The neovaginal microbiome of transgender women post-gender reassignment surgery

Kenzie D. Birse
Kateryna Kratzer
Christina Farr Zuend
Sarah Mutch
Laura Noël-Romas
Alana Lamont
Max Abou
Emilia Jalil
Valdiléa Veloso
Beatriz Grinsztejn
Ruth Khalili Friedman
Kristina Broliden
Frideborg Bradley
Vanessa Poliquin
Fan Li
Carolyn Yanavich
Adam Burgener
Grace Aldrovandi

Video Byte

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Abstract

Gender reassignment surgery can be gender-reaffirming for many transgender women. This process often involves using existing tissue to create a neovagina. For those assigned female at birth, optimal vaginal microbiota and microbes linked to increased risk of STIs and bacterial vaginosis are well characterized. In contrast, data about the microbial environment of the neovagina are limited. A new study aimed to further characterize the microbial composition and function of the neovagina. Researchers used metaproteomics to compare the microbiota found in neovaginal and rectal secretions from transgender women with those found in vaginal secretions from cisgender women. They found that bacterial taxa differed between neovaginal and cis vaginal samples. Interestingly, functional pathways upregulated in neovaginas were similar to those in cis vaginas during an inflammatory response to bacterial vaginosis, and estrogen-regulated keratins were expressed at a lower level in neovaginas. These results suggest that differences in the neovaginal compartment may increase susceptibility to inflammation and epithelial barrier damage. Although further study is needed, this study sheds light on the microbiome of neovaginal tissue, helping to improve the health of transgender women after gender reassignment surgery.