




CAIRIBU UROBIOME RESEARCH INTEREST GROUP (U-RIG)

CAIRIBU U-RIG RESEARCH HOURS


EXECUTIVE SUMMARY 10/20/2023 U-RIG RESEARCH HOUR

Goal: Facilitate knowledge exchange and spur collaborations in the urobiome and adjacent fields




CAIRIBU U-RIG RESEARCH HOUR

BRIDGING KNOWLEDGE GAPS IN THE UROBIOME



CAIRIBU UROMICROBIOTA RESEARCH INTEREST GROUP (U-RIG)



Catherine Putonti, PhD
Professor
Associate Dean for Interdisciplinary Initiatives & Academic Innovation
Loyola University Chicago
Sequencing the Urobiome - Going Beyond Profiling Genera

SPEAKER

FRIDAY, OCT 20
3:00 PM ET
2 PM CENTRAL | 12 PM PACIFIC

NOTES FROM DR. PUTONTI'S PRESENTATION AND GROUP DISCUSSION

Analyzing urine samples for bacteria using sequencing

- Dr. Catherine Putonti investigates the urobiome in collaboration with **Beth Mueller** and **Alan Wolfe**
- Has used variable region sequencing and phylogenetic analysis to identify 161 different species of bacteria in urine samples from females, with some variable regions providing limited species-level resolution

E. coli UTIs and urobiome diversity/species diversity

- In urine samples of women with UTIs, mixed *E. coli* species and strains were found, with some individuals having dominant strains and others with low biomass and DNA concentration

E. coli UTIs in postmenopausal women using meta-genomics

- Urine and rectal swab samples from postmenopausal women were collected to identify bacteria associated with UTIs
- In the analysis of 19 patients, instances were found where the same *E. coli* strain was present in both the rectal swab and urine samples

- **The phylogenetic tree showed that not all paired samples from the same participant were next to each other, with some strains found in different parts of the tree**

Tracking microbiome strains in different body compartments

- Using meta-genomic sequencing to analyze *E. coli* strains in urine and rectal swabs, **not all *E. coli*-associated UTIs appeared to be recent invasions from the rectum**
- Studies show similar microbiomes in vagina and urinary tract, suggesting sharing of microbiomes between different body compartments
- Analysis of data from shotgun metagenomics is challenging due to low representation of full genome sequences and difficulty identifying plasmids in publicly available databases

Computational tools for taxonomic analysis in metagenomics.

- Putonti has expertise in computational tools and sequencing technology; **opportunities for collaboration here**
- Taxonomic and comparative genomic analysis were discussed; challenges related to working with whole genome data were discussed
- There are limitations with tools used for taxonomic analysis, including Kraken and MetaPhlan, in identifying rare species

Challenges in analyzing microbiome data

- There are issues with database representation, sequencing technology, and probabilistic taxonomic classifiers
- Difficult to distinguish between different species of bacteria using 16S rRNA gene sequencing, despite its widespread use in taxonomic identification
- How to analyze microbiome data in the context of bladder health?
- **Proper documentation and annotation of genes and proteins is essential for accurate bioinformatics predictions!**

Suggestions for standardizing microbiome data sharing and analysis

- During discussion, investigators emphasized the importance of sharing detailed methods and results, including database information and version numbers, to facilitate comparison and replication of studies
- **How about centralizing microbiome data on CAIRIBU website for easy access and meta-analysis?**
- Need for a standardized way to report microbiome data to avoid confusion and improve collaboration

Needs related to establishing a biorepository for urobiome data

- Need for a centralized bio repository for urobiome data and samples; could potentially collaborate with investigators in other field, like the gut
- Proposal for a big data project bio repository for urology research, and the possibility of sharing concepts and ideas with other fields.

Recent publications Dr. Catherine Putonti:

- Urinary plasmids reduce permissivity to coliphage infection. *Microbiol Spectr* 2023
- Exploring the genotypic and phenotypic differences distinguishing *Lactobacillus jensenii* and *Lactobacillus mulieris*. *mSphere* 2023
- Coliphages of the human urinary microbiota. *PLoS One* 2023
- When plaquing is not possible: computation methods for detecting induced phages. *Viruses* 2023
- Comparative of genomic study of *Streptococcus anginosus* reveals distinct group of urinary strains. *mSphere* 2023
- Plasmids of the urinary microbiota. *Access Microbiol* 2022
- Link to PubMed-indexed publications by Catherine Putonti here: <https://pubmed.ncbi.nlm.nih.gov/?term=putonti+catherine&sort=date&size=100>

Future considerations

1. The group suggests a meeting to discuss a **centralized bio repository for urine samples**, with potential funding from grants; **CAIRIBU Interactions Core to coordinate**
2. **Could incorporate samples from other groups**, such as the pelvic floor disorders network, to create a prospective repository