MULTI-OMICS APPROACHES FOR PRECISION MEDICINE IN VIRAL HEPATITIS: FROM BIO-MARKER DISCOVERY TO PERSONALIZED THERAPY.

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ABSTRACT:

Background: Viral hepatitis is a great worldwide health challenge, causing appreciable morbidity & mortality, leading to chronic hepatitis, cirrhosis and hepatocellular carcinoma (HCC). Antiviral therapies improve non-subjective outcomes; however, a broad range in disease progression & response to treatment requires the development of precision medicine strategies. The technologies of multi-omics have emerged as powerful tools for comprehensive molecular profiling & hence enable individualized diagnosis and therapy. Objective: In this review, we summarize recent progress in multi-omics strategies for precision medicine in viral hepatitis, emphasizing their utility in biomarker discovery, disease prognosis, personalized therapy, & artificial intelligence (AI)-aided non-subjective decision-making.

Methods: A thorough literature search was performed using peer-reviewed articles, international clinical practice guidelines, reports published between 2016 and 2026. We critically evaluated current evidence on genomics, transcriptomics, proteomics, metabolomics, lipidomics, epigenomics, microbiomics and AI-driven multi-omics integration.

Results: The application of multi-omics technologies has improved our understanding of the pathogenesis of viral hepatitis through the identification of molecular signatures related to viral persistence, immune dysregulation, fibrosis progression, cirrhosis and HCC. Genomic and transcriptomic profiling allows risk stratification, prediction of the response to antivirals and pharmacogenomic-guided therapy. Proteomic and metabolomic analysis provides novel diagnostic and prognostic biomarkers. AI and machine learning integration of diverse omics datasets enhances biomarker discovery, patient stratification, disease prediction, and therapeutic optimization. However, widespread clinical implementation is limited by high costs, computational complexity,

lack of standardized analytical pipelines and insufficient large-scale validation. **Conclusion**: Multi-omics approaches are revolutionizing the field of precision hepatology by allowing personalized diagnosis, prognosis & treatment of viral hepatitis. Future integration of single-cell sequencing, spatial omics, CRISPR-based therapies, & explainable AI is expected to accelerate clinical translation & improve patient outcomes.

Keywords: Viral hepatitis; precision medicine; multi-omics; genomics; transcriptomics; proteomics; metabolomics; biomarkers; artificial intelligence; hepatocellular carcinoma.

INTRODUCTION:

Viral hepatitis continues to be a significant global health problem & one of the leading causes of chronic liver disease, liver cirrhosis, hepatocellular carcinoma (HCC) & liver-related mortality worldwide. Viral hepatitis causes more than one million deaths per year, according to the World Health Organisation (WHO), & chronic hepatitis B virus (HBV) and hepatitis C virus (HCV) infections are the main cause of the disease burden. Despite tremendous advances in vaccination programs, antiviral therapies and public health interventions, viral hepatitis remains a significant barrier to achieving the WHO goal of elimination of hepatitis as a public health threat by 2030 [1,12,22]

The five hepatotropic viruses, hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), hepatitis D virus (HDV) and hepatitis E virus (HEV) have unique virological features, routes of transmission and clinical consequences. Acute infection with HAV and HEV is usually self-limiting, whereas HBV, HCV and HDV often lead to chronic infections which can progress to hepatic fibrosis, cirrhosis, liver failure and HCC[8-11,16,18-21,25,26]

Disease progression varies considerably among individuals due to differences in host genetics, immune responses, viral characteristics, environmental factors, and metabolic status, highlighting the limitations of conventional treatment strategies [2,3,16].

Precision medicine is a new approach to disease prevention, diagnosis and treatment that considers molecular, genetic, environmental and clinical information to tailor care to individual patients. In contrast to the traditional "one-size-fits-all" approach, precision medicine recognises the biological heterogeneity of patients and aims to stratify therapeutic interventions according to individual molecular profiles[5,6,13,14]. As such, precision medicine could improve early diagnosis, predict disease progression, identify patients at higher risk of developing cirrhosis or HCC, optimise antiviral treatment, and enable long-term disease surveillance in viral hepatitis [2,3,27-29].

