The neovaginal microbiome of transgender women post-gender reassignment surgery

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Video Byte

Keywords: Transgender women, neovagina, gender reassignment surgery, microbiome, metaproteomics

Posted Date: October 28th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-99187/v1>

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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.