METABOLOMIC AND MICROBIOME PROFILING IN CHRONIC PROSTATITIS: NOVEL DIAGNOSTIC AND THERAPEUTIC PERSPECTIVES

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INTRODUCTION

Chronic prostatitis (CP) is a multifactorial condition characterized by persistent pelvic pain, urinary symptoms, and sexual dysfunction in men. Traditional diagnostics focus on pathogen identification and symptom-based management, yet many patients remain refractory to conventional therapies. Recent studies suggest that prostatic microbiome dysbiosis and metabolic alterations may play a central role in symptom persistence and disease heterogeneity. Understanding the metabolomic and microbial profiles of CP patients may enable personalized diagnostics and innovative non-antibiotic interventions. This approach is particularly relevant for Uzbekistan, where chronic prostatitis contributes to significant healthcare burden among men aged 25–55.

METHODS

A prospective observational study was conducted at a tertiary urology center between 2022–2025. 70 men with chronic prostatitis (NIH category IIIB) and 30 healthy controls were recruited.

- Microbiome analysis: Prostatic fluid samples were analyzed using 16S rRNA gene sequencing to identify bacterial community composition.
- Metabolomic profiling: Liquid chromatography–mass spectrometry (LC-MS) was used to quantify metabolite patterns associated with inflammation, oxidative stress, and energy metabolism.
- Clinical correlation: NIH-CPSI scores and VAS pain scores were recorded. Statistical analysis included multivariate regression and correlation of microbial/metabolite signatures with symptom severity ($p<0.05$ considered significant).

Results:

- Microbiome: CP patients demonstrated reduced microbial diversity, with overrepresentation of Enterococcus, Streptococcus, and Staphylococcus species compared to controls.
- Metabolomic changes: Elevated pro-inflammatory metabolites (e.g., kynurenine, leukotrienes) and reduced anti-oxidative metabolites (e.g., glutathione derivatives) were detected.
- Clinical correlation: Certain microbial species and metabolite patterns correlated strongly with NIH-CPSI pain and urinary scores ($r=0.62–0.78$, $p<0.01$).
- These findings suggest that microbiome and metabolomic alterations contribute to symptom persistence and may serve as diagnostic biomarkers.

Discussion:

This study highlights the role of microbial dysbiosis and metabolic disturbances in chronic prostatitis pathophysiology, independent of urothelial barrier or immune-targeted therapy. Microbiome-metabolome profiling could enable early stratification of patients, identification of new therapeutic targets (e.g., probiotics, metabolite modulators), and a move toward precision urology in CP management. Limitations include single-center design and the need for longitudinal validation.

Conclusion:

Microbiome and metabolomic profiling provides a novel lens for understanding chronic prostatitis, offering diagnostic biomarkers and potential non-antibiotic therapeutic pathways. Implementing such analyses in Uzbek urological practice may improve personalized treatment strategies and reduce recurrent symptomatic episodes.

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