Advances in high-throughput technologies have resulted in the emergence of multi-omics, an integrated approach that studies multiple biological layers in parallel, such as genomics, transcriptomics, proteomics, metabolomics, lipidomics, epigenomics, and microbiomics. In contrast to single-omics analyses, multi-omics approaches combine complementary molecular data to achieve a holistic understanding of host–virus interactions and the complex biological processes underlying disease initiation and progression. [3,4,7,13-15]

Genomic studies have revealed host genetic polymorphisms and viral genomic variations associated with susceptibility to chronic infection, antiviral response and HCC development. Transcriptomic profiling has identified gene expression signatures and regulatory non-coding RNAs involved in immune modulation, fibrosis

and hepatocarcinogenesis[3,16,17,27-29]. More recently artificial intelligence (AI), machine learning and advanced bioinformatics have allowed the integration of complex multi-omics datasets, allowing improved biomarker discovery, patient stratification, disease prediction and clinical decision-making [6,7].

Despite these promising advances, there are several challenges that preclude the routine clinical application of multi-omics-guided precision medicine. However, high analytical costs, limited standardisation, computational complexity, lack of validation in diverse populations, & regulatory barriers continue to be major barriers to widespread clinical adoption[7,13,29]. Emerging technologies such as single-cell multi-omics, spatial omics, CRISPR-based genome editing and explainable AI are expected to overcome many of these limitations and further improve precision hepatology[23,24,30].

This review presents a comprehensive overview of the current advances in multi-omics approaches to precision medicine for viral hepatitis, focusing on biomarker discovery, disease prognosis, personalised therapeutic strategies, artificial intelligence-assisted data integration, current challenges, and future directions for translating precision hepatology into routine clinical practice.

VIRAL HEPATITIS: PATHOGENESIS AND CLINICAL CHALLENGES:

Viral hepatitis is a group of liver diseases caused by five hepatotropic viruses: hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), hepatitis D virus (HDV) and hepatitis E virus (HEV). These viruses share a common target, hepatocytes, and induce liver injury through complex interactions between viral factors and host immune responses, differences in genome structure, routes of transmission, and replication strategies. [1,8-10,16,18-21,25,26].

Multiple host and viral factors including genetic susceptibility, immune responses, viral mutations, metabolic changes, epigenetic regulation, and environmental exposures influence disease progression. Therefore, two patients with the same viral load may have a very different course of the disease & different response to treatment.[2,3,16,17].

Current diagnostic methods such as biochemical tests, detection of viral nucleic acids, serological testing, and liver biopsy are still used for disease assessment .However, liver biopsy, the gold standard for fibrosis assessment, is invasive and not suitable for routine longitudinal monitoring[11,12,27,29].

Recent progress in systems biology has revealed that viral hepatitis is characterized by coordinated changes in the genome, transcriptome, proteome, metabolome, epigenome and lipidome. Combining these molecular layers with multi-omics technologies will enable a comprehensive view of host-virus interactions. This method helps to discover novel biomarkers for prognosis, risk stratification, early diagnosis, and tailored therapies. These advances have resulted in precision medicine, where viral hepatitis is treated at the individual patient level rather than the population level[3,7,13,15,28,30].

