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Associations between urinary bacterial load and UUI symptoms

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Abstract

Women are impacted twice as likely as men by urgency urinary incontinence (UUI) with nearly one-third of women suffering from UUI in their lifetime. The etiology of UUI is complex, but evidence suggests that shifts in the normal urinary microbiome may play a role in UUI. We aim to understand whether women with UUI have different urinary bacterial loads compared to women without UUI and whether this is correlated with severity of UUI symptoms.

Our prospective cohort study compares urinary microbiome in women with and without UUI. We recruited 25 women with and 36 without UUI between the ages of 45-85. UUI was defined as daily urinary leakage with urgency. Women with known neurological conditions, active urinary tract infections, recent antibiotic use and symptomatic pelvic organ prolapse were excluded. UUI severity was measured using the ICIQ-OAB symptom questionnaire. Bacterial load was estimated from a random sample of 50 catheter-collected urine specimens using SytoBC and flow cytometry.

There was no significant difference between cases and controls in menopausal status, sexual activity, or comorbidities. Cases were slightly older (59.4 vs 53.1, $p=0.05$), more likely to have had a hysterectomy ($p=0.03$), use estrogen products ($p=0.001$), and had higher BMI (29.6 vs 24.9, $p=0.003$). Average bacterial load was doubled in women with UUI compared to women without UUI (8,749±6,883 bacteria/mL in UUI, 4,121±4,993 in controls, $p=0.01$). Furthermore, we identified a significant negative correlation between bacterial load and symptom severity as measured by the ICIQ ($r=-0.63, p=0.02$).

This study provides evidence that women with UUI have significantly higher urinary bacterial load, but the higher bacterial load was associated with less severe symptoms. Larger bacterial load in women with UUI symptoms may represent a mix of both pathogenic and commensal bacteria and that symptom severity is dependent on proportion between these two types of bacteria rather than the overall abundance