ONLINE EXCLUSIVE

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
***ONF, 46*(2), E48–E59.**
DOI 10.1188/19.ONF.E48-E59

The human body hosts trillions of microbiotas, including bacteria, viruses, fungi, and archaea; this number is close to that of human body cells (Knight & Buhler, 2015; Sender, Fuchs, & Milo, 2016). The human microbiotas and their genomes are collectively called the human microbiome (Ursell, Metcalf, Parfrey, & Knight, 2012), which varies among different hosts and across body sites within a single host (Morgan & Huttenhower, 2012; Spor, Koren, & Ley, 2011). Within the human microbiome, a number of potential biomarkers of cancer diagnosis, treatment, and prognosis have been identified (Rajagopala et al., 2017; Zitvogel, Ayyoub, Routy, & Kroemer, 2016), particularly regarding the roles of the human microbiome in treatment response and efficacy (Wilson & Nicholson, 2017), treatment-related toxicities, such as infections and pain (Kelly, Lyon, Yoon, & Horgas, 2016; Touchefeu et al., 2014), and disparities in treatment outcomes (Abbasi, 2017).

Nurses involved in clinical research and practice are greatly encouraged to have a general understanding of what the human microbiome is, how to measure the human microbiome, what microbiome findings are feasible, and what the applications of microbiome study findings are to clinical care (Claesson, Clooney, & O'Toole, 2017; Goodrich et al., 2014) because findings from current research may affect and be integrated with clinical care processes in the future. As microbiome science moves forward, nurse researchers and practitioners should have a general knowledge of computational analysis of microbiome data and ideally understand the process of human microbiome analysis. In the near future, clinicians may include assessment of a patient's microbiome data in routine clinical practice. Several methods have been used to