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**New Research Uses Composition and Function to Identify Clinically Important  
Vaginal Microbiomes**  
***This could lead to precision treatments that protect women against STDs, HIV,  
and Preterm Birth***

Baltimore, Nov. 30, 2023— Researchers have long known that the composition of microbes in the vagina plays a large role in women’s genital health, including susceptibility to sexually transmitted diseases including HIV, and preterm birth. What has not been well understood is exactly how those microbes function together to create a healthy and protective vaginal microbiome.

Now for the first time, researchers from the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine (UMSOM) have applied metagenomic sequencing to understand the function of the bacterial strain communities in the vagina. While genomics looks at the genetic content of a single species, metagenomics looks at the DNA makeup of multiple species at the same time—and can show how the strains of the same species work together to contribute to health or disease.

Understanding how these microbiome communities function could lead to new targets for treatment of vaginal infections, as well as new diagnostic strategies for conditions like bacterial vaginosis. The research has been published in the Nov. 30 issue of *Microbiome*.

“Vaginal microbiomes cluster by similar bacterial species compositions, but each species consists of different strain combinations. These combinations likely play a significant role in the susceptibility to—and the course of—an infection,” said [Johanna Holm, PhD](#), a scientist at IGS, Assistant Professor of Microbiology and Immunology at UMSOM, and the paper’s lead author.

To capture the functional information, the researchers sequenced 1,890 vaginal metagenomes from more than one thousand women of reproductive age. They found 28 bacterial species common to the vagina. Within those species, they identified 135 distinct strain combinations—known scientifically as metagenomic subspecies.

It is the first time that scientists have identified different combinations of microbes within the vaginal microbiome. The researchers use these 135 combinations to develop a new functional

classification of vaginal microbiomes which they call, “Metagenomic Community State Types” or mgCSTs. In addition, they built a software classifier with open source coding for other scientists to use to create consistency in the way researchers study the vaginal microbiome.

"Our research highlights a previously unknown amount of functional diversity in the vaginal microbiome, which has, for a long time, been considered of low diversity and simple." said [Jacques Ravel, PhD](#), Acting Director of IGS, Professor of Microbiology and Immunology at UMSOM, and the corresponding author on the paper. "These new categories—based on their functional diversity—will help scientists to better understand how vaginal microbiomes interact within women to affect their reproductive health. This new knowledge can help us develop novel approaches to keeping the vaginal microbiome optimally protected."

However, even with a “good” microbiome—which previous research shows is dominated by the strain *Lactobacillus*—each strain can be functionally different and provide varying level of protection. This makes it critical for researchers to understand the community of strains, and what those strains are capable of doing in the vaginal microbiome.

In addition, the researchers identified functionally unique types of non-optimal vaginal microbiomes.

“We observed nine types of bacterial vaginosis-like communities, which research had previously characterized into only two groups. This presents an opportunity for one day improving treatment for bacterial vaginosis, through personalized treatment” said Dr. Holm.

“Our hope is that as more metagenomes are sequenced, other researchers use the mgCSTs to easily validate and reproduce their own studies,” added Dr. Holm. “Ultimately, our continuing work should reveal novel, therapeutic targets to provide women protection against infections without using antibiotics that often lead to yeast infections, as well as finding ways to treat other vaginal and reproductive health challenges.”

[WATCH a VIDEO THAT EXPLAINS THE RESEARCH](#)

**About the Institute for Genome Sciences:** The [Institute for Genome Sciences](#) (IGS) at the University of Maryland School of Medicine has revolutionized genomic discoveries in medicine, agriculture, environmental science, and biodefense since its founding in 2007. IGS investigators research areas of genomics and the microbiome to better understand health and disease, including treatments, cures, and prevention. IGS investigators also lead the development of the new field of microbial forensics. IGS is a leading center for major biological initiatives currently underway including the NIH-funded [Human Microbiome Project](#) (HMP) and the NIAID-sponsored [Genomic Sequencing Center for Infectious Diseases](#) (GSCID). Follow us on X @GenomeScience and @MDGenomics.

