Gastroenterologists explore relationship between bacteria in the gut and breast cancer

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The human body contains billions of microorganisms, and microbial cells found in the human gut are estimated to outnumber human cells by ten-to-one in healthy adults. However, little is known about the ways in which these minute life forms influence health and disease.

That is why gastroenterologists at Rush University Medical Center are working on a new research study funded by the U.S. Department of Defense to chart the presence of microorganisms found within the gut and to explore how microbial imbalances may impact diseases like breast cancer.

"Similar to what has been done with human DNA, we want to map out the composition of these microorganisms from their DNA and analyze how they correlate to diseases and changes within the immune system," said Dr. Ece Mutlu, gastroenterologist at Rush and principal investigator of the study. "If we are able to find the microbes responsible for particular diseases, it may increase the likelihood of developing new diagnostic tests and treatments for diseases like breast cancer."

Unlike the over 20,000 genes found in the human genome, the bacterial genomes, known as the microbiome, can rapidly evolve under the pressure of changing environmental factors. Therefore, changes in the gastrointestinal microbiota have the potential to explain rises in breast cancer incidence, which are difficult to attribute to alterations in the human genome alone.

About 20 to 25 percent of the risk of developing breast cancer is related to family history. Unfortunately, the known breast cancer susceptibility genes such as BRCA2 and BRCA 2 explain less than 5-10 percent of the total breast cancer cases attributable to familial factors.

Researchers are exploring the possibility that the gut microbiome passed on from mother to child may be another familial factor previously never accounted for in the genetic risk models.

"The currently recognized environmental risk factors are estimated to account for only 40 percent of the variance in breast cancer incidence, "said Mutlu. "There is a large body of evidence implicating that dietary factors such as alcohol, high fat foods are also possible breast cancer risk enhancers, and fruits and vegetables are protective."

Therefore, the gastrointestinal microbiota also has been an overlooked as a potential, major risk factor for breast cancer compared to better known genetic and environmental risk factors.

Researchers are also analyzing the effects of gut microbiome on carcinogens and sex hormone metabolism based on evidence that the gastrointestinal microbiota has an impact on estrogen balance and is important in estrogen metabolism. This might also enhance the knowledge of other sex hormone related diseases such as ovarian cancer, osteoporosis and endometriosis.

Supported by more than one million dollars in grants from the Department of Defense and NIH, Mutlu and her team are currently collaborating with Dr. Patrick Gillevet, at the MicroBiome Analysis Center, a new molecular ecology facility at George Mason University in Fairfax, Va., to chart the presence of microorganisms in patients suffering from breast cancer, Crohn's Disease, inflammatory bowel disease, cirrhosis of the liver and HIV.

Researchers will be using a technology for genomic sequencing called Multitag Pyrosequencing (MTPS) that allows them to examine, count and barcode hundreds of thousands of microorganisms per day within samples taken from various ecological systems including the human body. Because of this new technology for genomic sequencing, researchers will be able to identify 50,000 or 60,000 microbes per sample.

Rush is currently recruiting study participants who are female, 30 years of age or older, and newly diagnosed with breast cancer before any treatment has begun. Clinical data from the participant's medical records will be taken. Before a patient receives any cancer-related therapy, biopsies of the colon and stool specimens will be taken.

Source: Rush University Medical Center (news : web)