiqui MS, <i>et al.</i> ^[20] | 2019 | Retrospective | 1,904 / 292 | Diagnosis | APRI, FIB-4, AST/ALT ratio, NFS |
| Ioannou GN, <i>et al.</i> ^[22] | 2019 | Retrospective | 7,068 / 16,175 | Prognosis | HCC risk prediction models |
| Hagstrom H, <i>et al.</i> ^[27] | 2020 | Retrospective | 40,729 | Prognosis | FIB-4 |
| Balkhed W, <i>et al.</i> ^[28] | 2022 | Retrospective | 135 | Prognosis | FIB-4, NFS, APRI, dAAR |
| Labenz C, <i>et al.</i> ^[108] | 2022 | Prospective | 11,859 / 349,570 | Screening | SEAL algorithm |
| Younes R, <i>et al.</i> ^[26] | 2021 | Retrospective | 1,173 | Prognosis | APRI, BARD, FIB-4, NFS, Hepamet fibrosis score (HFS) |

Overall, routine clinical scores and blood-based markers work best as first-line tools for population-level risk stratification, primary care screening, and referral prioritization. Their main clinical value is in excluding advanced fibrosis and identifying patients who require second-line assessment with elastography, ELF, or specialist evaluation. However, because these scores are based largely on indirect variables such as age, aminotransferases, and platelet count, they are less suitable for refined fibrosis staging, precise individual-level monitoring, or mechanistic disease characterization. Therefore, these tools should be used as triage tools at the entry of a stepwise pathway rather than as standalone methods for comprehensive MASLD assessment. Omics-based approaches have become a useful tool for identifying molecular signatures of disease susceptibility, activity, and progression.

OMICS-DRIVEN NON-INVASIVE ASSESSMENT

Single-omics assessment

Early omics research was limited to single-omics approaches, investigating MASLD separately from the perspectives of DNA, RNA, proteins, and metabolites. The research objectives ranged from pathological exploration, diagnosis, and prognostic evaluation to treatment monitoring^[32-35]. The major strength of omics-based research is its ability to interrogate MASLD biology at the molecular level. By characterizing genetic susceptibility, transcriptional regulation, protein expression, metabolic remodeling, and microbial interactions, omics approaches can identify candidate biomarkers, reveal mechanistic pathways, and support biologically informed patient stratification.

Genomics helps identify genetic risks for MASLD, focusing more on baseline risk than changes in disease activity, and provides the most upstream biological information for MASLD by characterizing genetic susceptibility. From a clinical perspective, its principal value lies in identifying individuals with genetic risk for progressing to steatosis, advanced fibrosis, or hepatocellular carcinoma, thereby supporting long-term risk assessment over real-time disease monitoring^[36,37]. Representative studies on

variants such as *PNPLA3*, *TM6SF2*, *GCKR*, and *MBOAT7* have shown that host genetic background affects inter-individual heterogeneity in disease severity and clinical outcomes^[36,38-41]. However, because genomic information is largely static and cannot directly reflect short-term changes in inflammation, fibrotic remodeling, or treatment response, its role in MASLD should be understood more appropriately as a foundational risk layer that complements, not replaces, dynamic biomarkers.

Transcriptomics shows how molecular processes change and drive MASLD progression, beyond just genetic risk. Its principal contribution lies in providing information on steatosis, inflammation, and fibrosis, thereby bridging upstream risk factors and downstream clinical phenotypes. Transcriptomic studies have also identified pathway-level drivers of disease progression, highlighting their value in mechanistic stratification and therapeutic target discovery^[42]. However, RNA signals may vary according to disease stage, sample type, and cellular context, and the multicellular architecture of the liver further complicates their interpretation. Transcriptomics is useful for understanding mechanisms and finding biomarkers, but its clinical use will need better standardization, validation, and integration with other non-invasive methods.

Proteomics reveals the functional effector layer of MASLD by detecting proteins involved in hepatocellular injury, inflammatory signaling, and matrix remodeling. Because proteins are more directly linked to biological functions, and many proteins can be detected in blood, proteomics have strong clinical applicability for the development of non-invasive biomarkers. Sanyal developed models that could diagnose steatosis (AUC 0.95), inflammation (AUC 0.83), ballooning (AUC 0.87), and fibrosis (AUC 0.92), while a combined model achieved an AUC of 0.93 for identifying high-risk MASH^[43]. Nevertheless, issues such as technical variability, lack of standardization, and limited external validation continue to constrain its routine application.

Metabolomics captures the downstream dynamic layer of disease biology by reflecting the persistent metabolic disturbances closely associated with steatosis, inflammation, and fibrosis in MASLD. Compared with genomics, metabolomics is more sensitive to the current physiological state and may therefore be better suited for identifying active disease processes, monitoring disease progression, or assessing treatment-related changes^[44-47]. This is also what gives metabolomics its translational appeal for blood- or urine-based biomarkers, particularly for large-scale screening and repeated assessment^[44,48,49]. However, because metabolic profiles are highly susceptible to environmental influences, reproducibility across populations and the standardization required for clinical use remain important challenges. Representative studies of genomics, transcriptomics, proteomics, and metabolomics approaches for MASLD assessment are summarized in Table 3.

