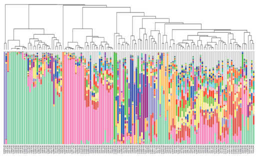
Nov 25, 2020 Version 4

Protocols for "The female urinary microbiota in relation to the reproductive tract microbiota." V.4



GigaByte

✓ Peer-reviewed method

DOI

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Protocol status: Working
We use this protocol and it's working

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Keywords: female urinary microbiota in relation, female urinary microbiota, urinary microbiota, detailed comparison of the urinary microbiota, common urinary bacterial community types in the cohort, urinary bacterial community, distinct bacterial communities in urine, common urinary bacterial community type, female reproductive tract microbiota, multiple sites of the female reproductive tract microbiota, reproductive tract microbial community, potential links between female urine, microbiota, female urine, distinct bacterial community, distinct microbial community, potential connectivity among microbiota, similar to the microbiota, human urine, bacteria, urine sample, relationship between urine, female urogenital system, live bacteria culture, urine, reproductive tract, streptococcus, lactobacillus, multiple sites of the reproductive tract, genital tract, rrna gene amplicon, chinese women of reproductive age, vagina, reproductive age, uterine cavity than to those of the vagina

Abstract

Human urine is traditionally considered to be sterile, and whether the urine harbours distinct microbial communities has been a matter of debate. Potential links between female urine and reproductive tract microbial communities is currently not clear. Here, we collected urine samples from 147 Chinese women of reproductive age and explored the nature of colonization by 16S rRNA gene amplicon sequencing, quantitative real-time PCR, and live bacteria culture. To demonstrate the utility of this approach, the intra-individual Spearman's correlation was used to explore the relationship between urine and multiple sites of the reproductive tract. PERMANOVA was also performed to explore potential correlations between the lifestyle and various clinical factors and urinary bacterial communities. Our data demonstrated distinct bacterial communities in urine, indicative of a non-sterile environment. *Streptococcus*-dominated, *Lactobacillus*-dominated, and diverse type were the three most common urinary bacterial community types in the cohort. Detailed comparison of the urinary microbiota with multiple sites of the female reproductive tract microbiota demonstrated that the urinary microbiota were more similar to the microbiota in the cervix and uterine cavity than to those of the vagina in the same women. Our data demonstrate the potential connectivity among microbiota in the female urogenital system and provide insight and resources for exploring diseases of the urethra and genital tract.

Troubleshooting

Files

SEARCH

Protocol

NAME

DNA extraction for human microbe samples.

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A Bioinformatics Analysis workflow for 16S rRNA Amplicon Sequencing data

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NAME

Quantitative real-time PCR for the four Lactobacillus species

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