Familial breast cancer not only inherited genetically, finds new study

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Mutations in known breast cancer genes such as BRCA1 and BRCA2 are identified in only approximately 20 per cent of women who are offered genetic testing for familial breast cancer.

Researchers at the University of Melbourne, led by Professor Melissa Southey, looked at 210 people from 25 multiple-case breast cancer

families. They identified 24 previously unknown epigenetic changes that alter a woman's risk of breast cancer and can be passed down through generations without involving changes in the DNA sequence of genes.

"For the majority of women who undergo genetic testing, there is no explanation for their breast cancer predisposition," said Professor Southey, from the Department of Clinical Pathology at the University of Melbourne and Chair of Precision Medicine at Monash University.

"This ground-breaking work is not only helpful for women from families with many cases of breast cancer, it will improve breast cancer risk prediction for all women, and pave the way for the development of epigenetic therapeutics for breast cancer."

The study, published in *Nature Communications*, looks at epigenetic changes called DNA methylation, where methyl group chemicals modify DNA without changing its sequence. DNA methylation can mimic genetic variation, predisposing a family to breast cancer. The study is one of the first to systematically scan the genome for places where DNA methylation is heritable, and is the first to apply this to familial breast cancer.

University of Melbourne statistician Dr James Dowty said: "Our methods were very successful when applied to breast cancer, and the exciting thing is that they can be applied to many other hereditary diseases. This work was the result of a very fruitful collaboration between molecular biologists and statisticians, like a lot of work in modern medical research."

University of Melbourne and Monash University research fellow Dr Eric Joo said: "Some individuals know they come from a family with a lot of breast cancer but do not have a mutation in a known breast cancer gene. This study should help answer why some of those families have a lot of

cancer. It's very exciting to be unlocking part of a big puzzle."

Dr Joo hopes more work will be done to develop tests to screen for the methylation markers associated with breast cancer.

More information: Heritable DNA methylation marks associated with susceptibility to breast cancer, *Nature Communications* (2018). DOI: 10.1038/s41467-018-03058-6

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