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Microbiome-Based Approaches in Urological and Renal Disorders

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Abstract

The human microbiome has emerged as an important component of health and disease, with growing evidence that microbial communities may influence the urinary tract, kidneys, immune system, and systemic metabolism. Traditionally, urine was considered sterile in healthy individuals; however, advances in culture-independent sequencing have demonstrated the presence of complex microbial communities within the urinary tract. Alterations in these communities, commonly described as dysbiosis, have been investigated in urinary tract infections, recurrent infections, overactive bladder, bladder pain syndrome, urological malignancies, nephrolithiasis, and chronic kidney disease. The gut microbiome may also influence renal health through microbial metabolites, immune signaling, intestinal barrier function, and the accumulation of uremic toxins. These findings have generated interest in microbiome-based approaches including probiotics, prebiotics, dietary interventions, fecal microbiota transplantation, targeted antimicrobial strategies, and microbial metabolite modulation. Nevertheless, microbiome research in urology and nephrology remains an evolving field, and significant questions regarding causality, standardization, patient selection, and clinical efficacy remain unresolved. This mini review discusses current evidence and emerging opportunities for microbiome-based approaches in urological and renal disorders and considers their potential role in personalized kidney and urinary tract care.

Keywords: Microbiome; Urinary Microbiome; Gut Microbiota; Urology; Nephrology; Chronic Kidney Disease; Urinary Tract Infection; Probiotics; Dysbiosis; Precision Medicine

Introduction

The human microbiome consists of diverse microorganisms and their genetic material residing throughout the body. These microorganisms participate in metabolic, immunological, and physiological processes that can influence human health. Although the gastrointestinal microbiome has received substantial attention, increasing evidence suggests that microbial communities may also exist in anatomical sites traditionally considered sterile, including the urinary tract [1].

The development of next-generation sequencing and metagenomic techniques has changed understanding of urinary microbial communities. Rather than viewing the urinary tract exclusively in terms of pathogenic organisms, researchers are increasingly examining the interactions between microbial communities and host tissues [2].

Microbial alterations have been investigated in several urological conditions, including recurrent urinary tract infections (UTIs), overactive bladder, interstitial cystitis or bladder pain syndrome, urinary stone disease, and urological

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cancers. At the same time, the gut-kidney axis has become an important area of nephrology research. Changes in intestinal microbiota may influence kidney disease through inflammation, altered intestinal permeability, microbial metabolites, and production of uremic toxins.

These observations have raised the possibility that manipulating microbial communities could become a therapeutic strategy. Potential interventions include probiotics, prebiotics, dietary modification, microbial metabolite targeting, and other approaches designed to restore or modify microbial balance [3].

However, microbiome research remains relatively young. Associations between microbial composition and disease do not necessarily establish that dysbiosis causes disease. Consequently, carefully designed clinical studies are required before microbiome-based interventions can become routine components of urological and renal care.

The Urinary Microbiome

The urinary tract contains microbial communities that vary according to anatomical location, sex, age, hormonal status, health conditions, and other factors.

Traditional culture techniques identify only a proportion of microorganisms present in clinical samples. Molecular sequencing has revealed greater microbial diversity and has encouraged researchers to investigate the urinary microbiome as a dynamic component of urinary tract health [4].

The urinary microbiome may interact with the urothelium and host immune system. Changes in microbial composition could potentially influence susceptibility to infection, inflammation, and urinary symptoms.

Importantly, the presence of bacteria in urine does not automatically indicate disease. Some microorganisms may form part of a healthy microbial community. This distinction is particularly important when considering recurrent urinary symptoms and asymptomatic bacteriuria [5].

Future microbiome-based diagnostics may therefore focus not simply on detecting individual organisms but on evaluating the overall microbial ecosystem [6].

Microbiome and Urinary Tract Infections

UTIs remain among the most common bacterial infections. Recurrent infections can significantly affect quality of life and may lead to repeated antibiotic exposure.

Traditional management focuses on identifying the causative organism and administering appropriate antimicrobial therapy. However, repeated antibiotic treatment may alter microbial communities and potentially contribute to dysbiosis and antimicrobial resistance [7].

Research into the urinary and vaginal microbiomes suggests that microbial community composition may influence susceptibility to recurrent UTI. In particular, changes in protective microbial populations may alter the urinary environment and host defense mechanisms. This has stimulated interest in microbiome-based prevention [8].

Probiotics containing selected bacterial strains have been investigated as a potential strategy for reducing recurrent UTI risk. However, clinical findings have been inconsistent, and the effectiveness of probiotics may depend on strain selection, dosage, route of administration, and patient characteristics.

Future approaches may involve individualized microbial profiling to identify patients who could benefit from specific interventions.

Microbiome and Overactive Bladder

Overactive bladder is characterized by urinary urgency, commonly accompanied by increased frequency and nocturia, with or without urgency urinary incontinence. Emerging research has identified differences in urinary microbial communities between individuals with urinary symptoms and controls. However, the relationship between microbiome composition and overactive bladder remains incompletely understood [9].

It is possible that microbial metabolites or interactions with urothelial and immune pathways may influence bladder sensory mechanisms.

