

A PROSPECTIVE STUDY TO EXAMINE THE ASSOCIATION OF THE URINARY AND FECAL MICROBIOME WITH PROSTATE CANCER AND BENIGN PROSTATIC HYPERPLASIA USING 16SRNA ANALYSIS

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BACKGROUND

There is accumulating evidence that variations in the human microbiota are associated with disease pathologies including cancer. This association has not been thoroughly investigated in prostate cancer.

STUDY OBJECTIVES

Our goal was to examine the association between urinary and fecal microbial profiles and the diagnosis of prostate cancer vs. benign prostatic hyperplasia (BPH) in patients undergoing transrectal ultrasound guided biopsy of the prostate.

STUDY METHODS

- Data, urine and fecal samples prospectively collected from 30 patients before transrectal biopsy of the prostate.
- DNA was extracted from urine collected after a prostate massage 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

- A total of 30 patients were included in our analysis (60samples, 1 urine and 1 fecal per patient).
- The majority of patients with prostate cancer (10/14) had similar bacterial communities within their urinary sample profile and clustered separately than patients with BPH (n=16).
- Analysis of the bacterial taxonomies of the fecal samples did not reveal any associations with prostate cancer.
- Patients who had a Gleason score (GS) of 6 (n=11) were present in both urine bacterial community clusters, but patients with GS 7 or greater (n=3) did not cluster closely with BPH patients.
- Antibiotics before biopsy, smoking, and diabetes did not affect the distribution of the bacterial community clusters

Figure 1: Effect of Disease state on urine sample clustering by PCOA.
Blue=samples that were collected from patients that had prostate cancer.
Red=samples that were collected from patients with BPH.