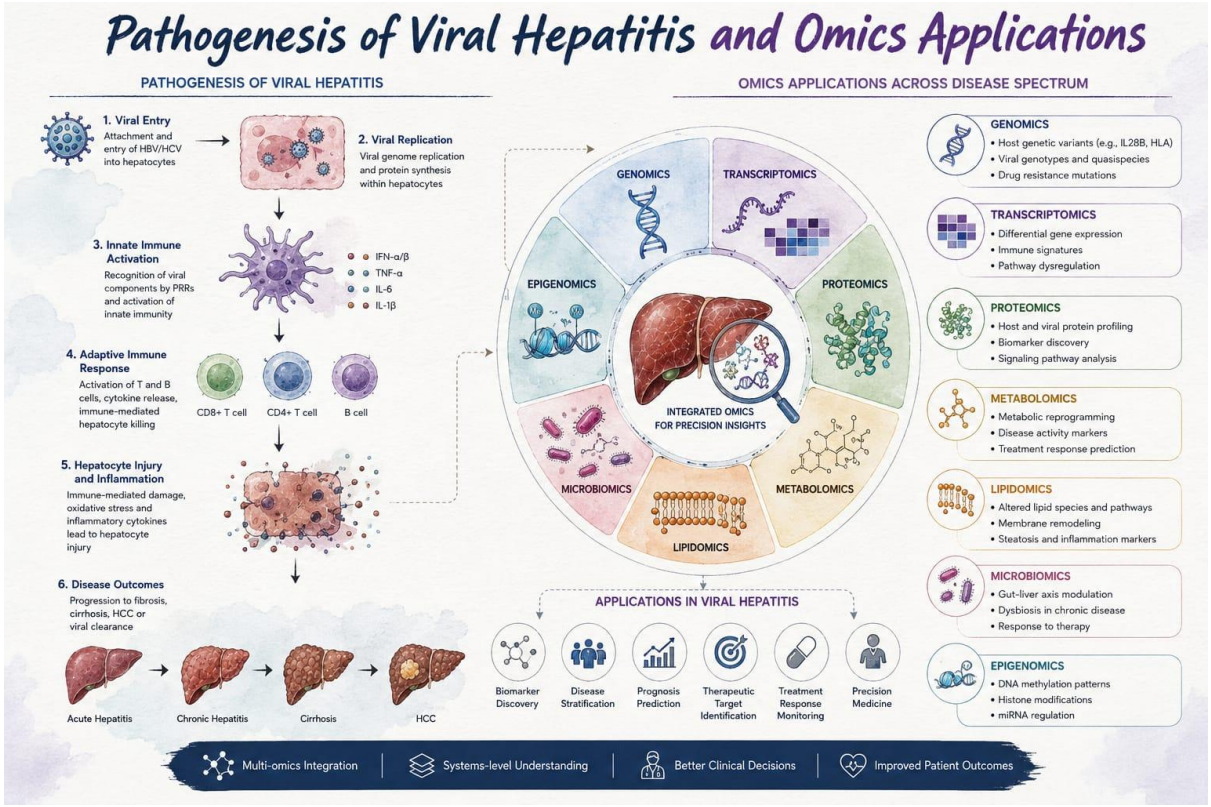


FIGURE 1: AI GENERATED PHOTO

TABLE 1: VIRAL HEPATITIS CLASSIFICATION

Feature	**HAV**	**HBV**	**HCV**	**HDV**	**HEV**
Genome	ssRNA	Partial dsDNA	ssRNA	ssRNA	ssRNA
Transmission	Fecal–oral	Blood, sexual, vertical	Blood	HBV-dependent	Fecal–oral
Chronic infection	No	Yes	Yes	Yes	Rare
Cirrhosis risk	Low	High	High	Very high	Low
HCC risk	No	High	High	High	Rare
Vaccine	Yes	Yes	No	HBV vaccine protects	Limited

MULTI-OMICS TECHNOLOGIES IN PRECISION MEDICINE

Precision medicine is about providing the right care to the right person, at the right time by bringing together data about our molecules. In contrast to formal approaches that rely mostly on non subjective manifestations and routine laboratory tests, precision medicine considers the natural heterogeneity among patients and tailors sanative interventions to the individual molecular characteristics of each patient. The rapid development of high-throughput technologies has allowed the complete analysis of natural systems at several molecular levels, leading to the concept of multi-omics. [4-7,13,14].

Multi-omics is the simultaneous analysis of different omics datasets like genomics, transcriptomics, proteomics, metabolomics, lipidomics, epigenomics, and microbiomics to give a holistic view of disease biology. While single omics approaches provide invaluable insights, integration of these complementary datasets allows a systems-level perspective of complex diseases that cannot be achieved by single omics analysis. [3,4,7,13,15]

The course of viral hepatitis is influenced by the complex interactions of viral and host factors, immune responses, metabolic changes and environmental factors. These interrelated molecular networks govern viral persistence, immune escape, fibrosis evolution, sanative response, and development of hepatocellular carcinoma. [2,3,16,17].

