

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:

- Inclusion: Patients with bladder cancer undergoing radical cystectomy and urinary diversion with either ileal conduit or neobladder

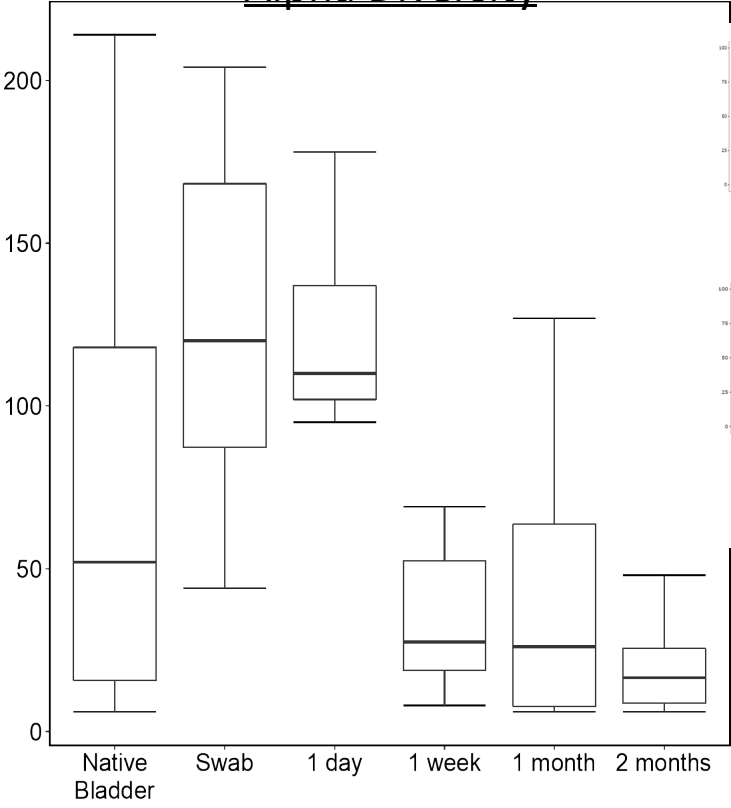


- Antibiotic prophylaxis was administered according to our institutional ERAS protocol.
- Bacterial 16S rRNA sequencing and microbiome profiling were performed.

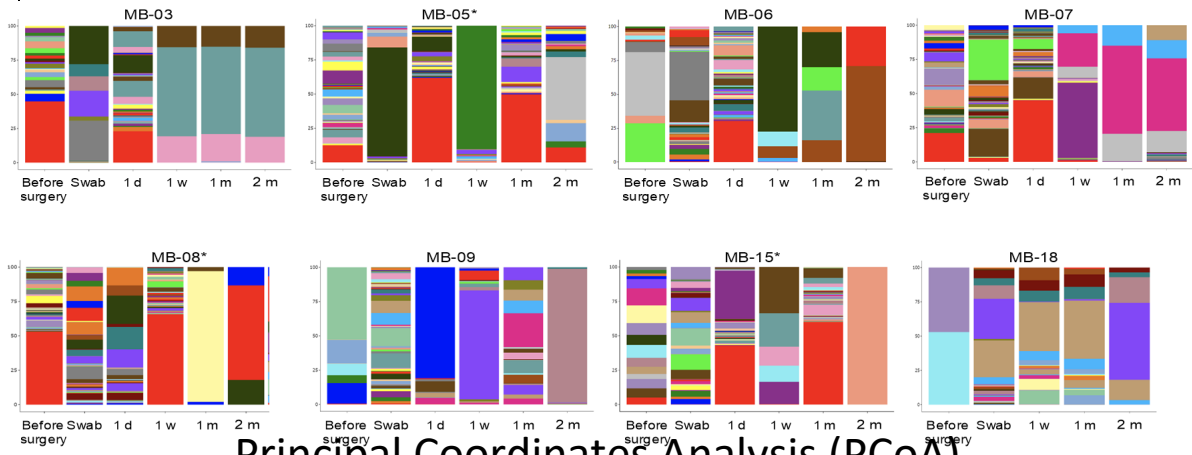
Results:

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

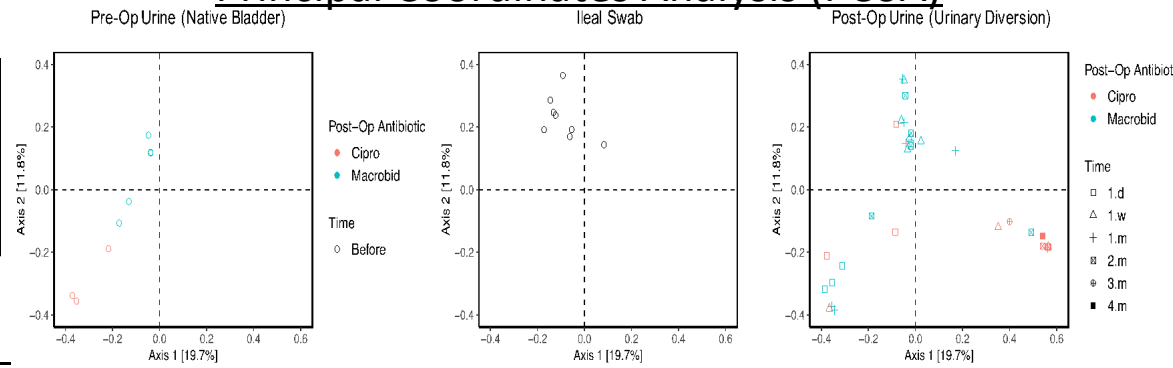
Alpha Diversity



Microbial Composition Barplot



Principal Coordinates Analysis (PCoA)



Conclusion:

- 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.