Table 3. Representative studies of single-omics approaches for non-invasive assessment of MASLD.

| Author(s) | Year | Study design | Sample size | Clinical Task | Omics |
|---|-------------|---------------------|--------------------|----------------------|------------------------------|
| Liu Y <i>et al.</i> ^[38] | 2014 | Retrospective | 375 | Prognosis | Genomics |
| De Vincentis <i>et al.</i> ^[109] | 2021 | Retrospective | 266,687 | Prognosis | Genomics |
| Eslam M <i>et al.</i> ^[110] | 2015 | Retrospective | 1,992 / 1,242 | Diagnosis | Genomics |
| Dongiovanni P <i>et al.</i> ^[36] | 2018 | Retrospective | 9,414 | Prognosis | Genomics |
| Verweij N <i>et al.</i> ^[111] | 2022 | Retrospective | 542,904 | Prognosis | Genomics |
| Bianco C <i>et al.</i> ^[112] | 2021 | Retrospective | 367,041 | Prognosis | Genomics |
| Chen VL <i>et al.</i> ^[113] | 2023 | Retrospective | 54,773 | Prognosis | Genomics |
| Sun J <i>et al.</i> ^[114] | 2024 | Retrospective | 546 | Prognosis | Transcriptomics, Genomics |
| Abul-Husn NS <i>et al.</i> ^[115] | 2018 | Retrospective | 46,544 / 12,527 | Prognosis | Genomics |

| | | | | | Transcriptomics |
|--|------|---------------|-----------------|--------------------------|-----------------------------|
| Jamialahmadi O <i>et al.</i> ^[37] | 2021 | Retrospective | 425,671 / 2,621 | Screening | Genomics |
| Valenti L <i>et al.</i> ^[40] | 2010 | Retrospective | 824 | Prognosis | Genomics Transcriptomics |
| Baselli GA <i>et al.</i> ^[116] | 2022 | Retrospective | 301 | Prognosis | Genomics Transcriptomics |
| Walker RW <i>et al.</i> ^[39] | 2020 | Retrospective | 27,744 | Prognosis | Genomics |
| Govaere O <i>et al.</i> ^[117] | 2020 | Retrospective | 206 / 175 | Diagnosis / Prognosis | Transcriptomics |
| Conway J <i>et al.</i> ^[118] | 2023 | Retrospective | 1,208 / 186 | Prognosis | Transcriptomics |
| Baboota RK <i>et al.</i> ^[42] | 2022 | Retrospective | 58 | Diagnosis / Prognosis | Transcriptomics |
| Tobaruela-Resola AL <i>et al.</i> ^[119] | 2024 | Retrospective | 100 | Diagnosis | Transcriptomics |
| Starmann J <i>et al.</i> ^[120] | 2012 | Retrospective | 87 | Diagnosis | Transcriptomics |

| | | | | | |
|---|------|---------------|------------|--------------------------|--------------------------------|
| Govaere <i>et al.</i> ^[121] | 2023 | Retrospective | 306 | Diagnosis | Transcriptomics |
| Bell LN <i>et al.</i> ^[122] | 2010 | Retrospective | 85 | Diagnosis | Proteomics |
| Feng G <i>et al.</i> ^[123] | 2023 | Retrospective | 285 | Diagnosis | Proteomics |
| Yuan X <i>et al.</i> ^[124] | 2020 | Retrospective | 56 | Diagnosis | Proteomics |
| Luo Y <i>et al.</i> ^[125] | 2021 | Retrospective | 216 | Diagnosis | Proteomics |
| Govaere O <i>et al.</i> ^[121] | 2023 | Retrospective | 306 | Diagnosis | Proteomics, Transcriptomics |
| Govaere O <i>et al.</i> ^[117] | 2020 | Retrospective | 403 | Diagnosis | Transcriptomics, Proteomics |
| Jiang Y <i>et al.</i> ^[126] | 2023 | Retrospective | 2,236 / 80 | Diagnosis | Proteomics |
| Sanyal AJ <i>et al.</i> ^[43] | 2023 | Retrospective | 636 | Diagnosis / Treatment | Proteomics |
| Rodríguez-Suárez E <i>et al.</i> ^[127] | 2010 | Retrospective | 18 / 45 | Diagnosis | Proteomics |

| | | | | | |
|---|------|---------------|----------------|-----------|--------------|
| McGlinchey AJ <i>et al.</i> ^[45] | 2022 | Retrospective | 627 | Diagnosis | Metabolomics |
| Zhu Q <i>et al.</i> ^[44] | 2022 | Retrospective | 83 | Diagnosis | Metabolomics |
| Perakakis N <i>et al.</i> ^[46] | 2019 | Retrospective | 80 | Diagnosis | Metabolomics |
| Chen J <i>et al.</i> ^[47] | 2024 | Retrospective | 250 | Diagnosis | Metabolomics |
| Khusial RD <i>et al.</i> ^[49] | 2019 | Retrospective | 559 | Screening | Metabolomics |
| Moolla A <i>et al.</i> ^[48] | 2020 | Retrospective | 275 | Diagnosis | Metabolomics |
| Kalhan SC <i>et al.</i> ^[128] | 2011 | Retrospective | 60 | Diagnosis | Metabolomics |
| Oh TG <i>et al.</i> ^[52] | 2020 | Retrospective | 163 / 237 / 49 | Diagnosis | Microbiomics |

Multi-omics assessment

Each individual omics layer shows one part of MASLD biology and therefore provides an incomplete representation of this multifactorial disease. For example, genomics cannot capture the influence of dietary and environmental factors on MASLD. By integrating multi-level biological information and combining it with artificial intelligence, multi-omics enables the construction of models from large-scale datasets and diverse data modalities to extract and identify disease-related information. This approach improves model performance as well as helps establish a more complete mechanistic chain of disease development^[32]. In multifactorial diseases such as MASLD, any single dimension is insufficient to directly characterize the origins and progression of the disease. In contrast, the integration of multidimensional information makes it possible to build more complex and interpretable models that illustrate the interactions and transformations among various biomolecules. This may enhance the clinical and biological interpretability of multi-omics models and, when combined with experimental validation, may help move the field from descriptive associations toward mechanistic inference and causal testing.