At present, microbiome assessment is not a routine diagnostic method for overactive bladder. Nevertheless, continued investigation may identify microbial signatures that help distinguish different biological subtypes of urinary symptoms [10].

Microbiome and Bladder Pain Syndrome

Bladder pain syndrome is a complex condition involving chronic bladder-associated pain, urinary frequency, urgency, and other symptoms.

Its pathophysiology is multifactorial and may involve urothelial dysfunction, immune activation, neural pathways, and altered bladder sensitivity.

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The urinary microbiome has been investigated as one possible contributor. Some studies have reported differences in microbial composition among patients with bladder pain syndrome, although findings have not been completely consistent.

The heterogeneity of this disorder suggests that microbiome alterations may represent one component of a larger biological network rather than a single disease mechanism.

Gut Microbiome and Kidney Disease

The relationship between the intestine and kidneys is commonly described as the gut-kidney axis. Kidney dysfunction can alter the intestinal environment through changes in diet, medication exposure, intestinal barrier function, and accumulation of metabolic products. In turn, altered gut microbiota may contribute to systemic inflammation and production of metabolites associated with kidney disease. This bidirectional relationship is particularly relevant in CKD.

Reduced kidney function can affect the clearance of microbial metabolites. At the same time, changes in gut microbial composition may increase the generation of compounds that contribute to the uremic toxin burden.

This creates a potentially self-reinforcing cycle:

Kidney dysfunction → altered intestinal environment → microbial dysbiosis → increased microbial metabolites → inflammation and metabolic disturbances → further kidney injury.

Breaking this cycle is an important area of current research.

Microbial Metabolites and CKD

Gut microorganisms produce numerous metabolites that can enter systemic circulation. Among the most studied are indoxyl sulfate, p-cresyl sulfate, and trimethylamine N-oxide (TMAO). Some microbial metabolites have been associated with cardiovascular disease, inflammation, endothelial dysfunction, and CKD progression. Because patients with CKD have increased cardiovascular risk, understanding the contribution of microbial metabolites may provide new opportunities for prevention.

Potential strategies include dietary modification, modulation of intestinal microbial activity, and development of therapies that reduce the production or absorption of harmful metabolites.

However, microbial metabolites should not automatically be considered harmful. Many microbial products have beneficial effects, and broad suppression of microbial metabolism could have unintended consequences.

Microbiome and Kidney Stone Disease

Kidney stone formation involves complex interactions among urinary chemistry, diet, genetics, metabolism, and environmental factors. The intestinal microbiome has received attention because certain microorganisms can influence oxalate metabolism. One example is the study of bacteria capable of degrading oxalate. Alterations in these microbial populations may influence intestinal oxalate availability and potentially affect urinary oxalate excretion. This has generated interest in microbiome-based strategies for preventing calcium oxalate stone recurrence. However, the relationship between intestinal microbial composition and stone formation is complex. Dietary intake, fluid consumption, host metabolism, and other factors also play major roles.

Microbiome and Urological Cancer

The microbiome may influence cancer biology through immune regulation, inflammation, metabolism, and interactions with therapeutic agents. Research has investigated microbial signatures associated with bladder, prostate, and kidney cancers. In bladder cancer, urinary microbial communities have been examined as potential biomarkers for disease detection or classification. Theoretically, microbiome-based biomarkers could complement existing diagnostic approaches and potentially identify molecular differences between tumors. However, this research remains exploratory. Differences in sample collection, sequencing platforms, patient populations, and analytical methods make comparisons between studies difficult. Large prospective studies are required before microbiome profiles can be considered reliable clinical biomarkers.

Microbiome-Based Therapeutic Approaches

Probiotics: Probiotics are live microorganisms administered with the intention of providing health benefits. In urological and renal medicine, probiotics have been investigated for recurrent UTIs and modulation of intestinal dysbiosis in CKD. Their effects appear to be strain-specific rather than universal. Therefore, simply using a generic probiotic formulation may not produce predictable outcomes.

Prebiotics: Prebiotics are substrates that can selectively support beneficial microorganisms. Dietary fibers and other

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fermentable substrates may influence intestinal microbial composition and metabolite production. In CKD, dietary interventions must be carefully individualized because restrictions on potassium, phosphorus, protein, and other nutrients may influence microbiome composition.

Dietary Modification: Diet represents one of the strongest influences on gut microbial composition.

Increased consumption of appropriate plant-based foods and dietary fiber may promote microbial diversity and production of beneficial short-chain fatty acids. However, dietary recommendations for patients with CKD must consider disease stage, electrolyte status, nutritional requirements, and comorbidities.

Fecal Microbiota Transplantation: Fecal microbiota transplantation involves transferring intestinal microbial communities from a screened donor to a recipient. Although it has an established role in recurrent Clostridioides difficile infection, its role in CKD and urological disease remains investigational.

More evidence is required to determine safety, durability, and clinical effectiveness.

Targeting Microbial Metabolites: Another promising approach is to modify microbial metabolite production without completely eliminating intestinal microorganisms. Strategies may include inhibition of specific microbial enzymes, dietary manipulation, adsorption of microbial metabolites, or modification of bacterial metabolic pathways. Such targeted approaches may eventually provide greater precision than broad antimicrobial interventions.