Recent advances in next-generation sequencing, high-resolution mass spectrometry, nuclear magnetic resonance spectroscopy and bioinformatics have made it possible to generate large-scale omics datasets. The combination of these datasets enables us to find disease-related molecular signatures, natural pathways and regulatory networks that result in improved diagnostic accuracy and sanative decision-making.[4,7,13,15]

The non-subjective uses of multi-omics in viral hepatitis have been rapidly and continuously expanded. Furthermore, the combination of multi-omics data with artificial intelligence (AI) and machine learning algorithms improves tolerant stratification, predicts nonsubjective outcomes, and facilitates personalized treatment approaches by revealing hidden molecular patterns within complex natural datasets [2,6,7,27-30].

Nevertheless, despite these advances, several challenges remain before multi-omics can be routinely implemented in non-subjective hepatology. However, continued improvements in sequencing technologies, computational biology and AI driven analytics are expected to accelerate the translation of multi-omics discoveries into precision hepatology, ultimately improving patient outcomes and supporting the global elimination of viral hepatitis [6,7,13,29,30].

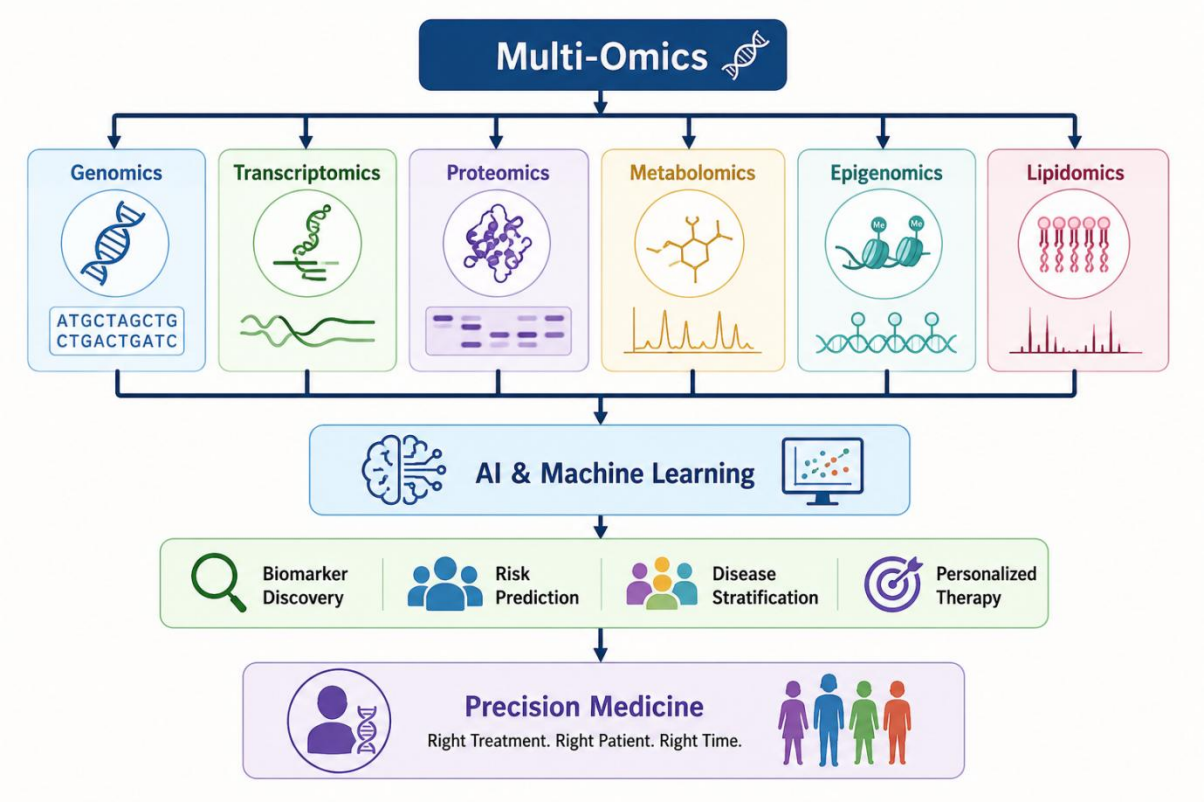


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TABLE 2 MAJOR TYPES OF OMICS:

Omics platform	Biological target	Major technology	Clinical application
Genomics	DNA	Whole-genome sequencing, GWAS	Genetic susceptibility, antiviral response
Transcriptomics	RNA	RNA-seq, scRNA-seq	Gene expression,
Proteomics	Proteins	LC-MS/MS	Biomarker discovery, therapeutic targets
Metabolomics	Metabolites	LC-MS, GC-MS, NMR	Disease diagnosis, metabolic profiling
Lipidomics	Lipids	LC-MS/MS	Lipid dysregulation, fibrosis biomarkers
Epigenomics	DNA methylation, histones	Bisulfite sequencing, ChIP-seq	Gene regulation, HCC prediction

GENOMICS: FOUNDATION OF PRECISION MEDICINE IN VIRAL HEPATITIS

Genomics investigates the complete genetic composition of an organism, to understand how genetic variations influence disease susceptibility, progression & therapeutic response. In viral hepatitis, genomic studies have transformed our understanding of host–virus interactions.These discoveries have established genomics as a cornerstone of precision medicine, enabling individualized risk assessment and therapeutic decision-making [2-5,13,15].

whole-genome sequencing(WGS) & whole-exome sequencing (WES) technologies help us look at the genomes of the host & the virus. It is more sensitive. Can look at a lot of genetic markers at the same time, that are relevant to viral hepatitis. This is really important for understanding the disease and for finding treatments. [4,13,15].

The virus itself can also change in ways that help it avoid being detected by the body's system making it harder to treat and increasing the risk of liver cancer. When we look at the changes in the virus especially in the HBV basal core promoter and pre-core regions we can use that information to create a treatment plan that is tailored to the individual and to keep a close eye on the disease over time. This helps us choose the antiviral therapy, for each person and makes it easier to monitor the disease in the long run[2,3,8-10,16].

Genomic profiling also aids in pharmacogenomics, a component of precision medicine that looks at the relationship between genetic variation and drug response. By identifying genetic markers that are associated with either antiviral efficacy or adverse drug reactions, clinicians can optimize their choice of treatment, minimize toxicity and improve therapeutic outcomes. Furthermore, the integration of host and viral genomic information allows for the risk stratification of fibrosis progression & surveillance of hepatocellular carcinoma, enabling more personalized patient management. [5,6,13].

While promising in the clinical setting, genomic medicine has faced many challenges. The high cost of sequencing, limited availability in resource limited settings, difficulties in interpretation of variants of unknown significance and ethical concerns regarding privacy of genetic data, continue to limit routine clinical implementation. Thus, genomics is increasingly integrated with other omics technologies to achieve a more complete understanding of viral hepatitis biology. [4,7,13]

TABLE 3: APPLICATIONS OF GENOMICS OF PRECISION MEDICINE IN VIRAL HEPATITIS

Application	**Clinical significance**
Hostgenetic polymorphisms	Predict susceptibility to chronic infection and disease progression
Viral genome sequencing	Detect viral mutations and antiviral resistance
GWAS	Identify disease-associated genetic variants
Pharmacogenomics	Optimize antiviral drug selection and minimize adverse effects
HCC risk prediction	Identify patients requiring intensive surveillance

Application	Clinical significance
Precision medicine	Support individualized diagnosis and treatment

TRANSCRIPTOMICS: UNDERSTANDING GENE EXPRESSION DYNAMICS IN VIRAL HEPATITIS

Transcriptomics is the study of all RNA transcripts expressed in a particular cell or tissue under defined physiological or pathological conditions. Transcriptomics gives a dynamic picture of gene expression and the regulatory mechanisms that influence disease progression. Transcriptomic profiling in viral hepatitis has greatly improved the understanding of host immune responses, viral persistence, inflammation, fibrosis and hepatocellular carcinoma (HCC), making it an essential tool for precision medicine. [3,4,7,13,15].

RNA sequencing, single-cell RNA sequencing, bulk transcriptomics & microarray technologies have provided sensitive, comprehensive and high-resolution analyses of coding & non-coding RNAs. These methods identify differential gene expression, signaling pathways & transcriptional networks associated with disease severity & therapeutic response. [4,15,24].

Sustained activation of inflammatory pathways causes immune exhaustion, hepatic fibrosis and progressive liver damage. Moreover, abnormal expression of genes involved in cell-cycle regulation, angiogenesis and DNA repair has been associated with hepatocarcinogenesis and has provided useful molecular signatures for disease prognosis.[2,3,16,17].