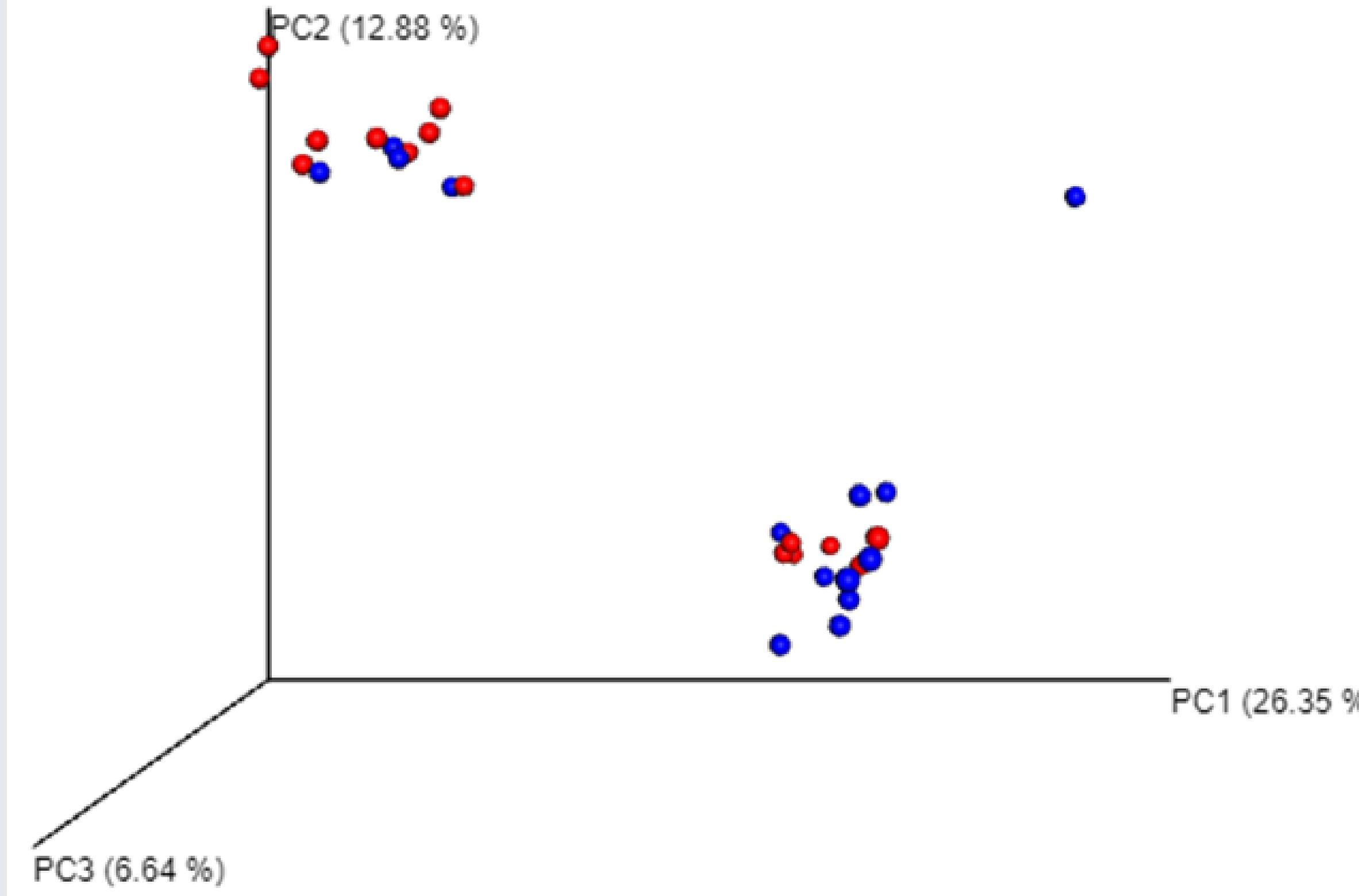
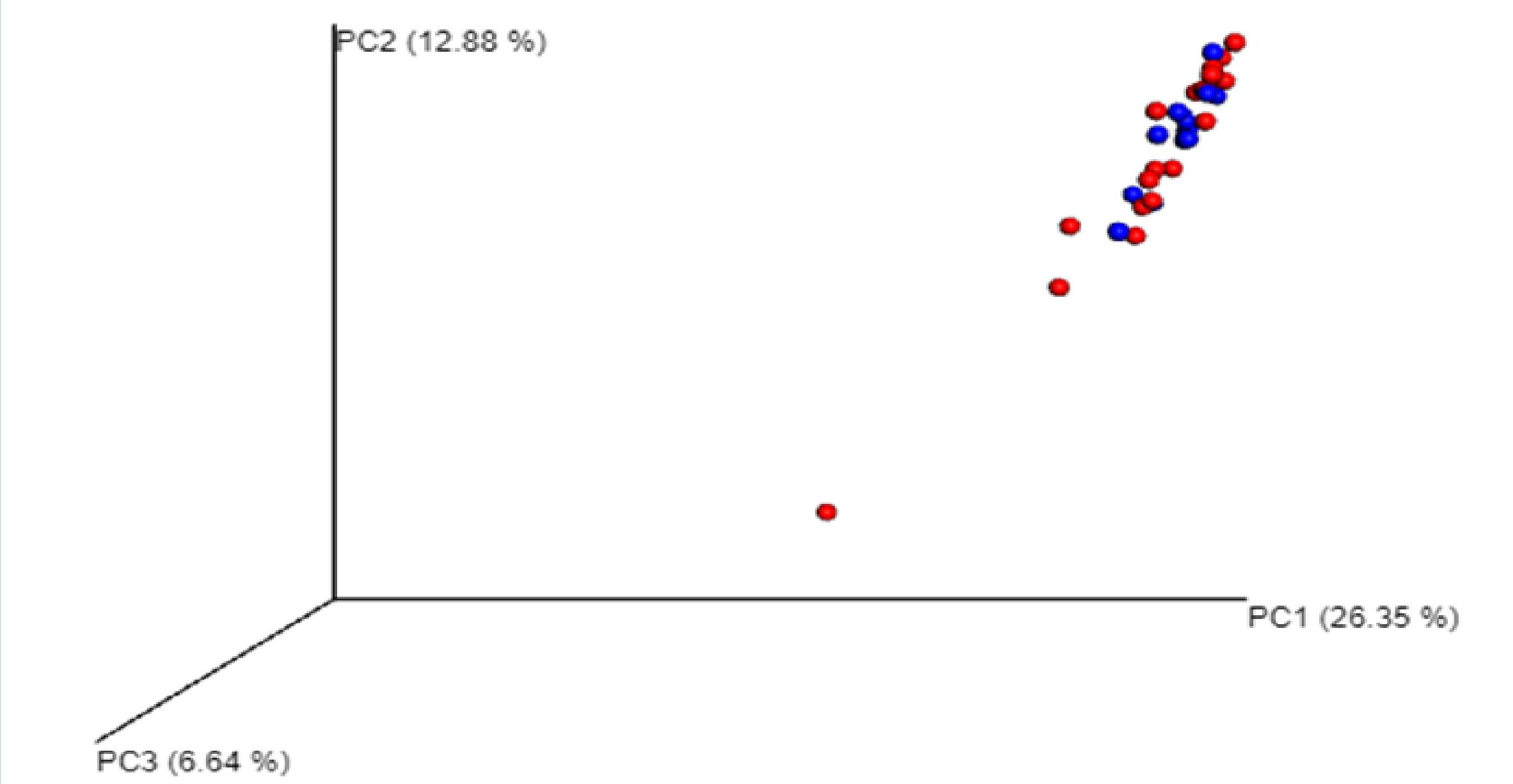


Figure 2: Effect of Disease state on fecal sample clustering by PCOA.
Blue=samples that were collected from patients that had prostate cancer.
Red=samples that were collected from patients with BPH.



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

Taxonomy Legend	Pre Biopsy Urine PC	Pre Biopsy Urine BPH	Pre Biopsy Fecal PC	Pre Biopsy Fecal BPH
Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	0.1%	0.6%	7.2%	7.7%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prevotellaceae;Prevotella	9.3%	3.2%	9.3%	12.6%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.1%	0.1%	2.7%	4.8%
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	10.1%	0.3%	37.9%	20.2%
Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Veillonella	13.9%	3.4%	0.1%	0.0%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	16.4%	11.2%	0.2%	0.2%
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	7.0%	18.0%	0.0%	0.0%
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	9.2%	2.6%	0.0%	1.9%
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	1.7%	0.3%	1.9%	1.7%
Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	2.8%	8.2%	0.1%	1.3%
Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Enterobacter	0.0%	0.0%	0.2%	0.1%
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0.1%	6.9%	0.0%	0.0%
Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	0.7%	10.3%	0.0%	0.1%

CONCLUSIONS

The difference in the urinary tract microbial profile supports a possible association for the bacterial environment inside the prostate and the development of prostate cancer. We plan on validating these results in a larger cohort of patients.