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New gene testing technology finds cancer risks 'hiding in plain sight'

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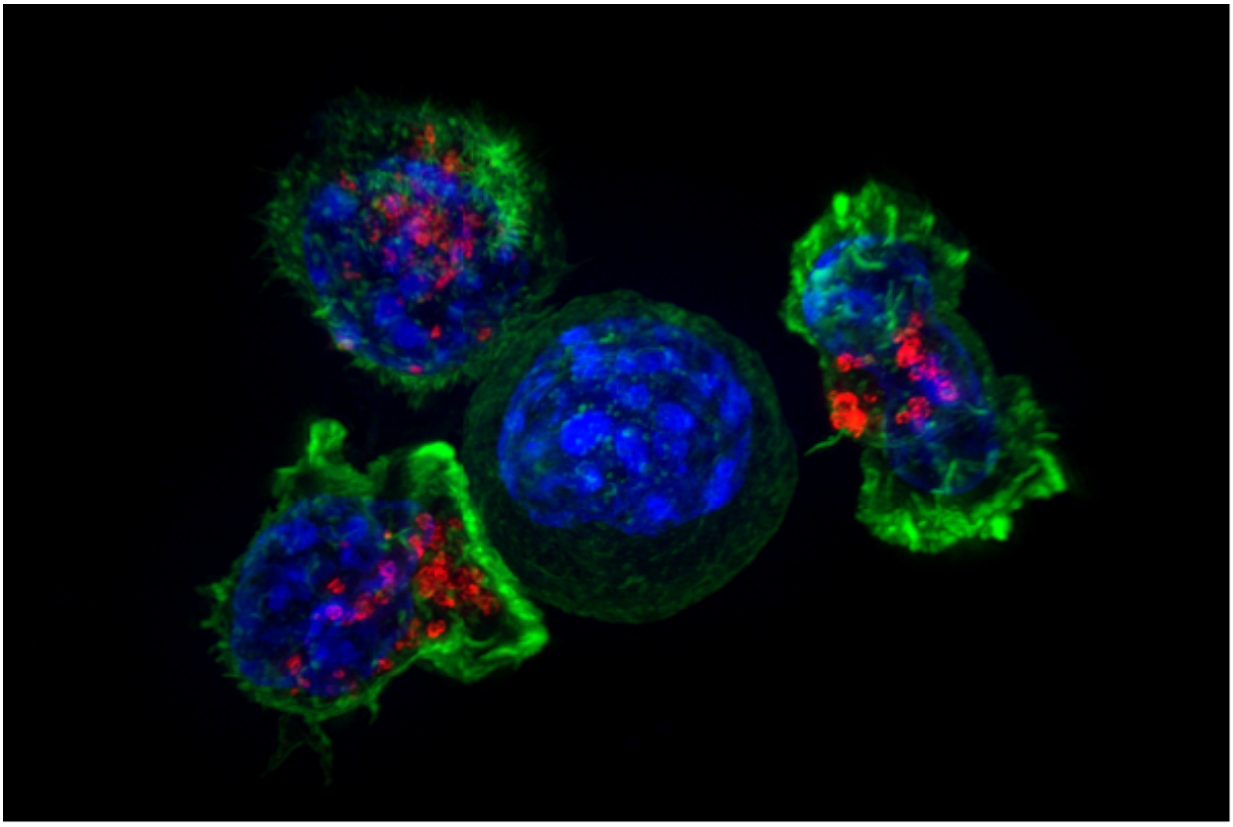

Killer T cells surround a cancer cell. Credit: NIH

A research team led by an award-winning genomicist at Western University has developed a new method for identifying mutations and prioritizing variants in breast and ovarian cancer genes, which will not

only reduce the number of possible variants for doctors to investigate, but also increase the number of patients that are properly diagnosed.

These potentially game-changing technologies, developed by Peter Rogan, PhD, students and his collaborators from Western's Schulich School of Medicine & Dentistry, reveal gene variants that were missed by conventional genetic testing.

Their method, described in *BMC Medical Genomics*, was first applied to 102 individuals at risk or with a diagnosis of inherited breast cancer. The team also studied 287 women with no known mutations for an article published in *Human Mutation*.

Rogan, Canada Research Chair in Genome Bioinformatics, says that 16 to 20 per cent of women in southwestern Ontario, who have their BRCA genes tested for breast and/or ovarian cancer risk, carry disease-causing gene variants that are well-understood by clinicians and genetic counselors. If a patient tests positive for an abnormal BRCA1 or BRCA2 gene and have never had breast cancer, there is a much higher-than-average risk of developing the deadly disease.

Basically, this means that doctors can make a decision on whether or not to proceed with specific treatments and can provide definitive genetic counseling for their children and other relatives.

The most widely known example of this type of patient is acclaimed actress, filmmaker and humanitarian Angelina Jolie. Testing indicated that Jolie had a gene variant associated with very aggressive form of this cancer, so she opted for a double mastectomy.

However, for the remaining 80-84 per cent of women who have been tested, the test, which is covered by health insurance in Ontario, does not give the patient and doctor a clear indication of how to proceed.

This is due to the fact that there is no current standard agreement of how to diagnose patients, who carry gene variants of uncertain significance. Rogan's *BMC Medical Genomics* study of 102 individuals identified 15,311 variants in seven complete genes. After completing the analysis, between 0 and 3 variants were prioritized in most patients.

"When a woman with a family history of breast cancer sees her physician, they want to know if they have a mutation in breast/ovarian cancer genes," says Rogan. "All of the patients that we studied had been sequenced for BRCA1 or BRCA2. The causative cancer gene variants are hiding in plain sight in these and other cancer genes, but the original testing laboratory didn't recognize them. Our approach can reveal gene variants that might explain their increased risk for cancer."

To increase the number of women who will benefit from genetic testing for breast cancer, Rogan says doctors and government policy makers should include additional genes in testing and consider new approaches that can interpret complete gene sequences.

Provided by University of Western Ontario

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