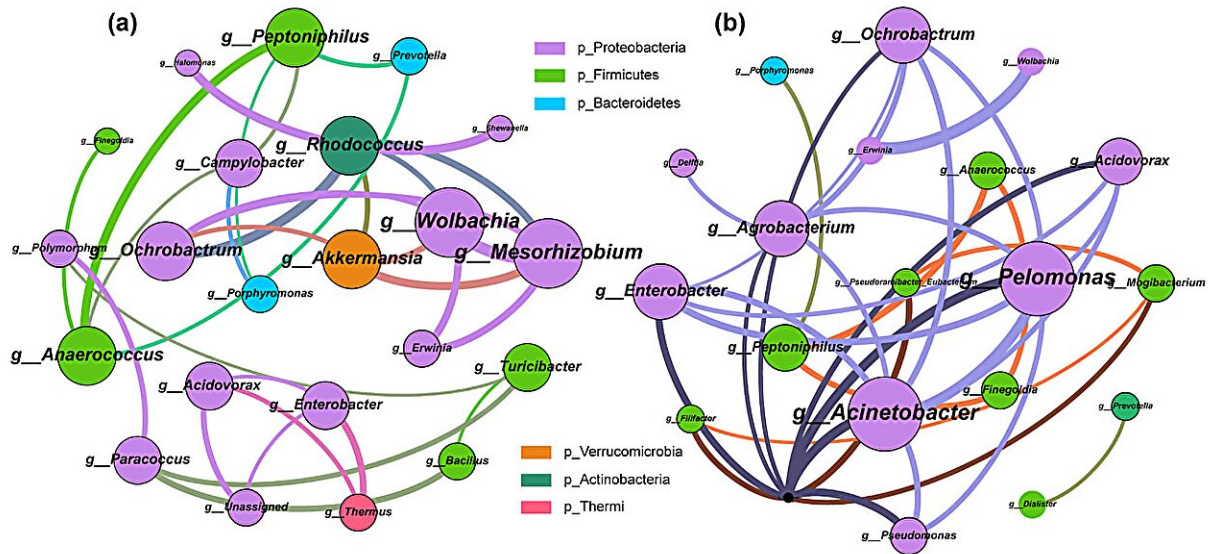# Specific microbial hallmarks in vagina could indicate gynecological cancers

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Analysis of vaginal microbial co-abundance network between Gynca and Control groups. The color of nodes indicates different phylum, node size represents node degree, connecting line indicates the interaction between genera, and the width of connecting line represents correlation. Credit: *Open Life Sciences* (2024). DOI: 10.1515/biol-2022-0850

A simple vaginal swab could reveal the presence of early-stage

gynecological cancers, according to a new, wide-ranging study published in *Open Life Sciences*. The study is the first to assess the diagnostic potential of vaginal microbes using a large sample of women with a range of gynecological cancers, making the results generalizable across a wider population.

Ovarian, endometrial, cervical and other gynecological cancers are often diagnosed at a late stage, making them difficult to treat and resulting in worse outcomes for patients. A convenient method to assess someone's risk of developing such cancers could allow clinicians to screen patients and identify more early-stage tumors.

Researchers are increasingly aware of the role microbes play in health and disease. A delicate microbial balance exists in the healthy vagina, with the bacterium Lactobacillus typically being present at high levels, releasing lactic acid which makes it hard for potentially harmful bacteria to take hold. Disruption to this balance can lead to inflammation, leaky tissue that allows microbes to penetrate deeper, and changes in tissue metabolism, all of which can contribute to cancer risk.

While previous research into the link between the vaginal microbiome and cancer has typically examined just one type of gynecological cancer, in relatively small groups of patients from one or two hospitals, this new study is the first to examine the phenomenon in a large group of patients of different ethnicities, in various countries, with a range of gynecological cancers.

Senior author, Professor Junnan Xu of the Cancer Hospital of Dalian University of Technology in China and colleagues obtained publicly available genetic information on vaginal microbes isolated from 529 women, including gynecological cancer patients. The researchers then

assessed the microbial differences between healthy women and those with gynecological cancer.

They observed a decrease in Firmicutes, Actinobacteria, and Lactobacillus bacteria and an increase in Bacteroidetes, Proteobacteria, Prevotella, Streptococcus, and Anaerococcus in the gynecological cancer group. An increase in bacterial diversity, a loss of Lactobacillus dominance, and an increased number of potentially pathogenic bacteria were also found in patients with cancer.

Using a statistical technique, the researchers then assessed if the microbial signature of gynecological cancer they had discovered would be useful as a diagnostic biomarker. They found that the microbial fingerprint had good diagnostic value, suggesting that it may have potential as part of a screening program to detect early-stage gynecological cancers or identify women at high risk of developing such cancers.

While the results are promising, further work will be required to fully unravel the role of the vaginal microbiome in cancer. "Additional larger studies are important for a more accurate understanding of vaginal microbiome changes in gynecological cancer," said Professor Xu. "Our work may contribute to the realization of noninvasive early screening of gynecological cancer."

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