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PRELIMINARY EVIDENCE OF URINARY MICROBIOME'S ROLE IN URINARY INCONTINENCE SUBTYPES

Hypothesis / aims of study
New data are emerging regarding the existence and function of the female urinary microbiota (i.e., the community of bacteria in the female lower urinary tract). Recent findings suggest that participants with urgency urinary incontinence (UUI) in the NIH-sponsored Anticholinergic versus Botulinum Comparison (ABC) trial were less likely to suffer from a post-instrumentation urinary tract infection (UTI) if their urine exhibited DNA-based evidence of bacteria than if it did not. In a separate population of women, new DNA-based evidence supports the potential role for the bladder microbiota in urinary incontinence, especially UUI.

Study design, materials and methods
With IRB approval, we obtained catheterized urine samples from women segregated into 4 different UI subtypes by symptoms [pure stress urinary incontinence (SUI), predominately SUI (SUI>UUI), predominately UUI (UUI>SUI), and pure UUI] using the Pelvic Floor Distress Inventory (a validated symptom questionnaire). Each sample was split: one portion was sent to the clinical microbiology lab for conventional urine culture and Gram stain analysis; the remaining portion was sent for DNA sequence analysis using the 454 platform to sequence the V1-V3 regions of the 16S rRNA gene of each bacterium. The detected 16S rRNA sequences were first classified by taxonomy, permitting us to identify the bacterial community (microbiota) in each sample. These microbiota were compared using a statistical method called Advanced Principal Coordinate Analysis (PCoA), which determined the degree of similarity amongst the microbiota in the patient samples. To validate our results, we re-analyzed the same 16 samples by sequencing the V4 region of the 16S rRNA gene using MiSeq, a newer sequencing platform that provides increased sensitivity over the 454 method because it yields many more sequences per sample.

Results
Subjects were free of clinical urinary tract infection. Analysis of the 454 data and subsequent PCoA demonstrated that the microbiota of UUI and UUI>SUI patients could be clearly distinguished from those of SUI and SUI>UUI patients. Furthermore, patients with UUI symptoms fell into at least two distinct groups (Figure 1). Preliminary analysis of the MiSeq data suggested that the SUI and SUI>UUI microbiomes were significantly less diverse than those of the UUI & UUI>SUI cohorts (data not shown).

Concluding message
These preliminary data are consistent with the hypothesis that bladder microbiota differ among different UI subtypes and that differing components or entire bacterial communities could affect UUI symptoms.

Disclosures
Funding: NIH **Clinical Trial:** No **Subjects:** HUMAN **Ethics Committee:** Institutional **Helsinki:** Yes **Informed Consent:** Yes