

Characterizing the Male Urogenital Tract Microbiome using 16S rRNA Gene Analysis



Kirsty Lee Garson¹, Enock Havyarimana², Katie Lennard², Clive Gray², Heather Jaspan^{2,3}, Nicola Mulder¹

¹Division of Computational Biology, Department of Integrative Biomedical Sciences, University of Cape Town, South Africa

²Division of Immunology, Department of Pathology, University of Cape Town, South Africa

³Seattle Children's Research Institute, University of Washington, USA

1. BIOLOGICAL CONTEXT

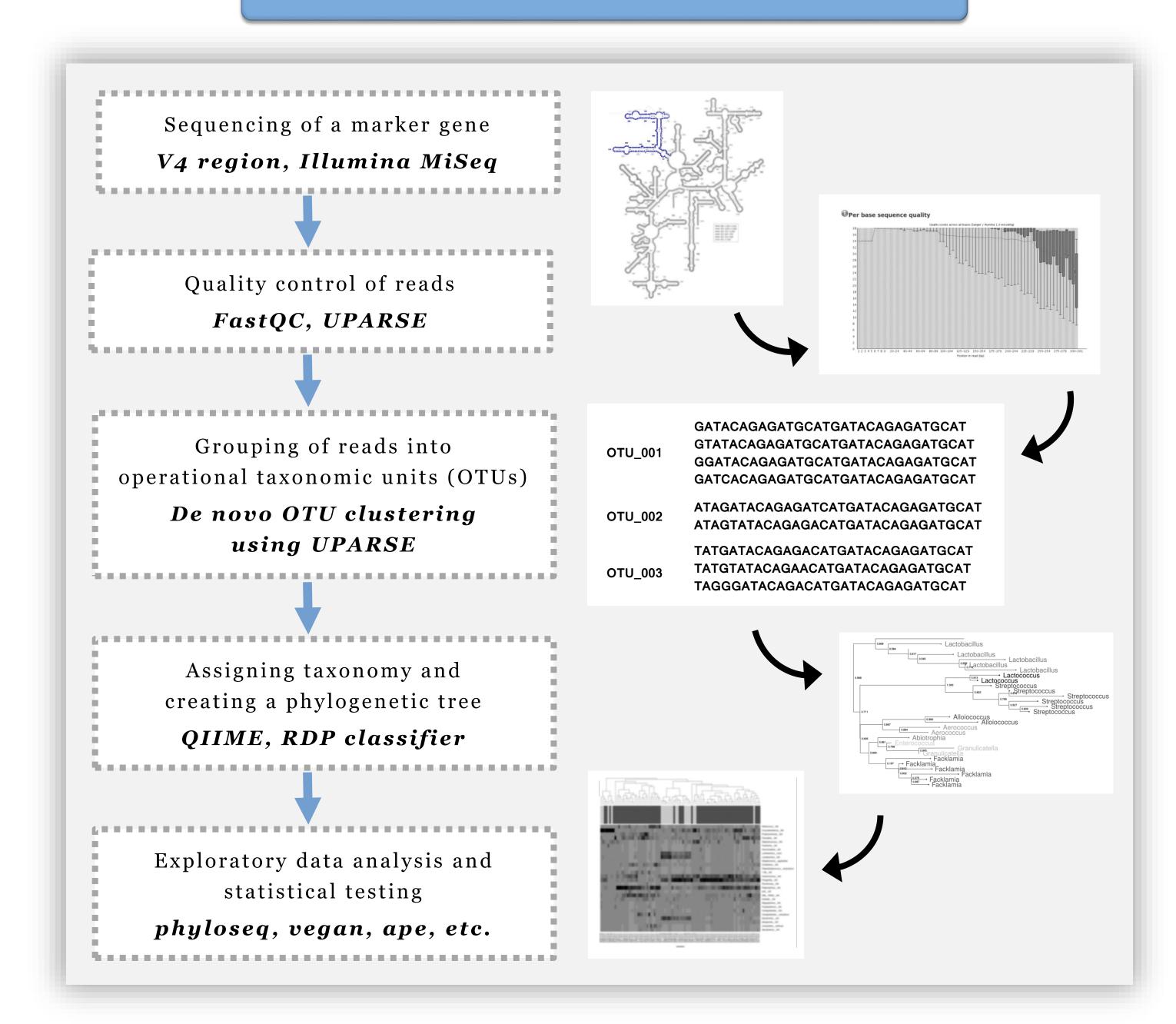
The male urogenital tract is the site of interactions between the microbiome, the immune system and various sexually-transmitted pathogens. A better understanding of these interactions may enable the development of interventions which decrease susceptibility to sexually transmitted infections (STIs), such as HIV.

A number of randomized, controlled trials have found that medical male circumcision reduces susceptibility to HIV.

- How does circumcision influence the composition of the male urogenital tract microbiome?
- What effect does circumcision have on the specific taxa (genera/species) which have been associated with increased/decreased HIV susceptibility?

To address these questions, young males scheduled to undergo circumcision were recruited into a longitudinal study. Penile swabs were collected at various time points pre- and post-circumcision for microbiome analysis.

