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Review Paper

A Review on the Role of Metabolomics in Kidney Disease: Current Applications and Future Perspectives

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ABSTRACT

Kidney diseases, such as chronic kidney disease (CKD), acute kidney injury (AKI), kidney transplantation complications, and nephrolithiasis, pose significant global health challenges. Current diagnostic tools often detect the disease at advanced stages, limiting opportunities for early intervention. This narrative review evaluated the role of metabolomics in enhancing the understanding, diagnosis, and management of major kidney disorders, drawing exclusively on recent peer-reviewed studies. The review synthesized findings from comprehensive urine and plasma metabolomic analyses using nuclear magnetic resonance (NMR) and mass spectrometry (MS) platforms in pediatric and adult patients across multiple kidney settings. Metabolomics reveals disease-specific metabolic signatures, enabling the early detection of renal injury, differentiation between disease subtypes, and prediction of outcomes. In CKD, altered profiles of amino acids, energy metabolites, and gut-derived compounds correlate with disease progression. In AKI, early fluctuations in citrate, branched-chain amino acids, and bile acids demonstrate diagnostic and prognostic potential. In kidney transplantation, metabolomics aids in the detection of acute rejection and drug-induced toxicity. For nephrolithiasis, changes in oxalate and citrate metabolism reveal insights into gut-kidney axis interactions. The integration of metabolomics with other omics (genomics, proteomics, and microbiomics) enhances mechanistic understanding and supports the development of precision nephrology. Metabolomics is redefining kidney disease evaluation by providing sensitive, real-time, and non-invasive insights into renal pathophysiology. Continued advances in analytics, data integration, and clinical validation will be essential for translating these findings into personalized nephrology practice.

Keywords: Metabolomics, Kidney disease, Chronic kidney disease (CKD), Acute kidney injury (AKI), Transplantation

Introduction

Kidney diseases, encompassing chronic kidney disease (CKD), acute kidney injury (AKI), nephrolithiasis, and transplant-related complications, represent a significant and growing global health burden. Rising incidence rates, combined with high morbidity and mortality, underscore the urgent need for improved strategies in early diagnosis, risk stratification, and personalized treatment, especially in children. The need for early and accurate diagnosis, as well as individualized treatment strategies, is greater than ever. Traditional biomarkers, such as serum creatinine, estimated glomerular filtration rate (eGFR), and urine output, remain limited in sensitivity and specificity, often reflecting damage only after significant functional loss has occurred. Furthermore, these conventional markers do not adequately differentiate between various renal pathologies or allow for precise disease stratification. Metabolomics—the comprehensive study of small molecule metabolites within biological samples—has emerged as a powerful approach to fill this diagnostic and prognostic gap. Through advanced analytical platforms, such as nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry (MS), metabolomics enables researchers to capture dynamic biochemical alterations associated with both early- and late-stage kidney diseases. These metabolic changes not only reflect organ-specific injury but may also uncover systemic responses, such as inflammation, oxidative stress, and energy metabolism dysregulation. A recent systematic review of pediatric and adult studies further confirmed consistent alterations in energy metabolism and inborn errors among CKD patients, emphasizing the diagnostic value of metabolomics. Recent studies in both adult and pediatric populations have demonstrated the value of urine and plasma metabolomic profiling in identifying early markers of renal injury, distinguishing between disease subtypes, predicting disease progression, and monitoring therapeutic response. As a result, metabolomics is not only enhancing our understanding of kidney disease pathogenesis but is also paving the way toward personalized nephrology. Metabolomics is emerging as a cornerstone of precision nephrology, with the potential to fundamentally reshape how kidney diseases are understood and managed [1]. This review aimed to highlight the importance of using metabolomics for the early detection and management of renal disease.

Overview of Metabolomics

Metabolomics is the comprehensive analysis of low molecular weight metabolites in biological systems, capturing a snapshot of physiological and pathological processes in real time. It sits downstream of genomics, transcriptomics, and proteomics, offering an integrated view of cellular activity that reflects both genetic programming and environmental influences [1]. In the context of kidney diseases, metabolomics enables the detection of subtle biochemical changes long before structural or functional impairment becomes clinically evident [2, 3]. Several analytical techniques are used in metabolomics, most notably NMR spectroscopy and MS, often coupled with chromatographic separation, such as liquid chromatography (LC) or gas chromatography (GC). Each platform has its strengths:

1) NMR spectroscopy offers non-destructive analysis, excellent reproducibility, and minimal sample preparation, making it particularly valuable for longitudinal studies [4, 5]; 2) MS, especially when paired with LC or GC, provides high sensitivity and the ability to detect a broad spectrum of metabolites at very low concentrations [6].