Several studies have systematically compared the diagnostic performance of single-omics strategies with that of multi-omics integration, consistently confirming the superiority of integrative approaches. Wood *et al.* and Zhou *et al.* developed diagnostic models and found that model performance was optimal after integrating all omics data^[50,51]. The integration of different omics datasets can significantly improve diagnostic performance. The likely reason is that different omics datasets carry complementary information, and this complementarity represents a major advantage of multi-omics. Compared with the relatively narrow and task-specific applications typically seen in single-omics studies, multi-omics may offer broader clinical and biological utility. Some multi-omics studies have established a workflow of exploring pathological mechanisms, building diagnostic models, and validating clinical performance, moving from descriptive association to mechanistic inference and, in

selected cases, experimental causal testing. Both Caussy *et al.* and Oh *et al.* used microbial features to reveal the influence of the gut microbiota on liver pathology and subsequently validated this relationship in predictive models^[52,53]. Quesada-Vazquez *et al.* further advanced mechanistic research toward functional validation: after integrating metabolomic, transcriptomic, and microbial data and identifying a negative association between plasma histidine and steatosis, they verified the therapeutic effect of histidine supplementation in multiple animal models, thereby completing a closed loop from association to causality^[54]. Therefore, the strengths of multi-omics studies lie not only in improved predictive performance, but also in their function to advance research from descriptive correlation to mechanistic interpretation and even causal validation. Such a research pathway gives multi-omics stronger scientific explanatory power in addition to its clinical utility.

Although multi-omics offers many advantages over single-omics approaches, most current studies on multi-omics remain at the research stage. Owing to factors such as testing costs, the complexity of clinical analytical workflows, and insufficient standardization, few studies have been used in real-world clinics. At the same time, most existing studies have been conducted in specific centers or selected populations, while multicenter external validation remains inadequate, resulting in limited reproducibility and generalizability.

Representative multi-omics integration studies for MASLD assessment are summarized in Table 4. In summary, omics-based approaches give a useful biological insight into MASLD heterogeneity and may support biomarker discovery, molecular subtyping, prognostic modelling, and treatment-response research. At present, however, most omics tools remain insufficiently standardized and externally validated for routine clinical screening, referral decisions, or longitudinal monitoring. Their most appropriate current role is therefore in mechanistic investigation, discovery of candidate biomarkers, and research-oriented precision stratification, with promise for future translation into

clinically deployable panels once analytical reproducibility, cost-effectiveness, and real-world validity are established. In contrast to omics approaches, which characterize molecular changes, quantitative imaging provides organ-level information on steatosis, stiffness, tissue composition, and architectural heterogeneity.

Table 4. Representative studies of multi-omics integration strategies for MASLD assessment.

| Author(s) | Year | Study design | Sample size | Clinical Task | Omics |
|--|------|---------------|-------------|---------------|--|
| Wood GC <i>et al.</i> ^[50] | 2017 | Retrospective | 576 | Diagnosis | Genomics, Proteomics |
| Oh TG <i>et al.</i> ^[52] | 2020 | Retrospective | 163 | Diagnosis | Microbiomics, Metabolomics |
| Younossi ZM <i>et al.</i> ^[129] | 2005 | Retrospective | 98 | Screening | Transcriptomics, Proteomics |
| Atabaki-Pasdar N <i>et al.</i> ^[130] | 2020 | Retrospective | 1,514 | Diagnosis | Genomics, Transcriptomics, Proteomics, Metabolomics |
| Zhou Y <i>et al.</i> ^[51] | 2016 | Retrospective | 318 | Diagnosis | Metabolomics, Genomics |
| Wen W <i>et al.</i> ^[131] | 2026 | Retrospective | 166 | Diagnosis | Transcriptomics, Epigenomics |
| Perakakis N <i>et al.</i> ^[46] | 2019 | Retrospective | 80 | Diagnosis | Lipidomics, Glycomics |
| Quesada-Vazquez S <i>et al.</i> ^[54] | 2023 | Retrospective | 651 | Treatment | Metabolomics, Transcriptomics, Microbiomics |
| Leung H <i>et al.</i> ^[132] | 2022 | Prospective | 180 | Prognosis | Microbiomics, Metabolomics |

| | | | | | |
|--|------|---------------|--|--------------------------|---|
| | | | 36,116 / | | |
| Sveinbjornsson G <i>et al.</i> ^[133] | 2022 | Retrospective | 9,491 / 4,809/ 35,559/ 47,151 | Diagnosis / Prognosis | Genomics, Transcriptomics, Proteomics |
| Li Z <i>et al.</i> ^[134] | 2025 | Retrospective | 61 | Diagnosis | Transcriptomics, Metabolomics, Proteomics |

Non-invasive imaging assessment

At the organ and tissue levels, non-invasive assessment of MASLD depends mainly on imaging-based biomarkers. Numerous imaging-based methods have been reported for the evaluation of liver fibrosis; however, a comprehensive review of all available techniques is beyond the scope of this article. The methods discussed in this review can broadly fall into three groups. The first group uses the mechanical properties of liver tissue, taking liver stiffness itself as the imaging biomarker. This includes Vibration-controlled transient elastography (VCTE), Shear wave elastography (SWE), and Magnetic resonance elastography (MRE). The second group involves leveraging endogenous contrast mechanisms to acquire information on tissue composition through specifically designed composition imaging sequences, followed by post-processing to derive quantitative compositional indices, such as T1, T1 ρ , and quantitative magnetization transfer (MT). The third group consists of approaches based on image post-processing and quantitative modeling, in which quantitative features are extracted from routine imaging and liver fibrosis is indirectly assessed through mathematical analysis or diagnostic models; representative methods include radiomics.