2. OVERVIEW OF THE ANALYSIS



3. RESULTS OF THE ANALYSIS

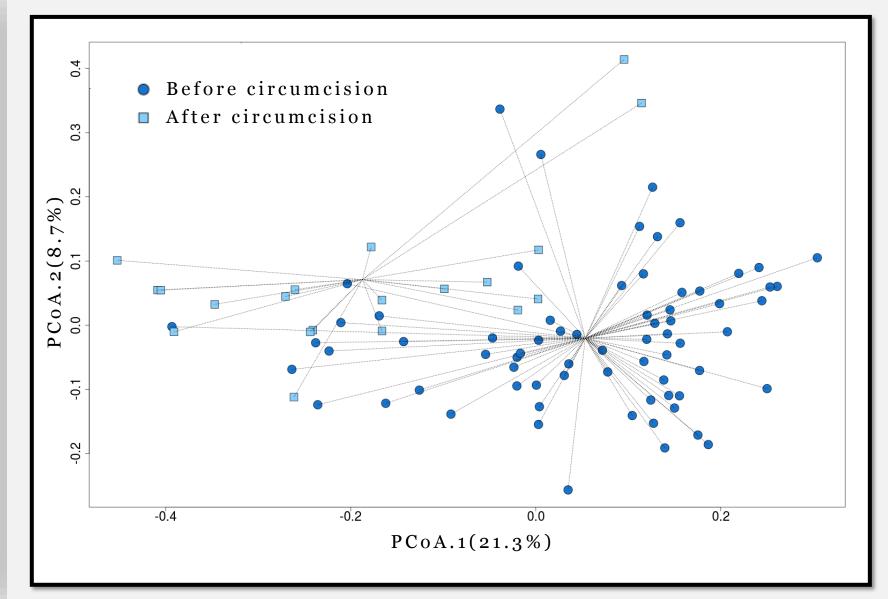


Figure 1: Principle
coordinates analysis (PCoA)
of samples by circumcision
status. Each sample is
represented by a single
point, with the distances
between points indicating
their degree of similarity.
A Permutation Multivariate
Analysis Of Variance
(PerMANOVA) confirmed
that the composition of the
two sets of samples were
distinct (p = 0.001).