For example, miR-122, the most abundant liver-specific microRNA, plays an important role in HCV replication and has become both a therapeutic target and a biomarker of liver injury. [2,17]

In the clinic, transcriptomic profiling has allowed the identification of gene-expression signatures that can predict the response to antiviral therapy, the progression of fibrosis and the risk of HCC. Such integrated analyses are increasingly combined with artificial intelligence (AI) algorithms to identify clinically relevant molecular patterns from large-scale datasets. [6,7,13,30]

Transcriptomics has several limitations. Transcript abundance does not always correlate with protein expression or biological function, highlighting the necessity of integrating transcriptomic data with complementary omics platforms. However, progress in single-cell sequencing, spatial transcriptomics, and AI-based data analysis is expected to enhance molecular characterization of viral hepatitis and foster clinical translation of precision hepatology.[7,13,24]

Table 4: Clinical applications of transcriptomics in viral hepatitis

Transcriptomic approach	Major findings	Clinical significance
RNA sequencing (RNA-seq)	Differential gene expression	Disease diagnosis & prognosis
Single-cell RNA sequencing	Cellular heterogeneity and immune landscape	Precision patient stratification

Transcriptomic approach	Major findings	Clinical significance
MicroRNA profiling	miR-122 & immune-regulatory miRNAs	Biomarkers & therapeutic targets
Long non-coding RNA analysis	Fibrosis and HCC-associated lncRNAs	Prognostic biomarkers
Integrated transcriptomics	Pathway & network analysis	Personalized therapeutic strategies

PROTEOMICS: DECIPHERING FUNCTIONAL PROTEIN NETWORKS IN VIRAL HEPATITIS

Proteomics is the study of proteins means how proteins are made & how they work together & what happens to them after they are made. Proteins are the molecules that do things inside cells.

Proteomics is different, from genomics & transcriptomics. Proteomics shows us what is actually happening inside cells when a virus is present & a disease is getting worse. Proteomics are important for giving the right treatment to people, which is called precision medicine. It help us to understand what is going on with hepatitis & other diseases.[3,4,7,13]

Recent advances in liquid chromatography–tandem mass spectrometry (LC-MS/MS), matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF), two-dimensional gel electrophoresis (2D-GE), & quantitative proteomics have enabled comprehensive profiling of liver tissue, serum, and plasma proteins. These technologies facilitate the identification of differentially expressed proteins involved in immune regulation, inflammation, fibrosis, and hepatocellular carcinoma (HCC), thereby providing valuable biomarkers for disease diagnosis and prognosis[13,14,15].

Increased expression of inflammatory mediators such as C-reactive protein (CRP), serum amyloid A (SAA), complement components, transforming growth factor-β (TGF-β), and matrix metalloproteinase (MMPs) has been correlated with progressive liver fibrosis and cirrhosis. Likewise, changes in proteins regulating cell proliferation, angiogenesis, and apoptosis contribute to hepatocarcinogenesis and may serve as potential therapeutic targets[2,16,17].

Despite these advances, proteomic research faces several challenges, including the wide dynamic range of serum proteins, variability in sample preparation, limited reproducibility across analytical platforms, and difficulties in translating experimental biomarkers into routine clinical practice. [7,13,14]

METABOLOMICS AND LIPIDOMICS: IDENTIFYING METABOLIC SIGNATURES IN VIRAL HEPATITIS

Metabolomics and lipidomics are fast developing parts of precision medicine that shed functional light on biochemical changes. Metabolomics is a holistic interrogation of small endogenous metabolites, whereas lipidomics is the qualitative and quantitative profiling of cellular lipids. Together, these approaches capture the

downstream effects of genomic, transcriptomic, and proteomic changes, offering a real-time window into cellular physiology and disease state[13,14,15].

Technological advances in liquid chromatography–mass spectrometry, gas chromatography–mass spectrometry & nuclear magnetic resonance spectroscopy have enabled high-throughput profiling of metabolites and lipid species in serum, plasma, urine and liver tissue. These platforms detect changes in amino acids, organic acids, bile acids, phospholipids, sphingolipids and fatty acids, which provide valuable information on perturbed metabolic pathways during viral infection.[13,14].