Owing to its availability and lower cost, VCTE remains one of the most widely used non-invasive techniques for the clinical assessment of liver fibrosis^[7]. Although MRE generally outperforms VCTE in terms of diagnostic performance and reproducibility, its use is limited by higher costs, less accessibility, and the need for specialized equipment. Assessment methods based on elastography or other mechanical parameters generally require dedicated equipment, specialized functional modules, or compatible probes. In contrast, compositional imaging methods based on endogenous contrast mechanisms and radiomics do not require additional standalone examination devices, thereby offering practical advantages in clinical implementation and application flexibility.

Assessment based on stiffness

Elastography has become a key non-invasive tool in the clinical management of

MASLD. Its clinical use spans primary screening of high-risk populations, accurate diagnosis of advanced fibrosis, longitudinal monitoring of disease progression, and prognostic evaluation of liver-related outcomes^[55]. VCTE, SWE, and MRE are currently the main elastography-based methods used for fibrosis assessment in MASLD; however, their value lies not so much in their technical differences as in their distinct positions within the clinical pathway. Owing to its simplicity and broad availability, VCTE is well suited for first-line triage. SWE provides an ultrasound-based alternative with good feasibility within routine imaging workflows, whereas MRE is generally reserved for settings requiring higher precision and reproducibility. Rather than viewing these modalities as competing technologies, it may be more useful to regard them as complementary tools with different levels of accessibility, accuracy, and resource needs. It should be emphasized that elastography-based techniques use liver stiffness as a surrogate marker of fibrosis. They do not directly measure extracellular matrix composition or interrogate the molecular pathophysiology underlying MASLD progression.

Among elastography-based techniques, VCTE is still the most widely used non-invasive tool in routine clinical practice because of its ease of operation, rapid acquisition, and established role in fibrosis triage^[56-64]. A cohort study of 6,295 individuals from Europe and Asia found VCTE-based fibrosis screening in primary care to be cost-effective^[65]. SWE can be integrated into conventional ultrasound platforms, offering practical advantages in workflow flexibility, and has demonstrated good reproducibility in several MASLD cohorts^[66-73]. A study evaluating the repeatability and reproducibility of SWE and VCTE showed that, in patients with MASLD, SWE had superior interday and interoperator reproducibility to VCTE and achieved the prespecified performance threshold^[74]. MRE generally provides the highest diagnostic accuracy and reproducibility, particularly in obese patients and specialist care settings, although its broader application is limited by cost, availability, and examination complexity^[75,76]. Overall, these techniques have become central to non-invasive fibrosis assessment,

although all of them are susceptible to confounding by factors other than fibrosis itself, such as inflammation, congestion, and cholestasis^[18]. Representative studies of VCTE, SWE, and MRE in MASLD are summarized in Table 5.

Table 5. Representative studies of elastography approaches for MASLD assessment.

| Author(s) | Year | Study design | Sample size | Clinical Task | Biomarker / Model |
|---|------|---------------|--------------|-----------------------------|-------------------|
| Boursier J <i>et al.</i> ^[64] | 2022 | Retrospective | 1,057 | Prognosis | VCTE |
| Wong VWS <i>et al.</i> ^[62] | 2012 | Prospective | 193 | Diagnosis | VCTE |
| Petta S <i>et al.</i> ^[63] | 2020 | Retrospective | 1,039 | Prognosis | VCTE |
| Shili-Masmoudi S <i>et al.</i> ^[61] | 2020 | Prospective | 2,245 | Prognosis | VCTE |
| Wong VWS <i>et al.</i> ^[57] | 2010 | Prospective | 246 | Diagnosis | VCTE |
| Karlas T <i>et al.</i> ^[59] | 2017 | Retrospective | 2,735 | Diagnosis | VCTE |
| Braude M <i>et al.</i> ^[60] | 2023 | Retrospective | 7,079 | Prognosis | VCTE |
| Boursier J <i>et al.</i> ^[58] | 2016 | Retrospective | 452 / 360 | Diagnosis / Prognosis | VCTE |
| Serra-Burriel M <i>et al.</i> ^[65] | 2019 | Prospective | 6,295 | Screening | VCTE |
| Mendoza YP <i>et al.</i> ^[73] | 2022 | Prospective | 104 | Diagnosis | VCTE, SWE |
| Indre M-G <i>et al.</i> ^[70] | 2025 | Retrospective | 2,223 | Diagnosis | SWE |

| | | | | | |
|---|------|---------------|-------|-----------|-----------|
| Ozturk A <i>et al.</i> ^[71] | 2020 | Retrospective | 116 | Diagnosis | SWE |
| Lee DH <i>et al.</i> ^[67] | 2020 | Prospective | 102 | Diagnosis | SWE |
| Herrmann E <i>et al.</i> ^[68] | 2018 | Retrospective | 1,134 | Diagnosis | SWE |
| Pierce TT <i>et al.</i> ^[74] | 2024 | Prospective | 40 | Diagnosis | SWE, VCTE |
| Jang JK <i>et al.</i> ^[66] | 2022 | Prospective | 132 | Diagnosis | SWE |
| Gidener T <i>et al.</i> ^[135] | 2021 | Retrospective | 829 | Prognosis | MRE |
| Imajo K <i>et al.</i> ^[104] | 2016 | Retrospective | 142 | Diagnosis | MRE |
| Park CC <i>et al.</i> ^[105] | 2017 | Prospective | 104 | Diagnosis | MRE |

Assessment based on non-invasive compositional imaging

The pathological hallmark of liver fibrosis is excessive deposition of collagen-rich extracellular matrix^[77]. This remodelling expands the extracellular matrix compartment and often shifts tissue water distribution as well. These tissue alterations provide a biological basis for compositional MRI sensitive to relaxation and MT. Quantitative MRI methods, including T1 mapping^[77-79] and T1 ρ mapping^[80-84], have been investigated as non-invasive approaches for assessing liver fibrosis. Both T1 and T1 ρ values have been reported to increase with fibrosis severity.