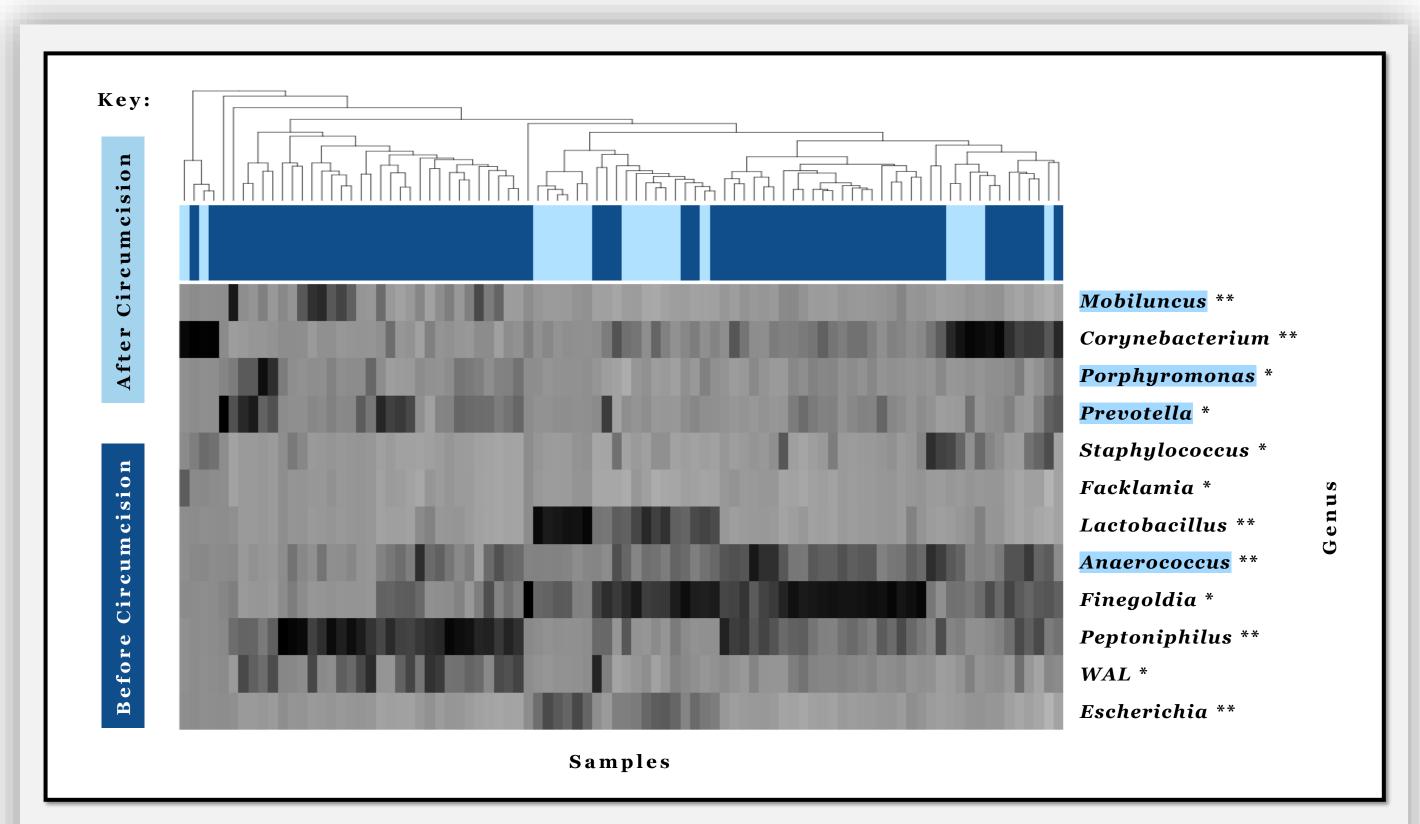


Figure 2: Average-linkage hierarchal clustering revealed patterns in the relative abundance of specific genera before and after circumcision (* p<0.05, ** p<0.01). Taxa highlighted in blue have been linked to increased HIV susceptibility¹.

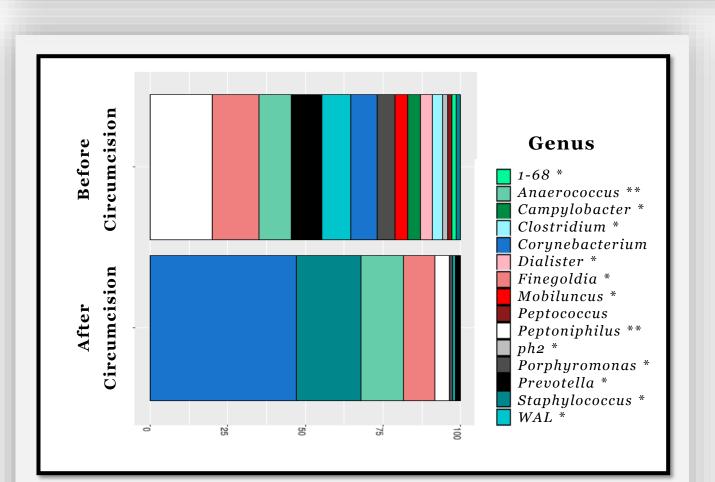


Figure 3: A comparison of the average composition of samples collected pre- and post-circumcision (* p<0.05, ** p<0.01).

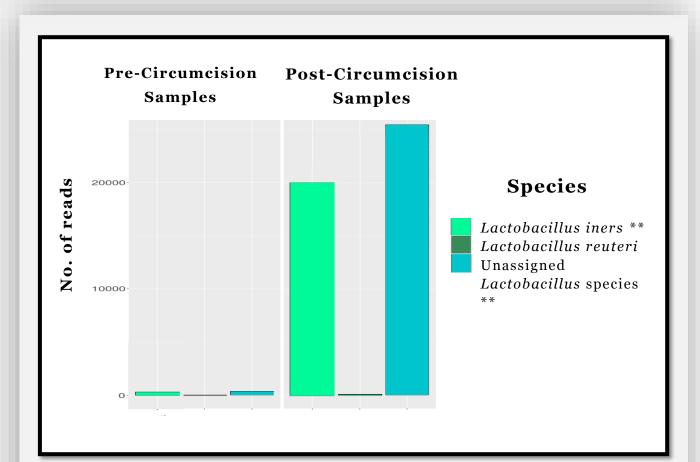


Figure 4: No. of reads assigned to the Lactobacillus genus, which has been linked to decreased HIV susceptibility. (** p<0.01).

The analysis of samples taken before and after circumcision revealed distinct bacterial community composition (Figure 1). Several taxa that have been linked to increased HIV susceptibility¹, were decreased post-circumcision (Figure 2, Figure 3).

In contrast, *Lactobacillus* species, which are considered to be protective in the female genital tract², were increased substantially after circumcision (Figure 4). These findings have implications for the development of potential methods to reduce HIV susceptibility by modulating the (uro)genital tract microbiome.

- ¹Liu CM et al. <u>Penile anaerobic dysbiosis as a risk factor for HIV</u> infection. mBio 8:4, 2017.
- ²Petrova MI et al. <u>Lactobacillus species as biomarkers and agents that</u> can promote aspects of vaginal health. Front. Physiol. 6:81, 2015.

4. ACKNOWLEDGEMENTS

- The analysis was funded by the SA National Research Foundation.
- It forms part of a study to investigate factors affecting HIV susceptibility in the genital tracts of young men, funded by the European & Developing Countries Clinical Trials Partnership.
- The analysis was carried out using the UCT High Performance Computing facility and the CBIO 16S Gene Analysis Pipeline.
- A travel fellowship was provided by the African Partnership for Chronic Disease Research.









