Abstract #479

The Role of Microbiota in Urinary Chronic Pelvic Pain Syndrome: A systematic Review

Hypothesis

Interstitial Cystitis/Bladder Pain Syndrome (IC/BPS) and Chronic Prostatitis/Chronic Pelvic Pain Syndrome (CP/CPPS) collectively known as Urologic Chronic Pelvic Pain Syndrome (UCPPS) are common conditions that significantly impact quality of life. The lack of straightforward diagnostic methods underestimates the true burden of UCPPS. The unknown etiology and pathogenesis make diagnosis and management challenging. Traditional definitions rely on sterile urine samples and exclusion of other diagnoses, but modern sequencing techniques challenge this approach. Imbalances in microbial communities (dysbiosis) can lead to various diseases, including genitourinary disorders. The microbiome in different body niches is linked to conditions like fibromyalgia, IBS, and rheumatoid arthritis. Dysbiosis is also associated with inflammatory bowel disease. The microbiota of organs like the gut and vagina may influence urinary diseases through central sensitization and interactions with the immune, metabolic, and nervous systems. This study aims to systematically review the role of microbiota in UCPPS due to the controversial and heterogeneous results in existing research.

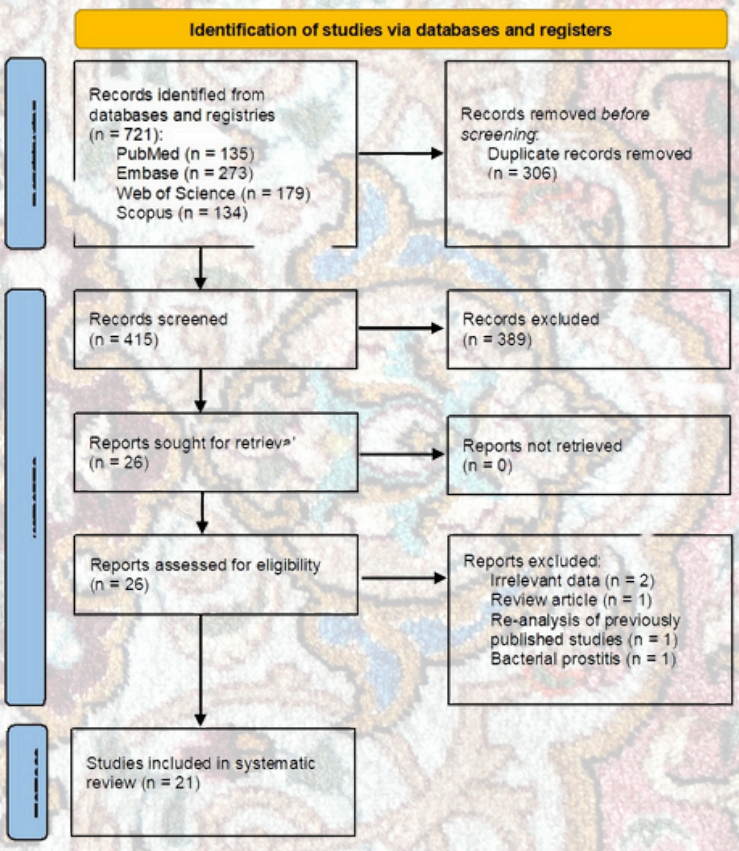
Study Design

This systematic review followed PRISMA guidelines and searched multiple databases for studies on the role of microbiota in UCPPS until December 6, 2023. Two authors independently screened and selected studies, including randomized clinical trials, cohort studies, and cross-sectional studies while excluding certain criteria. Data extraction was done using a standardized sheet, and quality assessment was conducted using the JBI appraisal tool. Disagreements were resolved through discussion or consultation with another author

Results:

This systematic review included 21 studies with a total of 1125 patients, focusing on UCPPS, IC/BPS, and CP/CPPS. The flow diagram in Figure 1 illustrates the literature search process and outcomes, with 21 studies meeting the inclusion criteria out of 721 abstracts screened. The quality of evidence assessed using JBI tools was generally medium to high. The dysregulation and altered composition of gut microbiota have been suggested as potential contributors to UCPPS development.

Changes in urine microbiota showed varying levels of certain operational taxonomic units, with some increasing in abundance while others decreased. Specific bacteria and fungi were associated with distinct clinical characteristics. However, some studies did not support the idea of UCPPS as a dysbiotic condition. For IC/BPS studies, voided urine samples were primarily used, with a few studies utilizing transurethral catheterized urine samples. UCPPS studies by Nickel et al. collected first-void urine (VB1) and midstream urine (VB2) samples to analyze urethral and bladder microbiota. CP/CPPS studies commonly utilized seminal fluid and expressed prostate secretions. Additionally, some studies investigated the role of gut microbiota in UCPPS using fecal specimens, while others collected vaginal swabs alongside urine samples.



Interpretation of Results

The urinary and intestinal microbiota may play a role in UCPPS, including IC/BPS and CP/CPPS. Nevertheless, due to the significant discrepancies among existing studies, further prospective trials are necessary to validate these observations.

Conclusion

The urinary and intestinal microbiota may play a role in UCPPS, including IC/BPS and CP/CPPS. Nevertheless, due to the significant discrepancies among existing studies, further prospective trials are necessary to validate these observations.

References

1. Clemens JQ, Mullins C, Kusek JW, Kirkali Z, Mayer EA, Rodríguez LV, et al. The MAPP research network: a novel study of urologic chronic pelvic pain syndromes. BMC urology. 2014;14:1-6.
2. Siddiqui H, Nederbragt AJ, Lagesen K, Jeansson SL, Jakobsen KS. Assessing diversity of the female urine microbiota by high throughput sequencing of 16S rDNA amplicons. BMC microbiology. 2011;11:1-12

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