However, both T1 mapping and T1 ρ mapping are sensitive to hepatic iron content, which can confound fibrosis assessment. To address this limitation, iron-corrected T1 mapping^[77-79] has been introduced for liver fibrosis evaluation, and iron correction strategies for hepatic T1 ρ mapping^[85] have also been reported. In addition to iron deposition, inflammation may also influence T1 and T1 ρ measurements. Furthermore,

reliable quantification requires close agreement between the assumed signal model and the acquired data. Careful sequence design, acquisition optimization, and post-processing can therefore help minimize possible sources of bias and improve measurement robustness.

Because collagen forms a gel-like macromolecular network, it is expected to exhibit a strong MT effect. Although the liver contains other proteins, these molecules are generally more mobile than collagen and are therefore expected to contribute less to MT. Triglycerides and lipids are hydrophobic and have limited MT effects. These properties suggest that quantitative MT imaging may provide a means to evaluate collagen deposition in the liver and thereby assess liver fibrosis. This concept has been demonstrated in both animal^[86] and human studies^[87-89]. Importantly, quantitative MT-based methods appear to be relatively less affected by hepatic iron deposition, which is an advantage for compositional imaging of the liver.

Conventional quantitative MT methods typically require T1 information and relatively long acquisition times, posing challenges for robust clinical imaging of the liver. In contrast, spin-lock radiofrequency-based methods^[90,91] have shown advantages for quantitative MT imaging because they can be designed to achieve higher saturation efficiency with reduced direct water saturation, enabling rapid mapping of macromolecular proton fraction (MPF) in the liver.

Compared with stiffness-based methods, compositional imaging approaches that more directly interrogate collagen-related tissue properties provide a distinct physical mechanism for fibrosis assessment. These methods do not require exogenous contrast agents or additional hardware and may have potential for detecting early-stage fibrosis. In early fibrosis, liver stiffness may not change substantially, whereas direct imaging of collagen-associated tissue alterations may provide greater sensitivity to early extracellular matrix remodeling. Such capability could be important for the

development of antifibrotic therapies, patient stratification, and treatment monitoring. By introducing complementary biophysical mechanisms, compositional imaging may help address current limitations in non-invasive liver fibrosis assessment. Nevertheless, despite the promise of these techniques, further technical development, standardization, and large-scale clinical validation are required before routine clinical implementation.

Assessment based on radiomics

Radiomics is another imaging-based strategy that can often be applied to routinely acquired clinical images without requiring additional scanner hardware, although robust implementation requires standardized acquisition, segmentation, preprocessing, and analysis pipelines. The basic idea is to extract large numbers of quantitative features from medical images automatically, and then use those features to build models for diagnosis, prognosis, treatment-response assessment, or disease monitoring^[92-94]. To improve reproducibility and comparability in radiomics research, Zwanenburg *et al.* standardized 169 radiomic features^[95]. Because of their widespread clinical use, CT and ultrasound have provided relatively large datasets for radiomics research, although their roles in MASLD care differ. Models developed by Zhang *et al.* and Meng *et al.* have both achieved encouraging results^[96,97]. In comparison, although Chen *et al.* and Xu *et al.* reported good performance using T2- and T1-weighted MRI sequences, respectively, limitations in sample size have constrained the generalizability of these models^[98,99].

However, most current radiomics studies in MASLD have focused mainly on diagnosis, whereas real-world clinical settings include both primary care clinics that require first-line screening tools and specialist clinics that address diagnosis, prognosis, and monitoring. Some clinical indicators currently used in primary care still play an important role in radiomics research. A study by Tang *et al.* showed that a combined clinical-radiomics model achieved an AUC of 0.930 for the diagnosis of moderate-to-severe fatty liver, whereas the radiomics-only model reached only 0.807; notably, the clinical model alone had already achieved an AUC of 0.904, meaning that

the added value of radiomics was only 2.6%^[100]. These findings suggest that, although radiomics may improve performance, its incremental benefit over readily available clinical variables may be modest in some diagnostic settings. Many radiomics studies therefore still require large-scale, multicenter validation to establish model robustness, generalizability, and true clinical value. The future of radiomics in MASLD will depend on its ability to provide reliable and useful clinical information beyond existing low-cost tools, rather than just slightly improving diagnostic accuracy. Representative radiomics-based studies discussed in this section are summarized in Table 6.