Two major approaches dominate the field:

1) Targeted metabolomics focuses on quantifying known metabolites within specific biochemical pathways, which is useful for hypothesis-driven research or clinical monitoring [1]; 2) Untargeted metabolomics aims to identify as many metabolites as possible in an unbiased manner, enabling the discovery of novel biomarkers and unforeseen metabolic shifts [3].

Importantly, metabolomic profiling is highly adaptable to various biological fluids, including urine, plasma, serum, dialysate, and even saliva, each offering a different window into systemic and organ-specific processes. Urine, in particular, is frequently used in nephrology due to its direct contact with renal tissue and its non-invasive nature of collection [4]. Together, these features make metabolomics a uniquely powerful tool in nephrology research, diagnostics, and biomarker discovery—offering opportunities to detect disease earlier, monitor it more accurately, and understand its underlying mechanisms with greater depth [3].

Metabolomics in CKD

CKD involves a progressive loss of renal function over time, often culminating in end-stage renal disease. While traditional biomarkers, such as serum creatinine and eGFR are widely used for clinical staging, they are late indicators of kidney damage and do not provide insight into the underlying pathophysiology [2, 3]. Metabolomics offers a powerful complementary approach, capable of identifying early metabolic disturbances and novel biomarkers for disease progression and complications [2]. Several studies have demonstrated that CKD is associated with widespread alterations in metabolic pathways. These include disruptions in the tricarboxylic acid (TCA) cycle, amino acid metabolism, purine and pyrimidine turnover, and fatty acid oxidation [2, 3]. Plasma and urine metabolomic profiling has consistently revealed increased levels of uremic toxins, such as indoxyl sulfate, p-cresyl sulfate, and kynurenine pathway metabolites, which are poorly cleared due to reduced kidney function [1, 3]. In addition, levels of protective metabolites, such as citrate, hippurate, and short-chain fatty acids tend to decrease with CKD progression, reflecting impaired tubular function and gut dysbiosis [2]. A notable advantage of metabolomics in CKD is its capacity for disease stage stratification. Profiles of plasma metabolites differ significantly across CKD stages, with progressive accumulation of certain toxic compounds and depletion of energy-related intermediates [7]. Such profiles are not only useful for disease monitoring but also for identifying patients at risk of rapid decline or cardiovascular complications [3]. In pediatric CKD, metabolomic studies have highlighted age-specific metabolic disturbances. Alterations in branched-chain amino acids, methyl histidine, and lipid species have been reported, suggesting early-onset disruptions in muscle and mitochondrial metabolism [8]. Moreover, differences in gut-derived metabolites between children and adults point to age-dependent interactions between the gut microbiome and renal function [1, 2]. Overall, metabolomics is contributing to a more nuanced understanding of CKD pathogenesis and holds the potential for improving early diagnosis, risk prediction, and individualized therapy. Future integration of metabolic profiles with clinical, genetic, and imaging data may further enhance precision nephrology approaches for CKD management [1, 3]. Recent targeted metabolomics research by Zhu et al. compared plasma metabolic profiles among pre-dialysis CKD stage 5 patients, hemodialysis (HD) patients, and peritoneal dialysis (PD) patients [9]. The study revealed significant alterations in cysteine and methionine metabolism, with elevated levels of kynurenic acid and S-adenosylhomocysteine in both dialysis groups compared to pre-dialysis patients, and a marked reduction in glutamine levels. These metabolite changes may contribute to the heightened cardiovascular risk observed in dialysis populations. Moreover, distinct differences were identified between HD and PD patients, suggesting that the mode of dialysis itself can shape the systemic metabolic milieu. These findings underscore the utility of metabolomics in characterizing treatment-specific metabolic shifts and tailoring therapeutic strategies in advanced CKD [9]. In addition to age-specific metabolic alterations, emerging evidence also underscores the impact of gut-derived metabolites on cardiovascular health in pediatric CKD patients. Schlender et al. reported that children with CKD exhibit an increased cardiovascular risk even in the absence of traditional factors, such as hypertension or diabetes [10]. This risk is linked to CKD-related dysbiosis, which reduces protective short-chain fatty acids and elevates harmful uremic solutes, like indoxyl sulfate and p-cresyl sulfate. These microbial metabolites impair gut barrier function, induce systemic inflammation, and promote endothelial dysfunction. Such findings emphasize the need to consider microbiota-targeted therapies as part of a comprehensive approach to managing pediatric CKD and its cardiovascular complications [10]. Although metabolomics has uncovered many CKD-related signatures, a study found no solute differences between HD patients with and without pruritus, suggesting its complex etiology beyond current detection methods [11].

