

# #602 Urinary Microbiome and its Correlation with Functional Disorders of the Genitourinary Tract

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## Introduction

Microbiota is a collection or community of microbes. "Microbiome" refers to the full collection of genes of all these microbes. Opposite the common misuse of these two terms they carry distinct meanings which enforces the careful use of the two. Microbial populations are present in the human body, residing in different organs such as the gastrointestinal tract, the skin, upper respiratory and the genital tracts. There are different elements contributing to shape characteristics of the microbiome communities in the body.

A standard urine culture does not identify slow growing, anaerobic and fastidious bacteria. However, rather positively; culture independent methods, in particular 16S rRNA gene sequencing, have established that standard urine culture protocols are incapable of distinguishing the preponderance of bacteria living in urine samples. In this study, we give an overview on all the available published literature on the relationship between the urinary microbiota and functional disorders of the genitourinary tract, including bladder pain syndrome, prostatitis, stone disease and bladder cancer.

## Methods and Materials

We present a systematic review of the available literature on microbiome and functional disorders of the genitourinary tract. The studies were searched through PubMed, Medline and Cochrane databases. The MeSH search was conducted through the association of microbiome and microbiota with genitourinary tract disorder, urinary tract symptom, urinary tract infections, overactive bladder, urinary incontinence, interstitial cystitis, bladder pain syndrome, chronic prostatitis, pelvic pain and kidney stones.

The initial search identified 743 studies. All included studies were written in English and were published between January 2007 and October 2018. Of the 753 identified citations, 504 were non-duplicate and thus admissible. 228 were excluded after screening the title and abstract. Of the remaining 276, 122 were eliminated, having reviewed the entire length of the articles. Ultimately; 124 studies were selected for inclusion in the review and Meta-Analyses (PRISMA) methodology. Of these 124, 40 were directly regarding microbiome and microbiota.

## Conclusions

The urinary microbiome is an exciting and fresh notion which has overwhelmingly captivated the fascination of medical research. The little while, beginning from its revelation, has been fruitful, producing mountainous publications by a variety of research teams, who have thus far revised our vision towards the role of bacteria in the urinary tract and the very perception of genitourinary health.

A main advantage the deeper understanding of the urinary microbiome should yield better methods to restore the microbiota to a healthy state, providing symptom relief. Opportunities to modify the urinary microbiome without antibiotic use are exciting possibilities for future research.

## Discussion

Evidence proves the bladder to contain microbiomes which under standard conditions are not perceivable. Whether they stand to benefit us or have pathogenic roots is dependent upon the singular microbiome characteristic. In regard to the uncovering of the relationship between microbiome and the lower urinary tract symptom, there has been a gargantuan amount of research in recent years.

All urine samples are collected using a transurethral catheter in order to elude the urine from bacterial contamination from the external tissues and in order to determine the resident microbial, the bacterial 16S rRNA is amplified through PCR and the NGS sequencing is performed through illumina MiSeq.

In all the studies concentrating on the relation among microbiome and OAB, the demonstration was made that Lactobacillus in patients suffering from OAB had increased in comparison to the subjects without the condition. However; in only one study a decrease in Lactobacillus was observed with an increase of Gardnerella spp.. In another study in patients suffering from OAB, an increase in Streptococcus compared to healthy subjects was observed.