Table 6. Representative studies of radiomics-based models for MASLD assessment.

| Author(s) | Year | Study design | Sample size | Clinical Task | Modality |
|---|------|---------------|-------------|---------------|------------|
| Zhang H <i>et al.</i> ^[97] | 2025 | Retrospective | 840 | Diagnosis | CT |
| Lubner MG <i>et al.</i> ^[136] | 2017 | Retrospective | 289 | Diagnosis | CT |
| Wang J <i>et al.</i> ^[137] | 2022 | Retrospective | 443 | Diagnosis | CT |
| Dichtel LE <i>et al.</i> ^[138] | 2023 | Retrospective | 16 | Diagnosis | CT |
| Cui E <i>et al.</i> ^[139] | 2021 | Retrospective | 332 | Diagnosis | CT |
| Tang S <i>et al.</i> ^[100] | 2023 | Retrospective | 227 | Diagnosis | CT |
| Chen ZW <i>et al.</i> ^[140] | 2021 | Retrospective | 22 | Diagnosis | PET/CT |
| Meng F <i>et al.</i> ^[96] | 2023 | Retrospective | 618 | Prognosis | Ultrasound |
| Xia F <i>et al.</i> ^[141] | 2024 | Retrospective | 87 | Diagnosis | Ultrasound |
| Chen ZW <i>et al.</i> ^[99] | 2022 | Retrospective | 203 | Diagnosis | MRI |

| | | | | | |
|---|------|---------------|-----|-----------|-----|
| Xu X <i>et al.</i> ^[98] | 2021 | Retrospective | 53 | Diagnosis | MRI |
| Li N <i>et al.</i> ^[142] | 2024 | Retrospective | 254 | Diagnosis | CT |
| Cannella R <i>et al.</i> ^[143] | 2019 | Retrospective | 54 | Diagnosis | MRI |
| Li F <i>et al.</i> ^[144] | 2025 | Retrospective | 146 | Diagnosis | MRI |

In summary, imaging-based tools occupy different positions across the MASLD care pathway. VCTE fits best for second-line triage and fibrosis risk stratification after initial blood-based screening, particularly in primary care or referral pathways. SWE can provide similar elastography-based information within conventional ultrasound workflows. MRE offers higher accuracy and reproducibility and is useful in specialist settings, clinical trials, and cases with indeterminate or discordant first-line tests. MRI-PDFF is well suited for quantifying steatosis and monitoring treatment-related changes in liver fat, whereas emerging compositional MRI methods and radiomics are still mostly at the research stage. Thus, established elastography and MRI-based biomarkers are clinically useful for staging, prognostic assessment, and longitudinal follow-up, whereas newer quantitative imaging and radiomics approaches require further standardization and external validation before routine implementation.

Multi-modality integration

In the past decade, non-invasive MASLD assessment has expanded from focusing mainly on imaging and lab tests to including blood biomarkers, imaging, AI, and omics profiling in research. These approaches interrogate different levels of disease biology. Blood-based biomarkers provide accessible systemic surrogates of liver injury, inflammation, and fibrogenesis; omics approaches capture molecular perturbations across biological layers; and imaging characterizes organ-level phenotypes of the liver and related tissues. VCTE, SWE, and MRE occupy different positions in the MASLD assessment pathway because they differ in accessibility, reproducibility, diagnostic

performance, cost, and suitability for repeated follow-up. From this perspective, a more relevant clinical question is which combination of tests provides actionable information for a specific decision point in the MASLD care pathway. From the perspective of translational medicine, multimodal integration should not be viewed merely as a strategy to improve predictive performance. More importantly, it provides a framework for linking non-invasive assessment with real-world clinical decision-making. In primary care and community settings, the priority is not detailed biological analysis, but scalable identification of individuals who are unlikely to have advanced disease and those who require referrals. In this context, low-cost and widely available blood-based tools such as FIB-4, together with sequential strategies incorporating second-line tests such as VCTE or ELF, remain attractive because they fit the practical demands of population-level triage and resource allocation. By contrast, specialist hepatology clinics face a different set of challenges, including refinement of fibrosis stage, identification of patients at risk of progression, selection of candidates for therapeutic intervention, and monitoring of longitudinal change. These tasks may benefit more from higher-resolution phenotyping, including elastography, advanced MRI-based methods, selected omics approaches, and composite non-invasive scores that combine imaging or elastography with laboratory variables, such as FAST, MEFIB, and MAST. The value of a non-invasive tool should be measured by how well it supports decision-making in specific clinical situations, rather than just its overall accuracy in a mixed group of patients. For longitudinal management, repeated acquisition of blood biomarkers and imaging features is also more feasible than serial biopsy for monitoring disease progression and treatment response, although clinically meaningful change thresholds and standardized acquisition protocols remain important.

Importantly, the value of multimodal integration lies both in the complementarity of data and in its potential to connect mechanistic understanding with clinical application. Clinical biomarkers can help identify high-risk populations, imaging can localize and quantify organ-level injury, and omics can help explain why disease progression differs

among individuals. When interpreted together, these data may support a more comprehensive model of MASLD and could facilitate patient stratification, individualized prognosis, treatment selection, and long-term follow-up. In this sense, multimodal integration is not simply a means of aggregating information, but a way to bridge disease mechanism, phenotypic heterogeneity, and clinical utility.

Overall, the future of non-invasive MASLD assessment is unlikely to depend on one modality replacing another. Rather, the field is moving toward a layered, clinically contextualized framework in which blood-based biomarkers support broad triage, imaging refines phenotypic and prognostic assessment, and omics provides deeper biological resolution for mechanism-informed stratification. Such a strategy may ultimately provide a more practical, reproducible, and biologically meaningful framework for reducing reliance on biopsy, while preserving histology for selected cases in which diagnostic uncertainty or trial requirements justify invasive assessment.