Increased lactate, abnormal glutamine metabolism, and disturbances of branched-chain amino acids have been described in patients with advanced liver disease and reflect mitochondrial dysfunction and impaired hepatic energy metabolism. Such metabolic signatures could be useful as non-invasive biomarkers for disease staging and prognosis. [2,15,27]

In chronic viral hepatitis there are also marked changes in the lipid metabolism. Accumulation of increased ceramides and free fatty acids contributes to oxidative stress, chronic inflammation and activation of hepatic stellate cells thereby promoting fibrosis and hepatocellular carcinoma. On the other hand, decreased phosphatidylcholine and bile acid homeostasis have been linked to liver dysfunction and disease progression. [2,3,16,28].

Metabolomic and lipidomic profiling has great potential for precision hepatology in the clinical setting. Integrated metabolic signatures can discriminate patients with acute or chronic hepatitis, identify patients with high risk of fibrosis or cirrhosis, predict response to antiviral treatments and allow early detection of HCC. These techniques, combined with traditional clinical markers and other omics datasets, improve disease stratification and aid in personalised therapeutic decision-making.[6,7,13,29]

Metabolic profiles are affected by diet, age, use of medication, gut microbiota composition and environmental factors, which may contribute to variability among studies. Additional difficulties are introduced by differences in analytical platforms, sample preparation & data processing, making comparisons across studies difficult. [7,13,14]

EPIGENOMICS: EPIGENETIC REGULATION IN VIRAL HEPATITIS

Epigenomics is the study of heritable, reversible changes in gene expression without the DNA sequence. These include DNA methylation, histone modifications, chromatin remodelling & non-coding RNA-mediated regulation. All of these are important in the control of cellular differentiation, immune responses and viral persistence. Epigenetic changes play a major role in the development of fibrosis, cirrhosis and hepatocellular carcinoma (HCC) in viral hepatitis, making epigenomics important in precision medicine. [3,13,14].

Chronic HBV and HCV infection induce global epigenetic reprogramming of the viral and host genomes. HBV covalently closed circular DNA is the transcriptional template for viral replication and is regulated by histone acetylation and methylation. These epigenetic marks are dynamic and influence viral gene expression and replication and, thus, treatment response and disease persistence. HCV infection also modifies host transcriptional programs, promoting chronic inflammation, oxidative stress and hepatocarcinogenesis [8,16,17].

DNA methylation is one of the most studied epigenetic mechanisms in the context of viral hepatitis. Aberrant methylation of the promoter regions of tumor suppressor genes such as RASSF1A, CDKN2A and SOCS1 has been associated with hepatic fibrosis and HCC development. These methylation signatures have been developed as promising biomarkers for early diagnosis and risk stratification in patients with chronic liver disease. [2,3,13]

For instance, aberrant levels of acetylated and methylated histones affect the expression of numerous genes encoding for proteins involved in interferon signaling, cytokine production, extracellular matrix remodeling, and hepatic stellate cell activation. Thus, there is a broad range of transcription & epigenetic-based mechanisms that contribute to the development of viral hepatitis [17,24].

It is clinically relevant to consider epigenomic biomarkers for precision hepatology because they can enable early diagnosis of fibrosis and hepatocellular carcinoma (HCC), predict treatment outcome, and identify those at higher risk for disease progression. Epigenomic therapies, such as CRISPR technologies that target DNA methylation and histone post-translational modifications, may also be used to silence viral functions and pathological gene expression. [23,24]

In addition to the mentioned achievements, clinical implementation of the described ways of epigenetic modifications is hampered by such factors as tissue-specificity and inter-individual variability. However, the integration of genomic, transcriptomic, proteomic, metabolomic, and epigenomic information will enable more accurate understanding of the molecular mechanisms underlying viral hepatitis & contribute to the individualization of diagnostic conclusions and treatment outcomes [7,13,14].

