

## Background

- Radical cystectomy (RC) and urinary diversion (UD) is a complex operation with associated morbidity.
- Recent studies have demonstrated the existence of a urinary microbiome which is thought to play a role in numerous disease states.
- Herein, we use 16S rRNA sequencing to characterize the microbiome of the reconstructed urinary tract of bladder cancer patients.

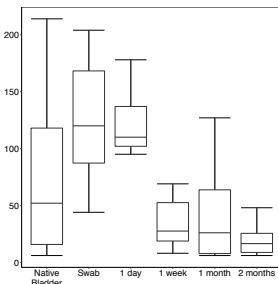
## Methods

- A catheterized urine specimen from the native bladder and a swab of the ileal segment used to create the UD were collected in the operating room.
- We then collected sequential catheterized specimens from the UD until 2 months post-op.
- Antibiotic prophylaxis was administered according to our institutional ERAS protocol.
- Bacterial 16S rRNA sequencing and microbiome profiling were performed.

## Results

- 20 patients enrolled, 8 with complete sample collection
- 17 (85%) male
- 13 (65%) ileal neobladder

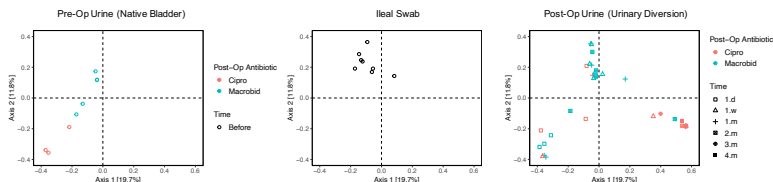
### Alpha Diversity



**Mean species richness**  
 Native bladder: 75.1 (S.D. 73.8)  
 Ileal segment: 127.3 (S.D. 56.9)  
 POD 1: 114.3 (S.D. 44.8)  
 1 week: 44.0 (S.D. 42.8)  
 1 month: 45.6 (S.D. 50.4)  
 2 months: 24.3 (S.D. 23.4)

**Abbreviations:** POD: Post-operative day;  
S.D.: Standard deviation

### Principal Coordinates Analysis (PCoA)



### Microbial Composition Barplot

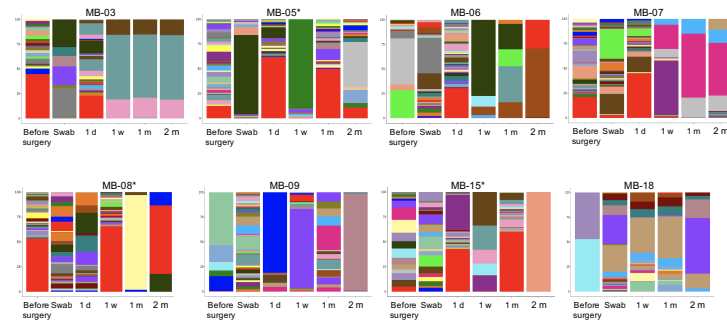


Figure 1: Microbial taxonomic profiles of each patient. 1 d = 1 day post-op, 1 w = 1 week post-op, 1 m = 1 month post-op, 2 m = 2 months post-op. \* = Patients with post-op UTI.

\*The microbial diversity at 1 month in 2/3 patients with UTI was high compared to all others (mean species richness 123.5 vs 19.7). Both patients experienced UTI at >60 days post-op.

## Conclusions

- The urinary microbiome immediately following UD shows alpha diversity similar to that of the native bladder and bowel, but this diversity decreases over time.
- Patients with infectious complications may have persistently higher alpha diversity despite prophylactic antibiotic use.
- Larger sample sizes are necessary to more completely characterize the urinary microbiome following UD.