Challenges from bench to bedside

Although omics, quantitative imaging, and AI have pushed the development of non-invasive assessment for MASLD, a stable, unified, and broadly generalizable strategy has yet to emerge. One reason is that much of the current literature remains technology-driven rather than clinically driven. Model development is often centered on maximizing AUROC in retrospective datasets, whereas the intended use case, target population, clinical pathway, and downstream decision point are insufficiently specified. As a result, high-dimensional or technically sophisticated models may show impressive performance in selected cohorts yet add limited value in practice if they do not outperform simpler tools, cannot be reproduced across centers, or are difficult to implement at scale. For MASLD, where screening and longitudinal follow-up must be scalable and sustainable, parsimony, external validity, calibration, and deployability may matter more than marginal improvements in discrimination.

A second limitation is that the reference standard itself is imperfect. Although liver biopsy remains the conventional histologic reference standard, it samples only a very small fraction of hepatic parenchyma, inter-observer agreement for steatohepatitis activity components is only moderate, and fibrosis staging remains semi-quantitative. These inherent shortcomings of the “gold standard” restrict, to some extent, the optimization and validation of non-invasive assessment methods. Given sampling variability and interobserver disagreement, the apparent performance of non-invasive tests may be constrained by a practical ceiling imposed by biopsy-based classification itself. This suggests that the field may ultimately require more robust reference frameworks, including composite outcome-based endpoints, central pathology review, AI-assisted digital pathology tools for MASH histology assessment, and longitudinal outcomes instead of sole reliance on single-time-point histology.

Another structural problem is the relative lack of direct head-to-head evidence across modalities and populations. The European LITMUS and US NIMBLE consortia have begun to fill this gap by evaluating non-invasive tests in more standardized and collaborative frameworks. However, robust direct comparisons across biomarkers, imaging modalities, and composite models in unselected real-world populations remain limited. Evidence from collaborative and external-validation studies suggests that the apparent performance of many tools is lower in less-selected populations than in the enriched tertiary or case-control cohorts in which they were often developed. In addition, the relative ranking of tests may change when disease prevalence, spectrum effects, and cohort enrichment are considered. Therefore, studies or guidelines that rely mainly on derivation-cohort AUCs without adequately considering enrichment effects may overstate real-world performance.

Evidence also remains relatively limited for the precise identification and dynamic monitoring of early fibrosis, especially at potentially reversible stages of disease. This gap is particularly important because future disease-burden reduction will depend not

only on detecting advanced fibrosis and cirrhosis, but also on identifying high-risk individuals earlier in the disease course.

At the quantitative imaging level, important practical limitations also remain. Liver stiffness-based methods are valuable for fibrosis assessment, but their implementation and interpretation are constrained by modality-specific limitations. Ultrasound-based elastography can be affected by operator dependence, body habitus, fasting status, and technical failure, whereas MRE is less widely available and more costly. Across stiffness-based approaches, liver stiffness may also be influenced by non-fibrotic processes such as inflammation, cholestasis, venous congestion, and edema. Elastography remains a cornerstone of fibrosis assessment because of its maturity and prognostic relevance, yet stiffness is still an indirect surrogate over a direct measurement of fibrotic architecture. MRI-based techniques may provide complementary phenotypic information. Although established methods such as MRI-PDFP and MRE are relatively well validated, many emerging MRI-based approaches still require broader standardization, cross-platform reproducibility assessment, and external validation. For advanced imaging to become clinically consequential, standardization, external validation, and workflow feasibility must be treated as primary endpoints.

Similarly, major translational challenges remain for high-dimensional approaches such as radiomics and multi-omics, as well as for AI models built upon them. Radiomics and other quantitative imaging signatures may capture tissue heterogeneity beyond conventional stiffness-based assessment, but their clinical utility remains constrained by variability in image acquisition, segmentation strategies, feature extraction, and cross-platform reproducibility. Multi-omics offers powerful opportunities for biological discovery, yet its translational gap remains substantial because molecular signatures are often affected by batch effects, platform heterogeneity, and differences in analytical pipelines. In both settings, high-dimensional signals may appear highly predictive in

selected datasets while remaining difficult to reproduce, interpret biologically, or implement clinically. Moreover, artificial intelligence can facilitate pattern recognition and multimodal integration, but it does not eliminate the fundamental risks of overfitting, shortcut learning, and hidden cohort-specific bias. Prospective validation, transparent reporting, calibration assessment, and evaluation across demographic and metabolic subgroups are therefore essential before such models can be adopted in clinical pathways. Therefore, the challenge is not simply to generate more features, but to identify which image- and molecular-derived signatures are robust, biologically meaningful, and actionable in real clinical pathways.

FUTURE DIRECTIONS: TOWARD PRECISION AND RISK-STRATIFIED MASLD CARE

Future development of non-invasive assessment in MASLD should shift from a model-performance-driven paradigm to a clinical problem-driven paradigm. The goal is not to focus on incremental improvements in diagnostic accuracy or predictive performance; future studies should be designed around specific clinical tasks and clearly defined use cases. Study design should move from retrospective case-control comparisons toward prospective, multicenter, pathway-based evaluation. In parallel, endpoint selection should focus on clinical needs, encompassing histological stage and progression to advanced fibrosis, liver-related events such as hepatic decompensation and HCC, and treatment response. Compared with costly efforts to achieve increasingly fine-grained histopathological classification, clinical practice is often more concerned with disease progression, long-term prognosis, and the consequences of management decisions.