Metabolomics in AKI

AKI is a rapid and often reversible decline in kidney function that is frequently encountered in critically ill patients. It is associated with increased morbidity, longer hospital stays, and a higher risk of progression to CKD. However, current diagnostic tools—primarily serum creatinine and urine output—lack sensitivity and specificity, particularly in the early stages [3]. Metabolomics has emerged as a promising method to fill this diagnostic void by detecting subtle biochemical changes that precede overt renal dysfunction [5]. Urine-based metabolomic profiling, especially using NMR spectroscopy, has shown considerable utility in identifying AKI-specific signatures. Studies in pediatric and neonatal intensive care units have demonstrated that metabolic profiles can distinguish AKI patients from both healthy individuals and critically ill non-AKI controls with high accuracy. A panel of four urinary metabolites—citrate, leucine, valine, and bile acids—was found to differentiate AKI patients with an area under the curve (AUC) exceeding 0.9. Citrate levels were consistently reduced, while branched-chain amino acids and bile acids were elevated, reflecting impaired tubular function and altered amino acid metabolism [5]. Moreover, metabolomics provides insights into the heterogeneity of AKI etiologies. For example, specific patterns have been associated with septic shock, hemolytic uremic syndrome, and dehydration, although discrimination among etiologies remains a challenge in small cohorts. Some markers, such as fumarate and cis-aconitic acid, also correlate with mitochondrial dysfunction and oxidative stress—central mechanisms in AKI pathogenesis [5, 6]. One of the strengths of metabolomic approaches is their ability to identify patients at risk of adverse outcomes. In validation studies, metabolite panels accurately predicted the need for renal replacement therapy and even short-term mortality. This predictive power may guide early clinical interventions and improve prognostic stratification [5]. Additionally, integrating metabolomics with clinical and demographic data has revealed the influence of age, particularly in neonates, on urine metabolic profiles. This underscores the need for age-specific reference standards when applying metabolomics in pediatric nephrology [5]. In summary, metabolomics provides a powerful, non-invasive tool for early diagnosis, subtype differentiation, and outcome prediction in AKI. As methodologies advance and validation studies expand, metabolomics is poised to become a cornerstone in the clinical management of acute renal injury [12]. Emerging evidence suggests that metabolomic profiling holds promise in predicting AKI in patients with cirrhosis. Traditional biomarkers often fail to detect early renal dysfunction in this population due to the complex interplay between liver and kidney pathophysiology. Metabolomics offers a comprehensive approach by capturing subtle metabolic alterations preceding overt kidney injury. Identifying specific metabolic signatures associated with AKI risk could facilitate early intervention strategies, potentially improving outcomes in cirrhotic patients. This perspective underscores the need for further studies to validate metabolomic biomarkers and integrate them into clinical practice for timely AKI detection in liver disease contexts [13]. In addition to ischemic and toxic etiologies, metabolomics has been instrumental in elucidating the pathophysiological mechanisms underlying heat stroke-induced AKI (HS-AKI). The other study conducted a comprehensive metabolomic analysis and identified significant disruptions in amino acid and lipid metabolism pathways in HS-AKI patients. Notably, alterations in the TCA cycle and increased levels of oxidative stress markers were observed, suggesting mitochondrial dysfunction as a central feature of HS-AKI. These findings underscore the potential of metabolomic profiling in identifying specific biomarkers for early detection and targeted therapeutic strategies in HS-AKI [14].

