Title

MP15-09 ALTERATIONS IN THE URETHRAL MICROBIOME IN PATIENTS WITH GENITOURINARY LICHEN SCLEROSIS

Journal

Investigative Urology, 199(4)

ISSN

0021-0005

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Publication Date

2018-04-01

DOI

10.1016/j.juro.2018.02.522

Peer reviewed

RESULTS: 42/506 (8.2%) Patients had significant pre-operative bacteriuria. Most common organisms were E. coli (30.4%) and E. faecalis (19.5%). 58/506 (11.4%) Patients had significant post-operative bacteriuria at time of hospital discharge with E. coli as most frequent organism (27.8%), followed by E. faecalis (22.2%). 36/506 (7.1%) Patients had significant post-operative bacteriuria 3 weeks after TURP with E.faecalis (44.4%) as most frequent bacteria, next to E.coli (36.1%). 31/506 (6.1%) Patients had significant positive blood cultures (at the recovery unit). E.coli and hemolytic Streptococci were the most frequent organisms (each 19.4%). 24/506 (4.7%) Patients had significant positive irrigation fluid cultures (upon arrival at the ward). E.coli was the most found organism (29.2%), followed by E. faecalis (25%). 47/506 (9.3%) Patients had a significant positive prostate tissue culture with E.faecalis (36.1%) and Staphyococci (14.9%) as most found organisms.18/506 (3.6%) Had uncomplicated fever during or after hospitalization and 1/506 (0.2%) patient had septicaemia.

CONCLUSIONS: A low rate of clinical infectious complications (fever or septicaemia) was observed (3.8%) despites the high rate of post-operative bacteriuria at time of discharge (11.4%) and after 3 weeks (7.1%). The high number of positive blood (6.1%), irrigation fluid (4.7%) and prostate tissue cultures (9.3%) also were of limited clinical relevance. In our opinion post-operative bacteriuria and positive blood cultures in the absence of clinical infection, should not be treated.

Source of Funding: none

MP15-09
ALTERATIONS IN THE URETHRAL MICROBIOME IN PATIENTS WITH GENITOURINARY LICHEN SCLEROSIS

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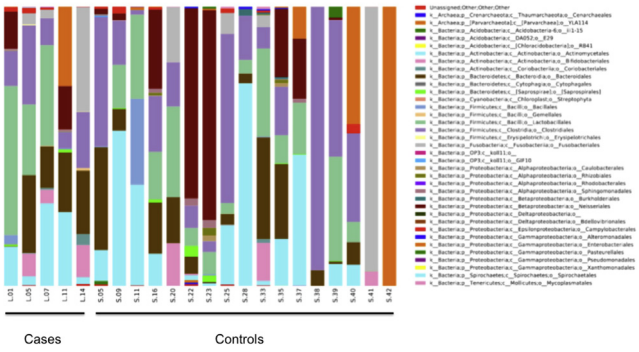
INTRODUCTION AND OBJECTIVES: Alterations in the urinary microbiome have been associated with urological disease, such as neurogenic bladder dysfunction and interstitial cystitis. Genitourinary lichen sclerosis (GU-LS) is a chronic, inflammatory condition of unknown etiology, and explorations in the urinary microbiome may shed light into the pathophysiology of this complex disease.

METHODS: We collected a mid-stream urine sample from men with GU-LS (cases) and men with urethral stricture disease (controls). Cases and controls were matched on age and IPSS score. Patients were excluded if they had recent genitourinary surgery/instrumentation (<2 months) or a recent urinary tract infection (<6 months). Samples were provided for DNA extraction, PCR amplification of the V4 hypervariable region of the 16s rRNA gene, and sequencing. Paired sequencing reads were quality filtered into operational taxonomic units (OTUs) using a 97% sequence similarity threshold. Alpha diversity was measured in richness (number of different OTUs), evenness (abundance of OTUs), and diversity (Shannon, Simpson, Inverse Simpson, and Faith's phylogenetic diversity). Beta diversity was measured via principal coordinates analyses.

RESULTS: Successful amplifications occurred in 24/41 (59%) samples; 22 (92%) of amplified samples had quality filtered read numbers above the specified rarefied threshold. There were 5 cases and 17 controls with analyzable data. No differences were observed in median age (57 v. 50, p=0.55) or median IPSS score (16 v. 15, p=0.88). Alpha diversity significant factors included richness (p=0.02) and diversity (Faith's phylogenetic diversity p=0.01, Simpson diversity p=0.05, and Inverse Simpson diversity p=0.05). Evenness and Shannon diversity did not reach statistical significance (p=0.41 and p=0.06, respectively). We found no differences in beta diversity. Compared to controls the microbiome of patients with GU-LS was enriched with Streptococcus taxa and depleted with respect to Enterobacteriaceae taxa.

CONCLUSIONS: Men with GU-LS had significantly higher microbiome diversity compared to control patients. However, the relative abundance of species within individual patients did not differ between controls and GU-LS patients. Further work will be required to elucidate the clinical relevance of these variations in the urinary microbiome.

Figure 1. Relative abundance summaries for order-level taxonomic classifications by sample type



Source of Funding: Alafi foundation

MP15-10
NEOVAGINAL MICROFLORA AFTER SURGICAL GENDER REASSIGNMENT IN HIV, HBV AND HCV SERONEGATIVE TRANSSEXUAL WOMEN

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INTRODUCTION AND OBJECTIVES: The investigation of the neovaginal microflora can help during the post-surgery follow-up of transgender women in order to ensure a proper therapy in case of the onset of an infectious disease. We mapped the neovaginal microflora during the early perioperative days after male to female (M-F) gender reassignment surgery in HIV, HBV and HCV seronegative and healthy transsexual women.

METHODS: Between November 2016 and January 2017 we collected 2 neovaginal swabs (one in the neo-vaginal fundus and one in the proximity of the urethral meatus) during the early perioperative days from 8 patients (pts) who underwent M-F gender surgical reassignment. The V3-16S rRNA Next Generation Sequencing (NGS) and a multiplex PCR technology were used to investigate the microbial composition and the presence of Sexual Transmitted Infections, respectively. QIIME 1.8.01 was used to process the NGS data.

RESULTS: Patients median age was 35 (24-49) years. For at least one year, all pts were taking an androgen deprivation therapy and an estrogen therapy, which was suspended at least 20 days before surgery. All pts were HIV, HBV and HCV seronegative and heterosexual. Swabs were performed between the 4th and the 10th postoperative days when no sign of infection was clinically present. All pts were using an iodone solution for the daily neovaginl hygiene. No STI, including Chlamydia tracomatis, Neisseria gonorrhoeae, Mycoplasma/Ureaplasma, HPV, Trichomonas vaginalis and Treponema pallidum, was detected in the samples analyzed. Prevotella was the predominant genus in the neovagina. Moreover, the samples showed the presence of Bacteroides, Escherichia, and Proteus while no Lactobacilli were reported.

CONCLUSIONS: We characterized the microbiome of the neovagina in the early postoperative days after M-F gender reassignment surgery. Despite estrogen substitute therapy, neovagina appeared massively colonized by microorganisms usually resident in the male urogenital tract and often responsible for genito-urinary infections in women while the native vaginal Lactobacilli were absent. To our knowledge, this is the first report describing the neovaginal microbiota in the early postoperative days after M-F gender reassignment surgery in healthy transsexuals women. Therefore, our study provides the standard model of vaginal microbiota of healthy transsexual women.

Source of Funding: none