



Commentary to: The urinary microbiome in patients with refractory urge incontinence and recurrent urinary tract infection

(Zhuoran Chen, Minh-Duy Phan, Lucy J Bates, Kate M Peters, Chinmoy Mukerjee, Kate H Moore, Mark Schembri)

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It has previously been demonstrated that the bladder microbiome in women with urge incontinence is eight times more diverse than in normal controls. Studies using culture-independent sequencing have revealed that the bladder of patients with urge incontinence is not sterile and that 40–60% of patients with refractory detrusor overactivity (DO) suffer recurrent urinary tract infections (rUTIs). The existence of intracellular bacteria in exfoliated urothelial cells from patients with urge incontinence has also been demonstrated, providing a link to a bladder reservoir for rUTI. Increasing evidence suggests the urinary microbiota may play a role in the pathology of urge incontinence and refractory DO. In the past, women without the classical symptoms of dysuria and foul-smelling urine may have not been identified as being at risk of recurrent and often multiresistant bacterial cystitis.

In this article, the urinary microbiome of women with refractory detrusor overactivity (DO) *and* concomitant recurrent urinary tract infection is explored for the first time in peer-reviewed literature.

Over 2 years, 39 patients with refractory urge incontinence and coexistent rUTI were studied. Midstream urine (MSU) samples were collected from patients with refractory urge incontinence and coexistent rUTI during acute symptomatic episodes, resulting in the collection of 102 MSU samples, 70 of

which were diagnosed as UTI (median of 8 UTIs/woman). Culture-independent (bacterial 16S RNA profiling) analysis of 38 of these samples revealed the existence of a diverse urinary microbiome. Strain typing of *E. coli* identified instances of rUTI caused by the same persisting strain and by new infecting strains.

The conclusions drawn were that patients with refractory urge incontinence and coexistent rUTI possess a diverse urinary microbiota with both new and preexisting organisms.

Instances where refractory DO patients suffer rUTI with the same strain suggest the existence of a chronic reservoir that may augment the pathology of their chronic condition and may have an impact on both the incidence of rUTI and the lack of response to antimuscarinic drugs.

A limitation of this study is that the urine samples collected were voided specimens rather than catheter specimens, and despite attention to labial toileting, this is likely to have increased the diversity of the microbiome.

The study adds to our understanding of the urinary microbiome in women with LUTS, and hopefully the stage is now set for the researchers to build on this significant contribution with clinically relevant outcomes that will help clinicians when managing this challenging group of patients.

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