Metabolomics in Kidney Transplantation

Kidney transplantation is the treatment of choice for end-stage renal disease, offering improved survival and quality of life compared to dialysis. However, long-term graft survival remains suboptimal due to complications, such as acute rejection, chronic allograft dysfunction, and drug-induced nephrotoxicity. Traditional monitoring strategies, like serum creatinine levels, proteinuria, and histological assessment via biopsy are limited by low sensitivity and invasiveness. Metabolomics offers a promising, non-invasive alternative for early detection and mechanistic insight into graft-related complications [8]. Urinary and plasma metabolomic profiles have been shown to reflect the functional status of the renal allograft. Studies using NMR and LC-MS platforms have identified distinct metabolic fingerprints associated with acute rejection. These include elevated levels of tryptophan-derived metabolites, bile acids, branched-chain amino acids, and reduced citrate levels. Such alterations mirror immune activation, mitochondrial stress, and proximal tubule dysfunction [15]. Importantly, metabolomic patterns have also been linked to chronic allograft injury, where lipid peroxidation products, changes in phospholipid metabolism, and increased levels of oxidative stress markers have been observed. These profiles may distinguish progressive fibrosis and atrophy from stable graft conditions even before histologic changes are apparent [8]. Moreover, metabolomics has shown utility in assessing nephrotoxicity related to immunosuppressive therapy. For example, alterations in taurine, creatine, and polyamine levels have been associated with tacrolimus-induced tubular injury. These findings could allow clinicians to tailor immunosuppressive regimens to minimize renal damage without compromising graft protection [16]. In pediatric transplant recipients, metabolomic profiling has helped to identify metabolic shifts unique to younger age groups, which differ from adult patterns due to developmental factors, drug metabolism, and immune responsiveness [8]. Furthermore, integrating metabolomic data with clinical, proteomic, and immunologic markers has enhanced diagnostic accuracy. Emerging predictive models combining these variables are being tested for early identification of subclinical rejection and long-term graft outcome prediction [1, 8]. In conclusion, metabolomics provides a sensitive, dynamic, and non-invasive means of monitoring kidney transplant function. Its integration into clinical workflows could reduce the need for invasive biopsies, enable early therapeutic adjustments, and ultimately improve graft longevity [17]. Recent advancements have highlighted the utility of metabolomic analyses in non-invasively monitoring kidney transplant recipients. Iwamoto et al. performed metabolomic profiling on plasma, urine, and saliva samples from transplant recipients, revealing distinct metabolic signatures associated with graft function and rejection episodes. Notably, elevated levels of 3-indoxyl sulfate were observed in both plasma and urine of patients experiencing T cell-mediated rejection, underscoring its potential as a biomarker for early detection of rejection. These findings emphasize the promise of integrating metabolomic assessments into routine post-transplant surveillance to enhance patient outcomes [14].

Metabolomics in Kidney Stone Disease

Nephrolithiasis, or kidney stone disease, is a prevalent urological condition characterized by crystal aggregation within the urinary tract. Although its diagnosis is often straightforward through imaging, understanding the underlying metabolic disturbances remains challenging. Metabolomics provides a unique opportunity to investigate systemic and urinary metabolic signatures associated with stone formation, recurrence, and stone composition [4]. Urine is the most informative biofluid in stone disease research, as it directly reflects renal excretory function and crystal-forming risk. Metabolomic profiling of urine has revealed specific alterations in patients with calcium oxalate and uric acid stones. In calcium stone formers, reduced excretion of citrate—a known inhibitor of crystallization—is a recurring finding, alongside increased excretion of oxalate, glyoxylate, and glycolate. These shifts suggest a disturbance in glyoxylate metabolism and impaired mitochondrial function [18]. In contrast, uric acid stone formation is often associated with acidic urine and altered purine metabolism. Metabolomic studies have demonstrated increased urinary levels of uric acid precursors and reduced levels of ammonium, pointing to defective acid buffering capacity and renal tubular dysfunction [4]. Notably, the gut microbiome plays an important role in modulating stone risk. Gut-derived metabolites, such as indoxyl sulfate, p-cresol, and trimethylamine-N-oxide (TMAO) are elevated in many stone formers, indicating microbial dysbiosis and its contribution to lithogenic potential [3, 4]. This gut-kidney axis offers a novel therapeutic target, potentially involving dietary modulation or probiotic intervention. Emerging research in pediatric nephrolithiasis shows that children exhibit distinct metabolomic signatures compared to adults. Changes in amino acid profiles, citrate, and phosphate metabolism suggest age-specific vulnerability to metabolic imbalances and stone recurrence [19]. In addition to diagnosis, metabolomics has the potential to predict recurrence risk. Longitudinal studies tracking urinary metabolite changes post-treatment or dietary interventions have identified patterns associated with stone recurrence, offering the potential for personalized prevention strategies [4]. Ultimately, metabolomics not only enhances our understanding of the biochemical pathways underlying stone formation but also opens avenues for targeted, non-invasive risk assessment and prevention in both adult and pediatric populations [3, 4]. Recent advancements in metabolomic analyses have shed light on the intricate biochemical pathways involved in nephrolithiasis. Kowalczyk et al. highlighted that alterations in amino acid metabolism, energy production, and gut-derived metabolites play pivotal roles in stone formation. Notably, disruptions in oxalate metabolism and the TCA cycle were observed, suggesting a link between systemic metabolic disturbances and stone pathogenesis. These findings underscore the potential of metabolomics in identifying novel biomarkers for early detection and personalized management of kidney stone disease [15].

