

BACKGROUND

Our understanding of the microbial environment of the prostate continues to be limited. New evidence indicates that the human urinary tract contains microbial communities; however, the role of these communities in urinary health has not been elucidated

STUDY OBJECTIVES

To prospectively examine the changes in microbiota within the urinary tract after transrectal prostate biopsy.

STUDY METHODS

- Data, urine and fecal samples prospectively collected from 30 patients (two urine and one fecal sample per patient) before and after transrectal biopsy of the prostate.
- DNA was extracted from urine collected after a prostate massage before and after prostate biopsy, and from fecal samples collected before the biopsy.
- DNA was sequenced using the bacterial 16S rRNA high-throughput next generation sequencing, and we analyzed changes in microbial profiles for taxonomy comparison between samples.

RESULTS

- Pre-biopsy urinary microbial profiles contained lactobacillales and staphylococcaceae bacteria.
- Post-biopsy urinary microbial profiles included lower levels of lactobacillales and higher levels of bacteroidales bacteria.
- Bacteroidales bacteria were predominant in fecal samples.
- We identified two clustering patterns containing both pre- and post-biopsy urine samples using principal component analysis (PCoA). Cluster 1 had a urine cluster pattern that was distinct from fecal, while cluster 2 was similar to fecal.
- We observed two different modes of microbial changes, 11 patients had both of their urine (pre and post) samples associated with a particular cluster group, while others (n=15) had movement between clusters 1 and two following the biopsy procedure.

Figure 1: PCOA clustering of samples by sample type and time of collection. Blue= fecal sample. Orange=Pre biopsy urine. Red=Post-biopsy urine

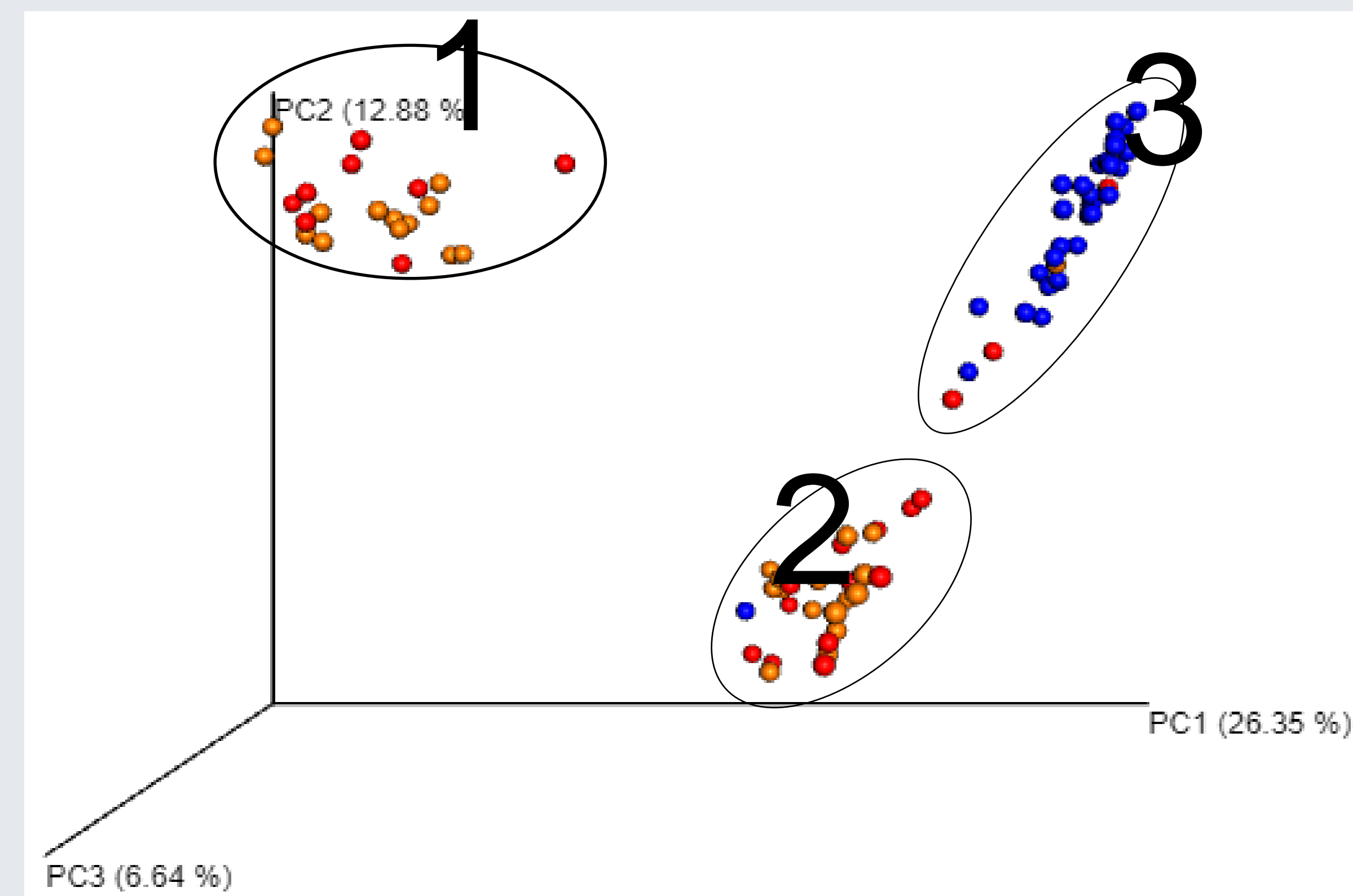


Figure 2: Identification of unique (top) and shared (bottom) genera among sample types.

Level 6 Taxa Unique	Pre Urine	Post Urine	Fecal	Total
Number of Genera Identified	16	16	25	157
Level 6 Taxa Shared	Pre and Post Urine	Pre Urine and Fecal	Post Urine and Fecal	All
Number of Genera Identified	16	4	18	30

Level 6 Taxonomic Summary of relevant abundance of taxa species within each sample type

Taxonomy Legend	Pre Urine %	Post Urine %	Fecal %
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Veillonella	8.5%	4.0%	0.0%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	13.7%	1.7%	0.2%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5.7%	2.1%	0.1%
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	12.7%	15.0%	0.0%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella	6.2%	11.7%	11.1%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	5.0%	4.5%	27.8%
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	5.8%	0.6%	1.1%
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	5.6%	8.9%	0.8%
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	0.4%	2.1%	7.6%

CONCLUSIONS

We describe two models of change in the urinary tract microbiota after prostate biopsy using 16S RNA gene analysis. Further research to determine what controls changes in the urinary microbiota after prostate biopsy can help us understand why some patients are more susceptible to develop post-biopsy infections.