ORIGINAL RESEARCH—TRANSGENDER AND GENDER NONCONFORMANCE

Rectal *Lactobacillus* Species and Their Influence on the Vaginal Microflora: A Model of Male-to-Female Transsexual Women

Ljubomir Petricevic, MD,* Ulrike Kaufmann, MD,* Konrad J. Domig, PhD,† Manuel Kraler, MS,†
Julian Marschalek, MD,* Wolfgang Kneifel, PhD,† and Herbert Kiss, MD, MBA*

*Department of Obstetrics and Gynecology, Medical University of Vienna, Vienna, Austria; †Department of Food Science and Technology, BOKU—University of Natural Resources and Life Sciences, Vienna, Austria

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ABSTRACT

Introduction. Based on *Lactobacillus* species co-colonizing the vagina and rectum, it has been hypothesized that the rectum may be an important reservoir for vaginal colonization by lactobacilli. There are no data on this issue in male-to-female transsexual women.

Aim. We undertook this observational study to characterize the *Lactobacillus* species present in the neovagina and rectum of male-to-female transsexual women and to determine the degree of neovaginal-rectal co-colonization in order to gain a better understanding of the potential role of the gut as a reservoir for genital lactobacilli.

Methods. Sixty-one male-to-female transsexual women with penile skin lined neovagina without clinical signs of infection were recruited on an ongoing basis from among male-to-female transsexual outpatients. Neovaginal and rectal smears were taken for molecular *Lactobacillus* species profiling by denaturing gradient gel electrophoresis (PCR-DGGE).

Main Outcome Measures. Matching *Lactobacillus* species between neovagina and rectum.

Results. Forty-three of the 61 male-to-female transsexual women (70.5%) simultaneously harbored the same lactobacilli in both the neovagina and rectum. We found 276 neovaginal and 258 rectal DGGE bands representing 11 *Lactobacillus* species, with 201 matches of the same *Lactobacillus* species in neovagina and rectum. 37 of the 61 women (61%) had two or more matching *Lactobacillus* species.

Conclusion. These data support the hypothesis that the rectum may play an important role as source of *Lactobacillus* species that colonies neovagina of male-to-female transsexual women. In view of the specific anatomical circumstances of the study population, these findings may be extended to the general population of women. **Petricevic L, Kaufmann U, Domig KJ, Kraler M, Marschalek J, Kneifel W, and Kiss H. Rectal *Lactobacillus* species and their influence on the vaginal microflora: A model of male-to-female transsexual women. J Sex Med 2014;11:2738–2743.**

Key Words. *Lactobacillus*; Vaginal Lactobacilli; Neovagina; Rectum; Transsexual Women; Gender Dysphoria

Introduction

Various bacterial species are known to concurrently colonize both the gastrointestinal and reproductive tracts, and it has been hypothesized that the rectum may function as a source of organisms colonizing the vagina [1]. The gut has also been suggested as a reservoir for vaginal colonization by *Lactobacillus* species, thereby contributing to the maintenance of a normal vaginal microflora [2,3]. This proposition has been supported by studies on the use of probiotics showing that lactobacilli can also be delivered to the vaginal environment by oral ingestion [4–7].

Antonio et al. found that co-colonization of the vagina and rectum by *Lactobacillus* species was associated with a lower prevalence of bacterial vaginosis [1]. El Aila et al. showed strong correlations between vaginal and rectal lactobacilli of pregnant women [8,9]. In one of our previous investigations, we found that 80% of pregnant and 40% of postmenopausal women harbored one or more *Lactobacillus* species in both vagina and rectum [10]. By contrast, Gustafson et al. reported a lack of correlation between the vaginal and rectal *Lactobacillus* microflora [11].

To obtain additional evidence of the microbial connection between vagina and rectum, we investigated the degree of matching *Lactobacillus* species in both neovagina and rectum in a population of male-to-female transsexual women. The neovagina is a skin-lined cavity without mucosa that does not communicate with internal pelvic organs. The physiology and pathophysiology of neovagina differs from that of the natal vagina. Thus, the neovagina is characterized by a constant neutral pH, and in the absence of monthly hormone cycles, the neovaginal microflora does not undergo cyclic shifts and is a mix of aerobe and anaerobe species, whereas lactobacilli were found in only 4% [12,13].

Although the penile skin lined neovagina had been thought to be unable to support the growth of lactobacilli, we detected *Lactobacillus* species from the neovagina of up to 75% of transsexual women [14]. Data on rectal lactobacilli are not currently available for transsexual women.

Aim

We undertook this study to characterize the Lactobacilli present in neovagina and rectum of male-to-female transsexual women and to determine the degree of neovaginal-rectal co-colonization. Due to the anatomical and hormonal similarities between transsexual male-to-female women receiving hormone substitution therapy and the general female population, transsexual women may be considered an ideal model for investigations on the origin of vaginal lactobacilli. Detection of the same lactobacilli in both neovagina and rectum of transsexual women would provide a further evidence for the gut as a reservoir for neovaginal lactobacilli.

Methods

This observation was performed in accordance with the Declaration of Helsinki and the guidelines for Good Clinical Practice after approval of the ethics committee of the Medical University of Vienna (EK 982/2010) had been granted. Informed consent was obtained from all study participants prior to enrolment.

We observed male-to-female transsexual women without clinical signs of infection who were recruited on an ongoing basis from among transsexual outpatients of the Medical University of Vienna during standard routine follow-up examinations. Transsexual women with diarrhea, constipation, rectal pathologies including previous gut operations, or urinary tract infection and patients having received antibiotic therapy in the previous 4 weeks or using either oral or vaginal probiotics were excluded from the study. All participants had undergone sex reassignment surgery (SRS) using the inverted penile skin flap technique [15] at least 1 year before enrolment. All transsexual women were treated according to the Standards of Care of the World Professional Association of Transgender Health (WPATH) [16].

From each participant, a smear from both lateral walls of the neovagina as well as a smear from rectum were taken and transferred to transport medium (Copan Innovation, Italy). The smears were analyzed by the culture-independent denaturing gradient gel electrophoresis (PCR–DGGE) technique based on the primers published by Walter et al. (2001) [17]. The bacterial cells from each swab were extracted in 1 mL sterile phosphate buffered saline. From this suspension the DNA was extracted, amplified with the primers mentioned above, and analyzed by DGGE. Bands with a migration pattern different from the lactobacilli marker bands were excised, re-amplified, and identified by sequencing. The technical details of the PCR-DGGE procedure applied have recently been published [14].

Statistics

Because this is the first study on neovaginal and rectal lactobacilli detection in transsexual women, no historical estimates for sample size calculations were available. We included all patients matching the inclusion criteria during one year. Demographic and background information is summarized and displayed using descriptive statistical techniques.

Main Outcome Measure

The main outcome measure was the molecularly detected diversity of *Lactobacillus* species and the matching of *Lactobacillus* species between neovagina and rectum of male-to-female trans-