Metabolomics in Glomerulonephritis (GN)

GN is a significant contributor to CKD, often leading to end-stage renal failure. Traditional diagnostic methods, such as kidney biopsies, are invasive and may not fully capture the disease's complexity. Recent advancements in omics technologies have opened new avenues for understanding GN's pathophysiology. A systematic review by Davies et al. evaluated 27 studies encompassing 1,818 participants, focusing on the use of proteomics and metabolomics in GN. The analysis revealed that these omics approaches could identify potential biomarkers related to disease phenotype, progression risk, and treatment response. Samples analyzed included urine, blood, and kidney biopsies, demonstrating the versatility of these techniques. The findings underscore the promise of metabolomics and proteomics in developing non-invasive diagnostic tools and personalized treatment strategies for GN. However, the review also highlights the need for larger-scale studies to validate these potential biomarkers and fully integrate omics technologies into clinical practice [16].

Integration with Other Omics Technologies

While metabolomics provides a real-time snapshot of the biochemical status of an organism, its full potential is realized when integrated with other "omics" platforms, such as genomics, transcriptomics, proteomics, and microbiomics. This systems-level approach enables a more comprehensive understanding of the complex mechanisms driving kidney diseases and supports the advancement of precision nephrology [1].

Table 1. Comparison of metabolomics analytical platforms in nephrology

Analytical Platform	Strengths	Limitations	Typical Applications
NMR spectroscopy	-Non-destructive analysis -High reproducibility -Minimal sample preparation	-Lower sensitivity -Detects fewer metabolites	-Longitudinal studies -Urine metabolite profiling
LC-MS	-High sensitivity -Broad metabolite coverage	-Complex sample preparation -Variability between runs	-Plasma profiling -Targeted and untargeted metabolomics
GC-MS	-Excellent for volatile and semi-volatile metabolites	-Requires derivatization -Longer run times	-Organic acids -Fatty acids profiling

Genomics and metabolomics

Genomic studies have identified several variants associated with susceptibility to kidney disease, including genes regulating tubular transporters and mitochondrial function. However, linking these variants to functional outcomes remains a challenge. Metabolomics fills this gap by revealing the downstream biochemical consequences of genetic variations. For example, polymorphisms affecting amino acid transporters have been linked with altered urinary profiles of glycine, valine, and leucine metabolites commonly perturbed in both acute and CKDs [20].

Transcriptomics and proteomics

Transcriptomic and proteomic analyses offer insights into gene expression and protein abundance, but they do not fully capture functional metabolic changes. Metabolomic data complements these layers by reflecting enzymatic activity, nutrient utilization, and stress responses. In kidney transplantation, for example, integrating metabolite markers (such as altered lipid and bile acid profiles) with transcriptomic signatures from biopsies has improved early detection of immune activation and rejection [8].

Microbiome–metabolome interactions

The gut microbiome is an increasingly recognized player in kidney disease pathogenesis. Microbial metabolites, including indoxyl sulfate, p-cresyl sulfate, and TMAO are elevated in both CKD and stone disease and contribute to inflammation, vascular damage, and tubular toxicity. Multi-omics integration has enabled the identification of specific microbial taxa associated with these uremic toxins, opening avenues for therapeutic modulation of the microbiota [3, 4].

Multi-omics in pediatric nephrology

In pediatric populations, where growth and development introduce additional variability, multi-omics integration is particularly valuable. Combining age-specific transcriptomic data with urine metabolomics has revealed unique metabolic fingerprints in young patients with AKI or CKD, supporting individualized treatment strategies [21]. Together, these integrated approaches offer a holistic view of kidney disease, linking genotype to phenotype and enabling the development of predictive models that inform early diagnosis, prognosis, and therapy selection [22]. Integrating metabolomic data with genomic analyses, as discussed by Moritz et al., can provide a comprehensive understanding of CKD pathogenesis. This multi-omics approach facilitates the identification of novel biomarkers and therapeutic targets, paving the way for precision nephrology [7]. This review emphasizes the importance of combining metabolomics with other omics approaches, such as proteomics and genomics, to gain a comprehensive understanding of GN's molecular mechanisms. This integrative strategy can enhance biomarker discovery and facilitate the development of precision medicine in nephrology [16].