TABLE 5: MAJOR EPIGENETIC MECHANISMS AND THEIR CLINICAL SIGNIFICANCE IN VIRAL HEPATITIS

Epigenetic mechanism	Biological role	Clinical significance
DNA methylation	Regulation of gene transcription	Biomarkers for fibrosis and HCC risk
Histone acetylation and methylation	Control of chromatin accessibility	Regulation of viral replication and inflammation
Chromatin remodeling	Modulation of gene expression	Disease progression and therapeutic response
MicroRNAs (miRNAs)	Post-transcriptional gene regulation	Diagnostic and prognostic biomarkers
Long non-coding RNAs (lncRNAs)	Epigenetic and transcriptional regulation	Fibrosis progression and HCC development

ARTIFICIAL INTELLIGENCE AND MULTI-OMICS INTEGRATION IN PRECISION HEPATOLOGY

The increasing availability of high dimensional multi-omics datasets has created unprecedented opportunities for precision medicine but has also introduced significant analytic challenges. Genomic, transcriptomic, proteomic,

metabolomic, and epigenomic datasets contain millions of variables that cannot be efficiently interpreted using conventional statistical approaches. Consequently, near intelligence (AI), machine learning (ML), and artful learning (DL) have become essential tools for integrating disparate datasets and extracting clinically suggestive biological information[6,7,15].

AI can help analyze patterns in molecular interactions, classify disease categories, determine treatments, and predict the possibility of fibrosis progression or hepatocellular carcinoma. Algorithms, such as supervised learning models, are applied to learn the associations between biomarkers and disease categories in the data; hence, they can identify biomarkers and classify the diseases. Furthermore, deep learning models can make accurate predictions by detecting complex associations in multidimensional data. [6,7]

In viral hepatitis, AI-assisted integration of multi-omics data has enabled identification of molecular signatures associated with antiviral response, immune dysregulation, and HCC development. Combining omics data with non-subjective variables, imaging findings, & electronic health records improves symptomatic precision & supports individualised treatment planning. Moreover, interpretable AI models are progressively being developed to enhance transparency and facilitate non-subjective implementation [2,6,30].

Despite the above-outlined opportunities, there are several challenges related to data standardization, model interpretation, computational complexity, and external validation that need to be addressed for adopting AI-based multi-omics techniques in routine clinical practice.

10. CHALLENGES AND FUTURE PERSPECTIVES

At the current state in medicine, the major setback to the clinical application of multi-omics technology to viral hepatitis is the large-scale data storage and analysis. Furthermore, the lack of sampling and processing standards within the multi-omics field has made validating multi-omics technology for viral hepatitis extremely challenging [7,13,14].

Economic barriers go hand in hand with the technological constraints. The developing nations that have the most cases of viral hepatitis lack the infrastructure to implement the expensive battery of high-throughput analysis. The defence of donor genomic data, informed consent gaps, data sharing, and bias in the analyses, have to be addressed. [5,6].

The future of precision medicine in hepatology is bright. Soon technology will allow medicine to explore virus & host interactions even further. The combination of these technologies and artificial intelligence will help integrate disease monitoring and personal treatment in real time.[23,24]

Nevertheless, ongoing improvements in sequencing technologies, computational biology, and AI driven analytics are expected to accelerate the translation of multi-omics discoveries into precision hepatology, ultimately improving patient outcomes and supporting the global elimination of viral hepatitis [6,7,13,29,30]

TABLE 6: CURRENT CHALLENGES AND FUTURE DIRECTIONS

Current challenge	Future solution
High analytical cost	Affordable sequencing technologies
Data integration complexity	AI-based computational platforms
Lack of standardized protocols	International harmonization guidelines
Limited clinical validation	Large multicenter prospective studies
Ethical and privacy concerns	Robust governance and secure data-sharing frameworks

11. CONCLUSION

Multi-omics technologies also support clinical artificial intelligence in the complex data analysis that is required for the discovery of new clinical biomarkers & the development of personalized medicine and targeted therapies. While there are hurdles that include high costs, a lack of standardisation, computational burden & a need for further clinical validation, we predict that the ongoing technological advancement will bring multi-omic technologies into everyday clinical practice.

When technologies such as single-cell resolution, spatial-omics, AI-centric analytics, & genome-editing become more refined and accessible, we can expect that diagnostic criteria & clinical prognostic evaluations will be more accurate in predicting disease states and create more targeted pharmaceutical interventions. Precision medicine is a multidisciplinary enterprise & viral Hepatitis is a prime example where we can expect more active participation in relevant domains to improve outcomes for patients and expand efforts to eradicate Hepatitis on a global scale.

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