Pediatr Urol Case Rep 2022; 9(3):185-186 DOI: 10.14534/j-pucr.20222675580

PEDIATRIC UROLOGY CASE REPORTS
ISSN 2148-2969
http://www.pediatricurologycasereports.com

The interaction of bladder bacteria and the severity of overactive bladder symptoms

Jan van Anker*
Department of Urology, Radboud University Medical Center, Nijmegen, Netherlands

✉ ***Jan van Anker***
Department of Urology,
Radboud University Medical Center,
Nijmegen, Netherlands,
E-mail: Janankre@radboudumc.nl
Received: 07-Jun-2022, Manuscript No. PUCR-22-68777; Editor assigned: 10-Jun-2022, PreQC No. PUCR -22-68777 (PQ); Reviewed: 27-Jun-2022, QC No. PUCR-22-68777; Revised: 04-Jul-2022, Manuscript No. PUCR-22-68777 (R); Published: 12-Jul-2022, DOI: 10.14534/j-pucr.2022267582

Description

It is widely accepted that microbial communities exist in the urinary tracts of healthy persons. Lower Urinary Tract Symptoms (LUTS) and overactive bladder are two benign urological disorders that are impacted by Overactive Bladder (OAB).

The impact of alterations to the urine microbiota on the severity of OAB symptoms is still unknown, though. The aim of this study is to investigate the relationship between OAB severity and urine microbiota.

Means and Standard Deviations (SD) or medians and interquartile ranges were used to describe continuous variables (IQR). Frequencies and percentages were used to characterise the categorization variables. T-tests, the Mann-Whitney U test, and Pearson Chi-square testing for categorical variables were used to analyse differences in baseline characteristics between cohorts.

The most common urotype in both groups was Lactobacillus, and OAB discovered similar effect in UUI patients. Additionally, we discovered that the moderate/severe group had a lower percentage of patients with Lactobacillus-dominant urine. Previous study also revealed that the UUI cohort had lower Lactobacillus sequence abundances than the control cohort, that Lactobacillus DNA was more prevalent in asymptomatic women than in OAB patients, and the people who experienced a post-treatment UTI had fewer Lactobacillus sequences.

In female vagina, the bacterial genus Lactobacillus is well known. By preserving the physiologically acidic environment of the vagina, it can prevent vaginitis. Functional abnormalities of the Lower Urinary Tract (LUT) may also be regulated or protected in part by the lactobacillus found in the bladder.

Our current study includes a number of key benefits. First, we used catheterized urine samples rather than urine that had been void midstream. The microbiome of voided urinate is collected by transurethral catheter was dramatically different, according to research by Wolfe and his colleagues. Catheterized urine samples had microbiomes that were much closer to those of the bladder and were free of genital tract microbial flora.

Second, the demographic details (such as age, BMI, race/ethnicity) of the two cohorts were identical, with the exception of the OABSS scores. Numerous factors that contribute to the variation in urine microbiota are so disregarded.

Third, there is a sizable sample size of OAB patients overall in this study. In order to rule out urinary tract infections, routine urine culture was also performed on urine samples from all patients.

The study's main drawback was the dearth of mild OAB patients. Only OABSS, which analyses symptoms from the patients' point of view and does not require bladder diary recording, was used in this study to determine the severity of the patients' symptoms.

As a result, patient perceptions could have a big impact on the outcomes. Furthermore, it is challenging to establish

a causal link between symptoms and urine microbiota in this cross-sectional investigation. Therefore, more extensive prospective investigations are needed to fully understand the significance of urine microbiota in the emergence of OAB.

Conclusion

In conclusion, our study's findings imply that the bladder microbiota and the severity of OAB are closely associated. Our study's findings supported the notion that greater bacterial richness and variety was linked to more severe OAB symptoms. Furthermore, a number of particular bacterial genera were linked to OAB sub-symptoms, indicating that a number of urinary dysbiosis may exacerbate functional bladder diseases. In the future, the urine microbiome may also have consequences for clinical diagnosis and treatment.