With the burden of MASLD-related end-stage liver disease continuing to increase, future research priorities should also shift further upstream toward early risk identification, targeted case-finding, and prevention. Rather than relying primarily on intervention at advanced stages, establishing robust, accurate, accessible, and scalable

risk-identification tools in primary care and community healthcare settings has clear practical value for reducing disease burden and allocating resources sensibly. Therefore, the development of initial risk-identification strategies suitable for primary care, community settings, and high-risk populations has clear practical value for future non-invasive assessment systems. In this setting, simple and scalable tools are likely to remain the entry point of care pathways, with more advanced tests reserved for second-line refinement.

Children and adolescents represent an important special population in MASLD assessment because disease phenotype, histological patterns, growth-related physiology, and clinical decision thresholds may differ from those in adults. Adult-derived scores such as FIB-4 and NFS are strongly influenced by age and routine laboratory variables and therefore should not be directly extrapolated to pediatric MASLD without dedicated validation. In pediatric settings, the primary clinical tasks are usually identification of clinically significant steatosis, exclusion of advanced fibrosis, monitoring of cardiometabolic risk, and selection of patients who require specialist referral or biopsy. Imaging-based tools may be particularly attractive because they avoid invasive sampling and can support longitudinal follow-up. MRI-PDFF provides quantitative assessment of hepatic steatosis and is useful in clinical studies and treatment monitoring, whereas VCTE and other elastography methods may help stratify fibrosis risk when pediatric-specific protocols, probes, and cutoffs are available. However, evidence for longitudinal change thresholds, prognostic prediction, and treatment-response monitoring in children remains more limited than in adults. Therefore, pediatric MASLD requires age-appropriate validation of non-invasive tools to direct adoption of adult thresholds, and future studies should define pediatric-specific cutoffs, monitoring intervals, and clinically meaningful endpoints.

Multimodal integration will remain central to moving MASLD assessment toward precision medicine, but it should be pursued in a clinically disciplined manner. The goal

is not to aggregate every available data type, but to determine which combinations of blood biomarkers, imaging, omics, pathology, and clinical variables provide actionable information at each stage of care. Early studies of composite models suggest that integrating clinical, laboratory, and imaging information can improve risk stratification. In the future, if digital pathology, electronic health records, and multi-omics data can be further incorporated, and if AI-based methods can be rigorously validated for integrating high-dimensional information, it may become possible to construct more precise risk-stratification systems, capture the heterogeneity of MASLD more fully, and support treatment decisions on a multimodal basis.

Longitudinal monitoring should receive much greater emphasis in future research. Repeated non-invasive assessment may be better suited than static single-time-point staging to capture dynamic changes in fibrosis, inflammatory activity, and treatment response. For longitudinal monitoring, available guidance and cohort data support a risk-adapted approach. In adults with MASLD, FIB-4 is commonly used as the first-line reassessment tool; it may be repeated every 2-3 years in lower-risk individuals and every 1-2 years in patients with prediabetes, type 2 diabetes, or multiple metabolic risk factors. A FIB-4 value below 1.3 generally supports continued follow-up in primary care, whereas values of 1.3 or higher should prompt second-line assessment with VCTE, ELF, or specialist evaluation; values above 2.67 indicate higher risk and usually warrant referral^[24,25]. For VCTE, liver stiffness values below 8 kPa generally indicate low risk, values of 8 to 12 kPa require further evaluation, and values above 12 kPa suggest a high probability of advanced fibrosis or compensated advanced chronic liver disease, depending on the clinical context^[64,101]. However, no universally accepted percentage-change threshold has been established for defining fibrosis progression or regression on serial VCTE, and longitudinal interpretation is therefore usually based on reproducible changes across clinically relevant risk categories rather than small numerical fluctuations^[64,102]. MRE-derived liver stiffness has shown good performance for fibrosis risk stratification in MASLD, and values around 3.5 to 3.6 kPa have been

reported as useful thresholds for identifying advanced fibrosis in biopsy-proven MASLD cohorts^[103-106]. For longitudinal follow-up, MRE remains a promising tool, but changes in liver stiffness should be interpreted in clinical context because inflammatory activity may increase stiffness and contribute to overestimation of early fibrosis stages^[18,106,107]. Therefore, longitudinal monitoring should integrate the magnitude and direction of change, baseline risk category, test reproducibility, and clinical context instead of relying on a single isolated measurement.

This is particularly relevant for identifying early fibrosis and potentially reversible disease states, as well as for evaluating therapeutic efficacy over time. A more dynamic assessment paradigm may ultimately prove more clinically meaningful than attempting to reproduce biopsy categories at a single time point.

Finally, in the long term, the MASLD field needs a more comprehensive and robust evaluation framework than liver biopsy alone. With deeper investigation into disease mechanisms and continued progress in multimodal data integration methods, it may become possible to develop a non-invasive assessment system that combines biological interpretability, clinical feasibility, reproducibility, and longitudinal relevance, thereby reducing, and in selected contexts partially replacing, the central role of liver biopsy in disease staging, risk stratification, and treatment-response assessment. This would not only help overcome the inherent sampling error and semi-quantitative limitations of biopsy but also facilitate drug development and therapeutic monitoring in MASLD. At the same time, implementation science should become an integral part of the research agenda, because a non-invasive tool is clinically meaningful only if it can be adopted, interpreted, acted upon, and sustained in real healthcare systems.

The future of non-invasive assessment in MASLD lies not in identifying a universally superior single test, but in developing clinically driven, stepwise, and biologically interpretable frameworks that align different modalities with specific needs across the

care pathway. Such an approach may provide a more practical and scalable alternative to biopsy-centered assessment for risk stratification, longitudinal monitoring, and precision, risk-stratified MASLD care.

DECLARATIONS

Availability of data and materials

Data is available on request.

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Conflict of interest

Not applicable.

Ethical approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

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