

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

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Introduction and objectives

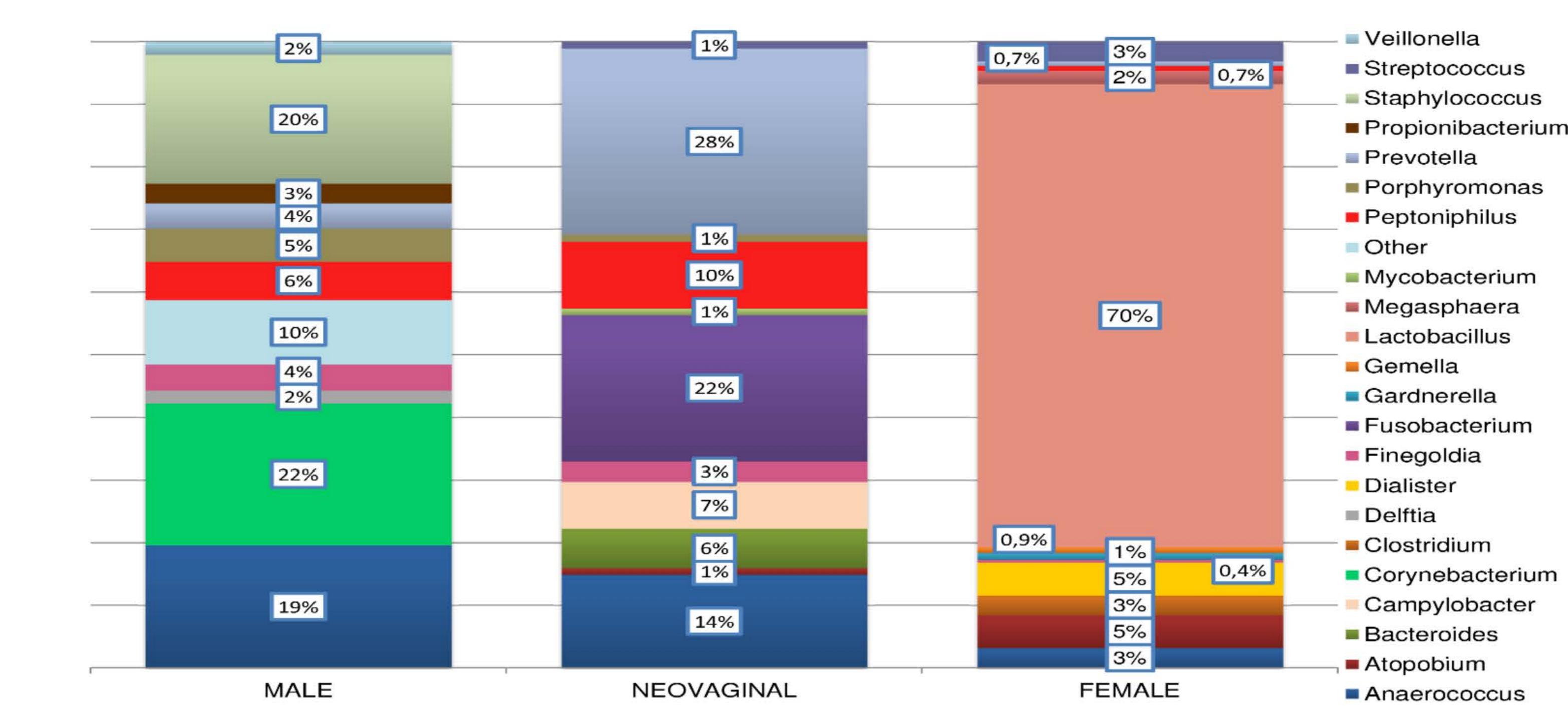
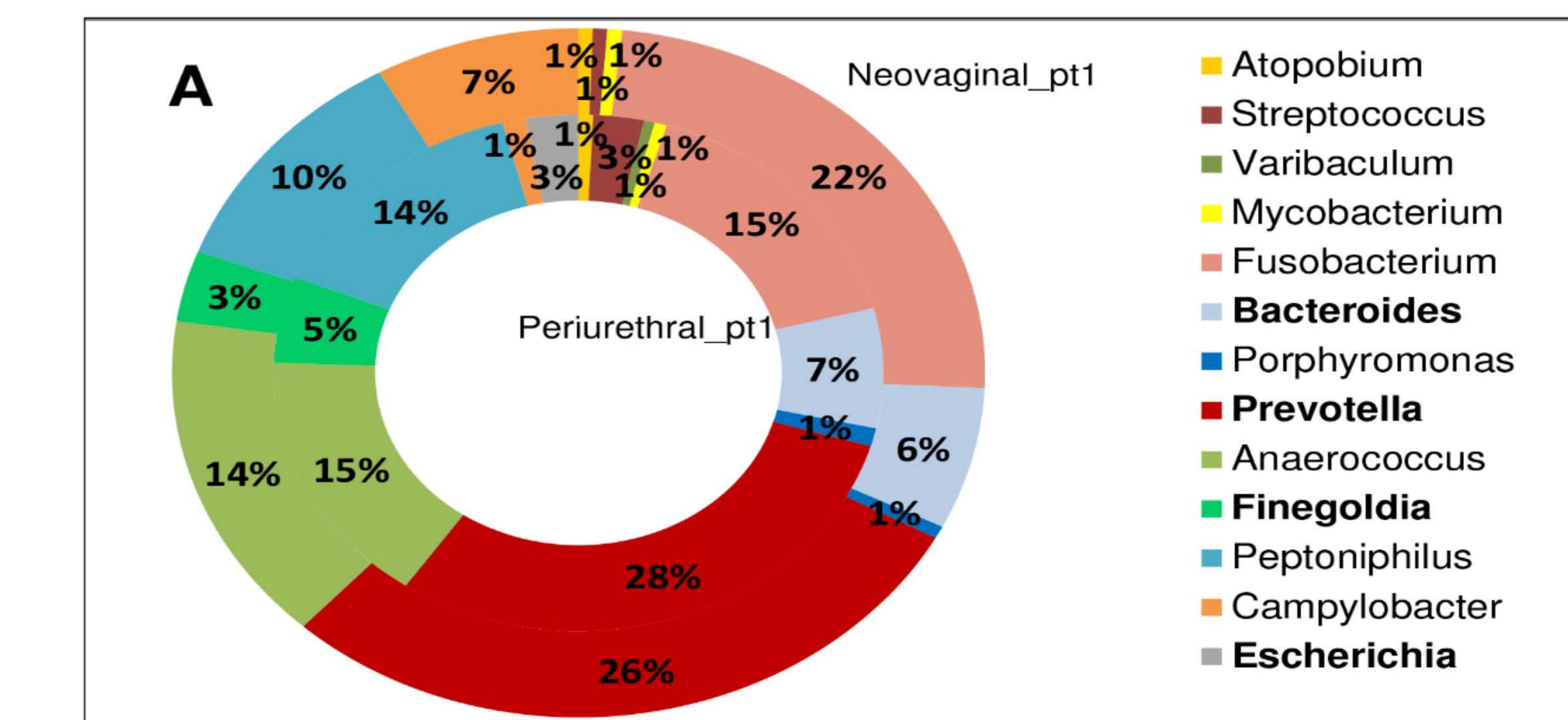
The investigation of the neovaginal microflora can help during the post-surgery follow-up of transgender women in order to ensure a proper therapy in case of the onset of an infectious disease. We mapped the neovaginal microflora during the early perioperative days after male to female (M-F) gender reassignment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

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 iodine solution for the daily neovaginal 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.

Materials and 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.



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.