Microbiome and Precision Medicine

Microbiome research aligns closely with the concept of personalized medicine. Microbial composition varies considerably between individuals. Age, diet, geography, medication exposure, genetics, lifestyle, and disease status can all influence microbial communities.

Consequently, a microbiome intervention that benefits one patient may not have the same effect in another. Future precision nephrology could potentially combine microbiome profiles with clinical characteristics, genomic information, metabolomics, and laboratory measurements. This may allow identification of specific patient subgroups with distinct microbial and metabolic profiles.

However, personalized microbiome medicine remains an emerging concept rather than established clinical practice.

Challenges and Limitations

Several important challenges must be addressed.

Lack of Standardization

Microbiome results can vary depending on sample collection, storage, DNA extraction, sequencing technology, and bioinformatic analysis.

Association Versus Causation

Finding a microbial difference in patients with disease does not demonstrate that the microorganism caused the disease.

Individual Variability

Microbiomes differ substantially between individuals, making it difficult to define a universal healthy microbiome.

Antibiotic Effects

Previous antimicrobial exposure can substantially alter microbial communities and complicate interpretation.

Limited Clinical Trials

Many studies remain observational or involve small populations.

Safety

Microbiome manipulation may have unexpected consequences, particularly in immunocompromised or medically complex patients.

Regulatory Issues

Microbiome-based therapies require appropriate standards for manufacturing, quality control, safety, and clinical evaluation.

Future Directions

Future research should move from descriptive microbiome studies toward mechanistic and interventional research. Large longitudinal studies could determine whether microbial changes precede disease development or simply occur as a consequence of disease. Standardized protocols for urine, stool, and other biological samples would improve comparability between studies.

Multi-omics approaches integrating microbiomics, metabolomics, genomics, and clinical information may

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provide a more complete understanding of host-microbe interactions. Artificial intelligence may also assist in identifying complex microbial patterns associated with disease progression or treatment response. Ultimately, the most important question is whether microbiome-based interventions can improve patient outcomes.

Future clinical trials should therefore focus on meaningful endpoints such as reduction in recurrent infections, slowing CKD progression, reduction in stone recurrence, improved symptoms, cardiovascular outcomes, and quality of life.

Conclusion

The microbiome is emerging as an important component of urological and renal health. Alterations in urinary and intestinal microbial communities have been associated with recurrent urinary infections, bladder disorders, kidney stones, CKD, and potentially urological malignancies. Microbiome-based approaches—including probiotics, prebiotics, dietary interventions, microbial metabolite modulation, and other targeted therapies—offer promising possibilities for individualized disease prevention and treatment.

Nevertheless, the field remains in an early stage. Significant uncertainty exists regarding causality, optimal interventions, patient selection, and long-term safety.

The future of microbiome-based urology and nephrology will depend on rigorous clinical research, standardized methodologies, and integration with precision medicine. Rather than viewing microorganisms solely as pathogens, future kidney and urinary tract care may increasingly recognize the microbiome as a modifiable component of human health.

References

1. Wolfe AJ, Brubaker L (2019) Urobiome updates: advances in urinary microbiome research. Nat Rev Urol 16(2): 73-74.

2. Whiteside SA, Razvi H, Dave S, Reid G, Burton JP (2015) The microbiome of the urinary tract—a role beyond infection. Nat Rev Urol 12(2): 81-90.

3. Brubaker L, Wolfe AJ (2017) The female urinary microbiota, urinary health and common urinary disorders. Ann Transl Med 5(2): 34.

4. Lewis DA, Brown R, Williams J, White P, Jacobson SK, et al. (2013) The human urinary microbiome; bacterial DNA in voided urine of asymptomatic adults. Front Cell Infect Microbiol 3: 41.

5. Aragón IM, Herrera-Imbroda B, Queipo-Ortuño MI, Castillo E, Sequeira-García Del Moral J, et al. (2018) The urinary tract microbiome in health and disease. Eur Urol Focus 4(1): 128-138.

6. Buffie CG, Pamer EG (2013) Microbiota-mediated colonization resistance against intestinal pathogens. Nat Rev Immunol 13(11): 790-801.

7. Ramezani A, Raj DS (2014) The gut microbiome, kidney disease, and targeted interventions. J Am Soc Nephrol 25(4): 657-670.

8. Vaziri ND, Zhao YY, Pahl MV (2016) Altered intestinal microbial flora and impaired epithelial barrier structure and function in CKD: the nature, mechanisms, consequences and potential treatment. Nephrol Dial Transplant 31(5): 737-746.

9. Evenepoel P, Poesen R, Meijers B (2017) The gut-kidney axis. Pediatr Nephrol 32(11): 2005-2014.

10. Wong J, Piceno YM, DeSantis TZ, Pahl M, Andersen GL, et al. (2014) Expansion of urease- and uricase-containing, indole- and p-cresol-forming and contraction of short chain fatty acid-producing intestinal microbiota in ESRD. Am J Nephrol 39(3): 230-237.

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