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Bacterial Composition of the Urinary Microbiome in South African Men with and without *Chlamydia trachomatis* Infection

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ABSTRACT

Background: The bacterial composition of the male urinary microbiota has been suggested to be related to sexually transmitted infections (STIs). *Chlamydia trachomatis* (*C. trachomatis*) is the most prevalent bacterial STI and the leading cause of STIs worldwide. Several studies have found that the genital microbiome plays a role in the host's susceptibility to chlamydial infection. Our study therefore assessed the bacterial composition of the urinary microbiome in South African men who have sex with men (MSM) with and without *C. trachomatis*.

Methods: This cross-sectional study used urine samples from MSM, 18 years and older, attending care at the King Edward VIII Hospital and the Aurum Institute in Durban, South Africa, between October 2021 and July 2022. A total of 200 urine samples were tested for *C. trachomatis* infection using the Applied Biosystems™ TaqMan® Assays. The urinary microbiota was characterized using 16S rRNA (V3 and V4) gene sequencing on the Illumina MiSeq platform.

Results: Of the 200 males, 12 (6.0%) tested positive for *C. trachomatis* infection. The amplicon sequence variants (ASVs) were identified across all samples. The ASVs were unique to 92 (representing 5.92% of the total number of sequences) of the positive samples, 302 (16%) of the negative samples, and 61 (78.08%) were shared between both groups. A higher abundance of *Streptococcus*, *Corynebacterium*, and *Staphylococcus* was observed in both the infected and uninfected groups. Urotypes corresponding to the female urinary tract such as *Prevotella, Gardnerella, Sneathia* and *Lactobacillus* were found to be components of the urinary microbial community of MSM.

Conclusions: It is clear from our study that unique bacterial communities, especially those associated with the female urogenital tract, are present in MSM.

Keywords: Urinary microbiome, *Chlamydia trachomatis*, MSM

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