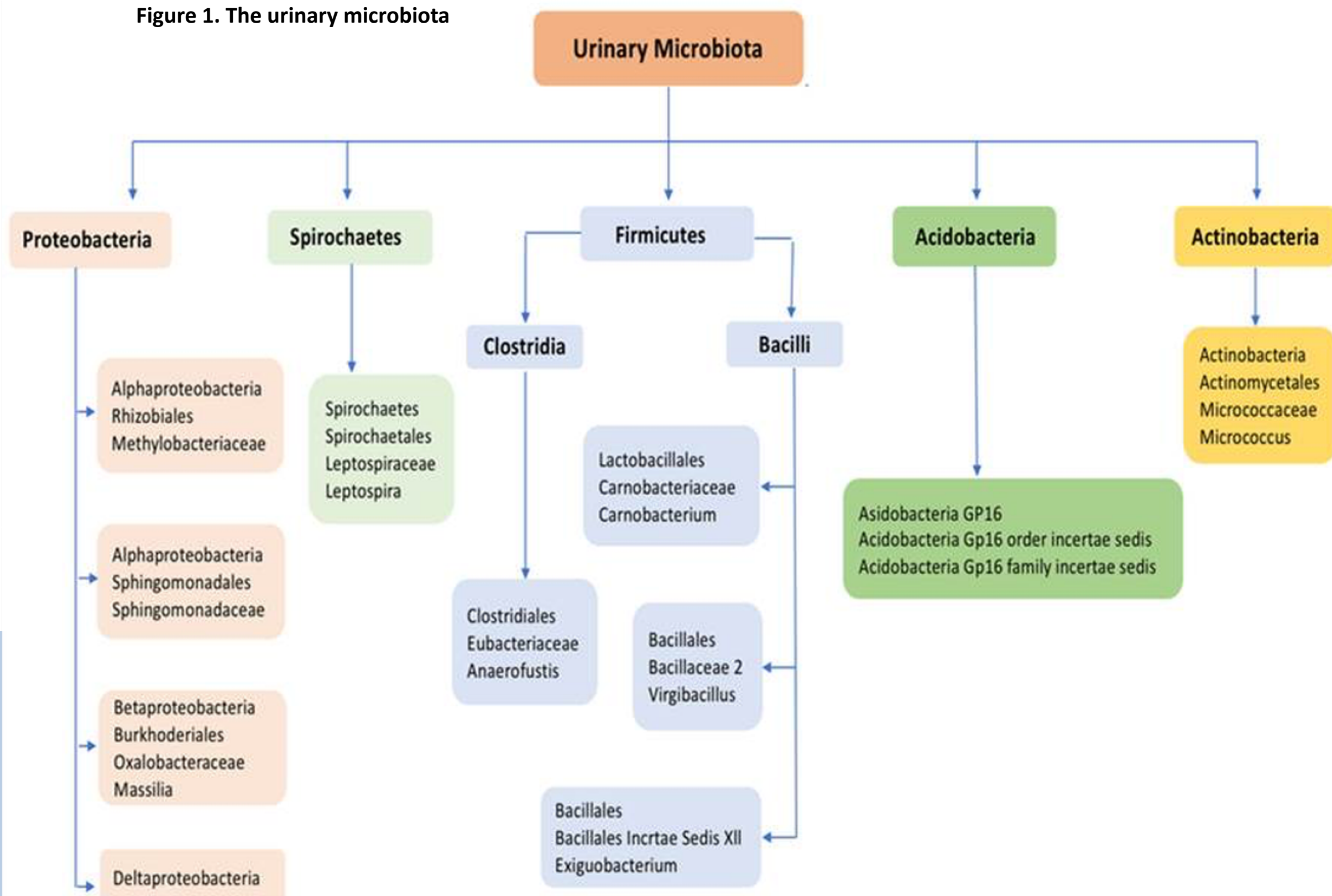
In the case of BPS/IC patients, it was evident that these patients had an increase in Lactobacilli. So far, there is still no evidence provided of a relation between the urinary tract microbiome and Detrusor Overactivity.

As regards to the CP/CPSP, in one study Burkholderia cenocepacia was detected. In a separate study, a increase in the Enterococcus levels was witnessed where as the Escherichia coli were decreased. In a third study, it was seen that the Clostridia and Bacteroidetes were increased.

Table 1. Summary of studies on the role of Microbiota in OAB, BPS/IC, CP/CPSP.

Study	OAB	BPS/IC	CP/CPSP
Wolfe et al. (2012)	<i>Lactobacillus</i> ↑		
Siddiqui et al. (2012)		<i>Lactobacillus</i> ↑	
Hilt et al. (2014)	<i>Lactobacillus</i> ↑		
Pearce et al. (2014)	<i>Gardnerella</i> spp. ↑ <i>Lactobacillus</i> ↓		
Siddiqui et al. (2014)	<i>Streptococcus</i> ↑		
Pearce et al. (2015)	<i>Lactobacillus</i> ↑		
Nickel et al. (2015)		<i>Lactobacillus</i> ↑	
Nickel et al. (2015)			<i>Burkholderia cenocepacia</i> ↑
Yu et al. (2015)			<i>Enterococcus</i> ↑ <i>E.coli</i> ↓
Thomas-White et al. (2016)	<i>Lactobacillus</i> ↑		
Shoskes et al. (2016)			<i>Clostridia</i> & <i>Bacteroidetes</i> ↑

Figure 1. The urinary microbiota



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