

Characteristics of urinary microbiota associated with overactive bladder



Okada K¹, Takezawa K¹, Tsujimura G¹, Imanaka T¹, Kuribayashi S¹, Ueda N¹, Fukuhara S¹, Kiuchi H¹, Motooka D², Nakamura S², Nonomura N¹

1. Department of Urology, Osaka University Graduate School of medicine

2. Department of infection Metagenomics, Genome Information Research Center, Osaka University Research Institute for Microbial Diseases

Background and Objective	Results		
Urinary microbiota was found to be present because of advances in the study of microbiota.	No. of participants48Median age (range)75(51-91)DD (use DD use DD		
We previously revealed that the instillation of lipopolysaccharide from Escherichia coli in mouse bladder increases urothelial ATP release and induces urinary frequency without inducing inflammation (Takezawa K, <i>et al.</i> Am J physiol, 2014. Ueda N, et al. Sci rep, 2020). We hypothesized that bacteria-rich urinary microbiota causes OAB by the mechanism. We aimed to clarify the characteristics of urinary microbiota associated with OAB. Bladder Urinary frequency Bacteria Urinary frequency	BR / non-BR group 7 / 41 1 The prevalence of OAB in the BR and the non-BR groups		
	BR non-BR	р	
	Prevalence of OAB 100%(7/7) 68%(28/41)	< 0.05	
	All participants in the BR group were OAB patients.		
	2-A Relative frequency of bacterial genera in each s The BR group The non-BR group	ample	
	100% OAB OAB r	າon-OAB	
Methods			

- 1. Investigation of the association between urinary bacterial counts and OAB
- ✓ We recruited female non-neurogenic OAB patients and female asymptomatic subjects and then collected their catheterized urine.
- We prepared smears from urinary sediment samples and performed Gram staining.
- ✓ We evaluated bacterial counts of urine smears by observing 5 fields of view under 400x magnification. the bacterial count ≥100 → Bacteria-rich (BR) group the bacterial count < 100 → Non-bacteria-rich (non-BR) group



- ✓ We compared the prevalence of OAB between the BR and the non-BR groups.
- ✓ Exclusion criteria: patients with any cancer, a history of antibiotic use within 6 months, pyuria

2. Investigation of the urinary microbiota characteristics of the BR group

✓ We analyzed the microbiota of the catheterized urine collected previously by 16S metagenome analysis.

Catheterized urine collection

DNA extraction

Several genera were dominant in the urinary microbiota of the BR group.

2-B Comparison of richness, evenness, phylogenetic diversity, and composition of urinary microbiota



The genus Escherichia and related genera had a higher composition in the BR group than in the non-BR group.





- 2-A Relative frequency of bacterial genera in each sample
- 2-B Comparison of richness, evenness, phylogenetic diversity and composition of urinary microbiota
 2-C Comparison of the abundance of OTUs between the urinary microbiota of the BR and the non-BR groups (P<0.05 and LDA score > [5.0]).

Discussion

We demonstrated that some OAB patients have bacteriarich urinary microbiota, which was characterized by a high composition of the genus Escherichia and related genera.

✓ The findings suggest that, in humans, the genus Escherichia may increase ATP release from the bladder urothelium by the similar mechanism, causing OAB symptoms.

Conclusion

✓ Bacteria-rich urinary microbiota may cause OAB.

✓In the urinary microbiota causing OAB, specific bacteria were suggested as potential therapeutic targets.