Pilot Study of Vaginal Microbiome Using QIIME 2™ in Women With Gynecologic Cancer Before and After Radiation Therapy

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OBJECTIVES: To characterize the vaginal microbiome using QIIME 2™ (Quantitative Insights Into Microbial Ecology 2) in women with gynecologic cancer.

SAMPLE & SETTING: 19 women with gynecologic cancer before and after radiation therapy at a comprehensive cancer center in Atlanta, Georgia.

METHODS & VARIABLES: This pilot study analyzed vaginal microbiome communities using a microbiome analysis pipeline, beginning with 16S rRNA gene sequencing and processing through use of a bioinformatics pipeline to downstream microbial statistical analysis.

RESULTS: The findings showed the methods to be robust, and most women with gynecologic cancer showed depletion of Lactobacillus. Compared to those pre–radiation therapy, women post–radiation therapy showed higher abundances of Mobiluncus, Atopobium, and Prevotella but lower abundances of Lactobacillus, Gardnerella, and Peptostreptococcus, which are associated with bacterial vaginosis.

IMPLICATIONS FOR NURSING: This study presents the fundamentals of human microbiome data collection and analysis methods to inform nursing science. Assessing the vaginal microbiome provides a potential pathway to develop interventions to ameliorate dysbiosis of the vaginal microbiome.

KEYWORDS vaginal microbiome; 16S rRNA gene; gynecologic cancer; radiation therapy

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