Challenges and Future Directions

Despite the remarkable potential of metabolomics in nephrology, several challenges remain that limit its widespread clinical application. These include technical, biological, and translational hurdles that must be addressed to fully realize the utility of metabolic profiling in kidney disease diagnostics and management [1, 3].

Technical limitations

Metabolomics data are highly sensitive to sample handling, processing, and instrument variability. Differences in analytical platforms—such as NMR versus LC-MS can result in inconsistent metabolite detection across studies. Furthermore, the lack of standardization in metabolite identification, quantification, and data normalization complicates cross-study comparisons and meta-analyses. This underscores the need for global harmonization of protocols and quality control frameworks [1]. A recent study failed to identify specific metabolomic markers for uremic pruritus in dialysis patients, reflecting the limitations of current platforms in capturing symptom-specific solutes [11].

Biological variability

The metabolome is influenced by numerous confounders, including age, sex, diet, microbiome composition, hydration status, medications, and comorbid conditions. In pediatric populations, the developmental stage significantly alters baseline metabolic profiles. As a result, interpreting metabolomic data requires careful contextualization and, ideally, matched control groups or longitudinal study designs [1, 5].

Clinical translation barriers

While many metabolite signatures have demonstrated diagnostic or prognostic value in research settings, few have transitioned into routine clinical practice. Key barriers include:

1) Limited validation in large, diverse cohorts; 2) Absence of regulatory approval for metabolomics-based tests; 3) Difficulty integrating complex metabolomic data into electronic health records and clinical decision-making [1].

Moreover, clinicians may require training to interpret metabolic patterns and apply them effectively in patient care [1]. Table 1 indicates a comparison of metabolomics analytical platforms in nephrology.

Future opportunities

Several innovations are poised to expand the clinical utility of metabolomics:

1) Point-of-care biosensors may allow real-time monitoring of metabolic markers; 2) Machine learning and AI algorithms are being developed to analyze high-dimensional metabolomic data and generate predictive risk scores; 3) Single-cell metabolomics could reveal cell-specific metabolic dysfunction in kidney biopsies; 4) Multi-omics consortia and open-access databases will facilitate data sharing and the discovery of universal biomarkers [1, 3].

Ultimately, the integration of metabolomics into precision nephrology depends on collaborative efforts among clinicians, researchers, data scientists, and regulatory bodies. With sustained investment and interdisciplinary innovation, metabolomics could become a standard component of kidney disease evaluation and personalized treatment strategies. Despite the promising findings, this review notes challenges, such as small sample sizes and the need for standardized protocols in omics research. Addressing these issues is crucial for translating omics-based discoveries into clinical applications for GN management [16, 22].

Conclusion

Metabolomics has rapidly emerged as a transformative tool in nephrology, offering deep insights into the biochemical alterations underlying kidney diseases. Unlike conventional markers, which often reflect only late-stage or nonspecific damage, metabolomics enables early, sensitive, and non-invasive detection of functional disturbances across a broad spectrum of renal disorders—from CKD and AKI to kidney transplantation and nephrolithiasis. Through advanced platforms, like NMR and MS, researchers have identified disease-specific metabolic signatures that not only enhance diagnostic accuracy but also aid in subtype classification, risk stratification, and monitoring of therapeutic interventions. In pediatric populations, metabolomics has uncovered age-dependent differences that underscore the importance of tailored approaches in young patients. Moreover, the integration of metabolomics with genomics, proteomics, and microbiome data is paving the way toward a holistic understanding of kidney pathophysiology. These multidimensional analyses support the development of precision nephrology, where molecular profiling informs individualized treatment and prevention strategies. Despite current limitations—such as analytical variability, biological complexity, and barriers to clinical translation—ongoing advances in technology, data analytics, and multi-center collaboration are steadily moving the field toward clinical implementation. In conclusion, metabolomics represents a paradigm shift in kidney disease research and care. With continued investment and validation, it holds the promise of becoming an integral part of future nephrology practice, improving outcomes through early detection, deeper understanding, and personalized management of renal disorders.

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Ethical Considerations

Compliance with ethical guidelines

The method was approved in accordance with the scientific and moral standards of Tehran University of Medical Sciences, Tehran, Iran and all procedures were performed in accordance with the Declaration of Helsinki guidelines and regulations. STROBE reporting guidelines for observational research were used and adhered to throughout the study.

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Authors' contributions

Supervision: Mastaneh Moghtaderi; Data analysis and writing: All authors.

Conflict of interest

The authors declared no conflict of interest.

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